

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 19:02:58 ; Search time 5525.28 Seconds
 (without alignments)
 2823.852 Million cell updates/sec

Title: US-10-063-670-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLTSIWTRLL.....NPEESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10063670/runat_06102005_112746_227/app_query.fasta_1.910
-DB=GenEmbl -QFMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063670_@CGN_1_1_4930_@runat_06102005_112746_227 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
 1: gb_ba.*
 2: gb_htg.*
 3: gb_in.*
 4: gb_om.*
 5: gb_ov.*
 6: gb_pat.*
 7: gb_ph.*
 8: gb_pl.*
 9: gb_pr.*
 10: gb_ro.*
 11: gb_sts.*
 12: gb_sy.*
 13: gb_un.*
 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1657	100.0	1285	9	AF127670 Homo sapi
2	1657	100.0	1755	6	AX136227 Sequence
3	1657	100.0	1755	6	BD123566 Secretary
4	1657	100.0	1755	9	AK075443 Homo sapi

5	1657	100.0	2029	6	BD222718	Human sig
6	1657	100.0	2029	6	AR204700	Sequence
7	1657	100.0	2312	6	CO720788	Sequence
8	1657	100.0	2372	6	BD172392	Secreted
9	1657	100.0	2372	6	BD172711	Secreted
10	1657	100.0	2372	6	BD173030	Secreted
11	1657	100.0	2372	6	BD173349	Secreted
12	1657	100.0	2372	6	BD175383	Secretary
13	1657	100.0	2372	6	AR410761	Sequence
14	1657	100.0	2372	6	AR439125	Sequence
15	1657	100.0	2372	6	AR473145	Sequence
16	1657	100.0	2372	6	AR527131	Sequence
17	1657	100.0	2372	6	AR566164	Sequence
18	1657	100.0	2372	6	AX092274	Sequence
19	1657	100.0	2372	6	AX454446	Sequence
20	1657	100.0	2372	6	AX490924	Sequence
21	1657	100.0	2372	6	AX697609	Sequence
22	1657	100.0	2372	6	BD075532	Secretary
23	1657	100.0	2372	9	AY358925	Homo sapi
24	1643	99.2	2282	9	BC026231	Homo sapi
25	1638	98.9	2313	9	AF118108	Homo sapi
26	1174	70.9	1613	4	AY372937	Bos tauru
27	1103	66.6	2027	10	BC038653	Mus muscu
28	1103	66.6	2027	10	BC038892	Mus muscu
29	1095	66.1	1516	10	MMU311501	Mus muscu
30	803	48.5	716	6	AX136529	Sequence
31	803	48.5	716	6	BD123769	Secretary
32	755	45.6	165698	9	AC009532	Homo sapi
33	726.5	43.8	603	4	AY304537	Sus scrof
34	592	35.7	451	6	BD076146	5' EST of
35	572	34.5	1419	5	BX932088	Gallus ga
36	389	23.5	235382	2	AC130104	Rattus no
37	389	23.5	239307	2	AC129402	Rattus no
38	306	18.5	469	6	CQ093590	Sequence
39	306	18.5	469	6	CQ132364	Sequence
40	306	18.5	469	6	CQ170929	Sequence
41	306	18.5	469	6	CQ215560	Sequence
42	306	18.5	469	6	CQ254154	Sequence
43	306	18.5	469	6	CQ291166	Sequence
44	285	17.2	363	6	AX939196	Sequence
45	285	17.2	363	6	BD077623	5'EST of
46	284.5	17.2	59529	2	AC110451	Continuation (4 of
47	281.5	17.0	457	6	CQ093209	Sequence
48	281.5	17.0	457	6	CQ290845	Sequence
49	277	16.7	373	6	AX968782	Sequence
50	277	16.7	373	6	BD073800	5'EST of
51	241	14.5	3322	5	BC074228	Xenopus 1
52	234.5	14.2	1537	6	AR365492	Sequence
53	234.5	14.2	1537	9	BABECMR	Baboon lymph
54	233.5	14.1	1089	10	CRUCD44	Hamster hya
55	231	13.9	2747	6	AX401912	Sequence
56	231	13.9	2747	10	RATCD44A	Rattus norv
57	229.5	13.9	1177	10	MUSCDA44A	Mouse CD44
58	229.5	13.9	1337	10	MUSPGP1	Mouse phago
59	229.5	13.9	3328	5	BC061327	Xenopus t
60	229	13.8	1932	10	BC061531	Rattus no
61	227	13.7	1383	10	RNU52179	Rattus norv
62	227	13.7	1384	10	RNU46957	Rattus norv
63	227	13.7	1384	10	AF065147	Rattus no
64	226	13.6	1183	10	MUSCDA44B	Mouse CD44
65	226	13.6	2799	10	BC005676	Mus muscu
66	224.5	13.5	1418	10	MMPGP1M1M	M.musculus
67	224	13.5	3164	10	RATNETAA	Rattus norv
68	224	13.5	3207	6	I19505	Sequence 1
69	223	13.5	3207	6	A30543	R.norvegicu
70	222	13.4	141	6	CQ106718	Sequence
71	222	13.4	141	6	CQ145372	Sequence
72	222	13.4	141	6	CQ180810	Sequence
73	222	13.4	141	6	CQ228565	Sequence
74	222	13.4	141	6	CQ266722	Sequence
75	222	13.4	141	6	CQ303674	Sequence
76	221.5	13.4	4038	10	RNU96138	Rattus norv
77	220.5	13.3	1520	10	MMPGP1M2M	M.musculus

78	220.5	13.3	1618	5	AY029553	AY029553 Anas plat
79	219	13.2	1072	5	AF332869	AF332869 Anas plat
80	218	13.2	1208	10	MUSPGP1A	J05163 Mouse phosp
81	216	13.0	1927	10	MAU10881	U10881 Mesocricetu
82	215	13.0	1342	9	HUMCDW44A	M24915 Human CDw44
83	215	13.0	1354	6	BD015203	BD015203 TliSa cel
84	213.5	12.9	1355	4	BTCD44MR	X62881 B.taurus mR
85	213.5	12.9	1355	4	S63418	S63418 CD44=cell-s
86	213.5	12.9	1766	10	MMPGP1M3M	X66083 M.musculus
87	213	12.9	1794	6	AX587906	AX587906 Sequence
88	213	12.9	1794	6	AX658338	AX658338 Sequence
89	213	12.9	1794	9	HUMCD44B	M59040 Human cell
90	212.5	12.8	2962	10	MAU10880	U10880 Mesocricetu
91	212	12.8	1083	6	AX824985	AX824985 Sequence
92	212	12.8	4606	9	HSM803952	AL832642 Homo sapi
93	212	12.8	5165	6	CQ413028	CQ413028 Sequence
94	210	12.7	1297	6	AR380331	AR380331 Sequence
95	210	12.7	1297	9	HSU40373	U40373 Human cell
96	210	12.7	1339	9	AY101193	AY101193 Homo sapi
97	210	12.7	1356	9	BC067348	BC067348 Homo sapi
98	210	12.7	1997	10	MMPGP1M4M	X66084 M.musculus
99	207.5	12.5	1107	4	AF045939	AF045939 Ceratotho
100	206.5	12.5	1094	5	AY032667	AY032667 Anas plat
101	206	12.4	3518	10	BC051388	BC051388 Mus muscu
102	205.5	12.4	1368	5	CR386646	CR386646 Gallus ga
103	205.5	12.4	3091	6	CQ875295	CQ875295 Sequence
104	205.5	12.4	3091	9	HSA251595	AJ251595 Homo sapi
105	204.5	12.3	2613	10	MMU251594	AJ251594 Mus muscu
106	204.5	12.3	5303	6	CQ766842	CQ766842 Sequence
107	203.5	12.3	2035	5	AF153205	AF153205 Gallus ga
108	203	12.3	1483	6	AX060538	AX060538 Sequence
109	202.5	12.2	1055	4	CPCD44AG	Z27115 C.familiari
110	202.5	12.2	1468	6	AX060536	AX060536 Sequence
111	199.5	12.0	1482	6	CQ766874	CQ766874 Sequence
112	199.5	12.0	1737	9	HSCD441	X56794 H.sapiens C
113	199.5	12.0	1824	6	AX769855	AX769855 Sequence
114	199.5	12.0	2100	6	AX056982	AX056982 Sequence
115	199.5	12.0	2100	6	AX824987	AX824987 Sequence
116	199.5	12.0	2292	9	AY101192	AY101192 Homo sapi
117	199.5	12.0	2308	6	BD015204	BD015204 TliSa cel
118	199.5	12.0	2316	9	HSCD44E	X55150 Human mRNa
119	199.5	12.0	4675	6	AR454624	AR454624 Sequence
120	198.5	12.0	1586	9	S66400	S66400 CD44=CD44SP
121	197	11.9	2097	6	AX824989	AX824989 Sequence
122	197	11.9	2265	9	HSEPIC	X66733 H.sapiens m
123	197	11.9	2387	9	BC004372	BC004372 Homo sapi
124	196	11.8	1823	9	HUMKCA	M25078 Human Herm
125	186	11.2	1338	4	ECCD44	X66862 Equus cabal
126	178.5	10.8	1697	6	CQ723838	CQ723838 Sequence
127	170	10.3	106	6	CQ106350	CQ106350 Sequence
128	170	10.3	106	6	CQ303364	CQ303364 Sequence
C 129	158	9.5	157583	5	BX571951	BX571951 Zebrafish
	157	9.5	133410	5	BX470202	BX470202 Zebrafish
C 130	157	9.4	1608	9	AK129808	AK129808 Homo sapi
	155	9.3	270	6	AX033418	AX033418 Sequence
132	153.5	9.2	7447	4	BTU76615	U76615 Bos taurus
133	152.5	9.1	2863	6	AX747085	AX747085 Sequence
134	151	9.1	2863	9	AK091600	AK091600 Homo sapi
135	151	9.1	2863	9	GGU78555	U78555 Gallus gall
136	149.5	9.0	6597	5	CHKSFCP	L21913 Chicken cho
137	148.5	9.0	6452	5	CHKAGGRECA	M88101 White legho
138	147	8.9	6477	5	HUMZD93D04	AF086484 Homo sapi
139	145.5	8.8	769	9	CQ730585	CQ730585 Sequence
140	145.5	8.8	781	6	CQ730585	AJ419936 Homo sapi
141	145.5	8.8	834	9	HSA419936	BC030205 Homo sapi
142	145.5	8.8	1430	9	BC030205	AF314813 Sus scrof
143	145.5	8.8	1481	4	AF314813	D13542 Chicken mRN
144	145.5	8.8	12307	5	CHKPRGL	CQ713460 Sequence
145	145	8.8	466	6	CQ713460	AJ421518 Homo sapi
146	145	8.8	834	9	HSA421518	AR063905 Sequence
147	145	8.8	1414	6	AR063905	AR144434 Sequence
148	145	8.8	1414	6	AR144434	AR281307 Sequence
149	145	8.8	1414	6	AR281307	U83903 Mus musculu
150	144	8.7	1605	10	MMU83903	

151	144	8.7	1616	10	BC021155	BC021155 Mus muscu
152	143	8.6	1683	10	RNU46958	U46958 Rattus norv
153	142.5	8.6	8444	6	AX686192	AX686192 Sequence
154	141.5	8.5	3625	6	AX149461	AX149461 Sequence
155	141.5	8.5	8495	6	AX686194	AX686194 Sequence
C 156	141	8.5	208621	2	AC150078	AC150078 Gallus ga
	157	8.5	3911	10	BC031166	BC031166 Mus muscu
158	140.5	8.5	7931	10	AF290914	AF290914 Mus muscu
159	140	8.4	8069	9	AK160380	AK160380 Homo sapi
160	139.5	8.4	7104	4	CFU65989	U65989 Canis famil
161	138.5	8.4	1411	6	AX202114	AX202114 Sequence
162	138	8.3	7382	10	MUSAGGRECA	L07049 Mus musculu
163	137	8.3	1406	4	RABPS4EA	M86381 Oryctolagus
164	137	8.3	3260	6	AX686401	AX686401 Sequence
165	137	8.3	3260	9	AF160476	AF160476 Homo sapi
166	137	8.3	3591	6	CQ719622	CQ719622 Sequence
167	137	8.3	4492	9	AY227444	AY227444 Homo sapi
168	137	8.3	4575	9	AK024503	AK024503 Homo sapi
169	137	8.3	5604	9	AK074051	AK074051 Homo sapi
170	137	8.3	6939	10	RATPGCA	J03485 Rat alterna
171	137	8.3	8214	9	AB052958	AB052958 Homo sapi
172	137	8.3	8251	9	AY311388	AY311388 Homo sapi
173	137	8.3	8266	9	HSA295695	AJ295695 Homo sapi
174	136	8.2	4706	10	AY007370	AY007370 Rattus no
175	136	8.2	8157	10	AF364951	AF364951 Mus muscu
176	135.5	8.2	3076	10	BC052032	BC052032 Mus muscu
177	135.5	8.2	3153	10	MMBREVGEN	X87096 M.musculus
178	133.5	8.1	1734	6	AR220822	AR220822 Sequence
179	132.5	8.0	2160	6	AX748299	AX748299 Sequence
180	132.5	8.0	2160	9	AK093774	AK093774 Homo sapi
181	132.5	8.0	4178	9	BC036445	BC036445 Homo sapi
182	131.5	7.9	5144	6	CQ723852	CQ723852 Sequence
183	131	7.9	3245	9	BC010571	BC010571 Homo sapi
184	131	7.9	3275	9	BC009117	BC009117 Homo sapi
185	131	7.9	3292	9	BC027971	BC027971 Homo sapi
186	131	7.9	3438	6	AX704756	AX704756 Sequence
187	131	7.9	3476	6	AX056675	AX056675 Sequence
188	131	7.9	3476	6	AX574524	AX574524 Sequence
189	131	7.9	3476	9	AY358372	AY358372 Homo sapi
190	130.5	7.9	2534	10	RNRNABGPI	X86406 R.norvegicu
191	130.5	7.9	2868	10	RNALPBRE	X79881 R.norvegicu
192	130.5	7.9	3077	10	RNU37142	U37142 Rattus norv
193	130.5	7.9	4040	5	AF325324	AF325324 Xenopus 1
194	130.5	7.9	7137	9	HUMAGPRO	M55172 Human large
195	130.5	7.9	7909	9	D87433	D87433 Homo sapien
196	130.5	7.9	7916	9	AB052956	AB052956 Homo sapi
197	130	7.8	7870	9	HSA275213	AJ275213 Homo sapi
198	128.5	7.8	1540	6	CQ716123	CQ716123 Sequence
199	128.5	7.8	3259	4	BTBREV	X75887 B.taurus Br
200	128.5	7.8	7136	6	CQ716466	CQ716466 Sequence
201	127.5	7.7	1893	9	AY262759	AY262759 Homo sapi
202	127.5	7.7	1985	6	BD172402	BD172402 Secreted
203	127.5	7.7	1985	6	BD172721	BD172721 Secreted
204	127.5	7.7	1985	6	BD173040	BD173040 Secreted
205	127.5	7.7	1985	6	BD173359	BD173359 Secreted
206	127.5	7.7	1985	6	BD175393	BD175393 Secretory
207	127.5	7.7	1985	6	CQ881212	CQ881212 Sequence
208	127.5	7.7	1985	6	AR410771	AR410771 Sequence
209	127.5	7.7	1985	6	AR439135	AR439135 Sequence
210	127.5	7.7	1985	6	AR473155	AR473155 Sequence
211	127.5	7.7	1985	6	AR527141	AR527141 Sequence
212	127.5	7.7	1985	6	AR566174	AR566174 Sequence
213	127.5	7.7	1985	6	AX375960	AX375960 Sequence
214	127.5	7.7	1985	6	AX697621	AX697621 Sequence
215	127.5	7.7	1985	6	BD075542	BD075542 Secretory
216	127.5	7.7	1985	9	AY358500	AY358500 Homo sapi
217	127.5	7.7	2004	9	BC062320	BC062320 Homo sapi
218	127.5	7.7	2558	9	AF229053	AF229053 Homo sapi
219	127.5	7.7	2878	9	AF228710	AF228710 Homo sapi
220	127.5	7.7	3306	9	BC022938	BC022938 Homo sapi
221	127.5	7.7	79444	2	AC150153	AC150153 Gallus ga
222	127.5	7.7	143178	2	AC150117	AC150117 Gallus ga
C 223	127.5	7.7	166863	2	AC150140	AC150140 Gallus ga

C 224	127.5	7.7	168751	2	AC068969	AC068969 Homo sapi	297	113.5	6.8	4634	5	AF116856	AF116856 Gallus ga
C 225	127.5	7.7	170883	9	AC067805	AC067805 Homo sapi	C 298	113.5	6.8	64675	2	BX322628_3	Continuation (4 of
C 226	127.5	7.7	197370	9	AC103982	AC103982 Homo sapi	C 299	113.5	6.8	110000	2	BX322628_2	Continuation (3 of
227	127	7.7	2465	6	AX400824	AX400824 Sequence	300	113.5	6.8	170883	9	AC067805	AC067805 Homo sapi
228	127	7.7	2465	10	AF072892	AF072892 Rattus no	301	113.5	6.8	218103	5	BX465199	BX465199 Zebrafish
229	126.5	7.6	199942	2	AC150038	AC150038 Gallus ga	302	113.5	6.8	271812	2	BX530095	BX530095 Danio rer
230	126	7.6	10427	10	MUSPGM	D28599 Mouse mRNA	303	113	6.8	1925	9	BC050524	BC050524 Homo sapi
231	125.5	7.6	2780	10	AF098460	AF098460 Mus muscu	304	113	6.8	2087	6	AX338947	AX338947 Sequence
232	125.5	7.6	4738	10	BC066853	BC066853 Mus muscu	305	113	6.8	2087	9	HUMPGH3A	D32039 Human pgH3
233	125	7.5	201	11	BV206501	BV206501 sqnm22108	306	113	6.8	2809	5	XELLDLR2A	M62978 X.laervis lo
234	125	7.5	1414	6	AX3336169	AX3336169 Sequence	307	113	6.8	8224	6	CQ728127	CQ728127 Sequence
235	125	7.5	1414	9	HUMTSG6A	M31165 Human tumor	308	113	6.8	8224	6	AR362654	AR362654 Sequence
236	124.5	7.5	2430	10	AF139572	AF139572 Mus muscu	309	113	6.8	8224	6	AX658277	AX658277 Sequence
237	124	7.5	1682	5	CR762351	CR762351 Xenopus t	310	113	6.8	8224	9	HSVERS	X15998 H.sapiens m
238	124	7.5	249541	2	AC095672	AC095672 Rattus no	311	113	6.8	138091	2	AC113583	AC113583 Tetraodon
239	124	7.5	249774	2	AC126196	AC126196 Rattus no	C 312	113	6.8	199942	2	AC150038	AC150038 Gallus ga
240	123	7.4	2116	4	AF060459	AF060459 Bos tauru	313	112	6.8	340	6	CQ704239	CQ704239 Sequence
241	123	7.4	5077	4	AF060458	AF060458 Bos tauru	314	112	6.8	1173	14	AJ626532	AJ626532 Human her
242	123	7.4	7330	4	AF060457	AF060457 Bos tauru	315	112	6.8	1173	14	AJ626542	AJ626542 Human her
243	123	7.4	10291	4	AF060456	AF060456 Bos tauru	316	112	6.8	1173	14	AJ626547	AJ626547 Human her
244	122	7.4	1183	4	RABAGGRECA	L38480 Oryctolagus	317	112	6.8	1190	6	I67656	I67656 Sequence 1
C 245	122	7.4	150209	2	CR759744	CR759744 Danio rer	318	112	6.8	2026	5	BC068325	BC068325 Danio rer
246	121.5	7.3	959	6	CQ723845	CQ723845 Sequence	319	112	6.8	3070	8	AK110196	AK110196 Oryza sat
247	121	7.3	1587	6	AR432563	AR432563 Sequence	320	112	6.8	12979	14	HEHSV1SU	X02138 Herpes simp
248	121	7.3	1587	6	BD078622	BD078622 Human pro	C 321	112	6.8	26245	14	HSLIUS	L00036 Human herpe
249	121	7.3	1704	9	AY007241	AY007241 Homo sapi	C 322	112	6.8	79444	2	AC150153	AC150153 Gallus ga
C 250	120.5	7.3	155548	2	CR848047	CR848047 Danio rer	C 323	112	6.8	143178	2	AC150117	AC150117 Gallus ga
251	120	7.2	1626	9	AB119257	AB119257 Danio rer	324	112	6.8	152261	14	HEICG	X14112 Human herpe
252	120	7.2	1630	9	AC090712	AC090712 Homo sapi	325	112	6.8	166863	2	AC150140	AC150140 Gallus ga
253	120	7.2	29864	9	BC029864	BC029864 Homo sapi	326	112	6.8	176022	2	BX294110	BX294110 Danio rer
254	120	7.2	2954	5	BC046259	BC046259 Xenopus l	327	112	6.8	208621	2	AC150078	AC150078 Gallus ga
255	120	7.2	4069	5	BC078043	BC078043 Xenopus l	C 328	112	6.8	232749	2	CR354535	CR354535 Danio rer
C 256	120	7.2	300750	1	AP005217	AP005217 Corynebac	C 329	111.5	6.7	15515	1	AE000044	AE000044 Mycoplasm
257	119.5	7.2	1236	14	AJ626545	AJ626545 Human her	330	111	6.7	1478	4	ECCRTL1G	BD195591 70 human
C 258	119.5	7.2	221762	2	BX908731	BX908731 Danio rer	331	111	6.7	1720	6	BD195591	BD195591 70 human
259	119	7.2	480	10	MMLINK4	AF137277 Mus muscu	332	111	6.7	1720	6	CQ775636	CQ775636 Sequence
260	119	7.2	1736	10	AB049055	AB049055 Mus muscu	333	111	6.7	1720	6	AR352646	AR352646 Sequence
261	119	7.2	197370	9	AC103982	AC103982 Homo sapi	C 334	111	6.7	184365	2	AC079639	AC079639 Mus muscu
262	118.5	7.2	1794	9	AB049054	AB049054 Homo sapi	C 335	110.5	6.7	193188	10	AL844155	AL844155 Mouse DNA
263	118.5	7.2	5923	9	HSU26555	U26555 Human vers1	C 336	110.5	6.7	229628	2	BX908768	BX908768 Leptospir
264	118.5	7.2	11185	6	CQ776629	CQ776629 Sequence	C 337	110.5	6.7	300299	1	AE017288	BD231671 31 human
265	118.5	7.2	11185	6	AX330530	AX330530 Sequence	338	110	6.6	1308	6	BD231671	BX322628 Danio rer
266	118.5	7.2	11185	6	AX410665	AX410665 Sequence	339	110	6.6	110000	2	BX322628_0	Continuation (2 of
267	118.5	7.2	11185	9	HSU16306	U16306 Human chond	C 340	110	6.6	110000	2	BX322628_1	Continuation (2 of
268	118.5	7.2	12319	6	AX281831	AX281831 Sequence	341	110	6.6	140093	8	AP005091	AP005091 Oryza sat
269	118.5	7.2	164846	2	AC107727	AC107727 Mus muscu	342	110	6.6	147748	8	AP005704	AP005704 Oryza sat
270	118	7.1	2318	10	MUSPGM3B	D32040 Mouse pgM3	C 343	110	6.6	183682	9	AL133330	AL133330 Human DNA
271	118	7.1	7375	6	CQ777492	CQ777492 Sequence	C 344	110	6.6	271812	2	BX530095	BX530095 Danio rer
272	118	7.1	7375	10	MUSPGMV	D16263 Mus musculu	C 345	110	6.6	292007	2	AC128762	AC128762 Rattus no
273	117.5	7.1	1194	14	AJ626546	AJ626546 Human her	346	109.5	6.6	1335	4	SSLINK	Y00165 Sus scrofa
274	117.5	7.1	61052	2	AC123513	AC123513 Dictyoste	347	109.5	6.6	103201	2	AC149525	AC149525 Xenopus t
C 275	117.5	7.1	136240	3	AC117070	AC117070 Dictyoste	348	109	6.6	2447	10	AF060879	AF060879 Rattus no
C 276	117.5	7.1	107418	2	AC109112	AC109112 Rattus no	349	109	6.6	6310	9	AF026547	AF026547 Homo sapi
277	117.5	7.1	246369	2	AC125707	AC125707 Rattus no	350	109	6.6	6312	6	CQ727544	CQ727544 Sequence
278	117	7.1	209852	2	AC151363	AC151363 Gasterost	351	109	6.6	110000	2	AC096220_0	AC096220 Rattus no
C 279	117	7.1	214941	2	AC150409	AC150409 Branchios	352	109	6.6	232127	2	AC113724	AC113724 Rattus no
C 280	116.5	7.0	226416	2	AC103519	AC103519 Rattus no	C 353	109	6.6	235684	2	AC129422	AC129422 Rattus no
C 281	116.5	7.0	230817	2	AC106909	AC106909 Rattus no	354	109	6.6	272258	2	AC123370	AC123370 Rattus no
282	116	7.0	1785	9	BC052287	BC052287 Homo sapi	355	108.5	6.5	1194	14	AJ626543	AJ626543 Human her
283	116	7.0	1910	5	CHKLNKPA	M13212 Chicken car	C 356	108.5	6.5	1378	1	AY127887	AY127887 Anaplasma
284	116	7.0	136886	2	AC149262	AC149262 Spheroeid	C 357	108.5	6.5	1399	1	AY127894	AY127894 Anaplasma
285	115	6.9	1249	10	BC022136	BC022136 Mus muscu	C 358	108.5	6.5	4128	1	AF527423	AF527423 Anaplasma
286	114.5	6.9	5191	6	I56080	I56080 Sequence 1	C 359	108.5	6.5	4185	1	AMU60779	U60779 Anaplasma m
287	114.5	6.9	5191	10	RATNCAN	M97161 Rattus norv	360	108.5	6.5	37711	3	CEZK896	Z82288 Caenorhabdi
288	114	6.9	1406	10	AB049056	AB049056 Rattus no	C 361	108.5	6.5	110000	8	CR382129_31	Continuation (32 o
289	114	6.9	8924	6	CQ580640	CQ580640 Sequence	362	108.5	6.5	189608	5	AL929208	AL929208 Zebrafish
C 290	114	6.9	55863	2	AC018100	AC018100 Drosophil	363	108	6.5	317	10	RATLNKPA	M22339 Rat link pr
C 291	114	6.9	110000	3	AC116305_1	Continuation (2 of	364	108	6.5	685	4	AY226857S06	AY226857 Bos tauru
292	114	6.9	157225	3	AC010042	AC010042 Drosophil	365	108	6.5	1319	10	AY269788	AY269788 Mus muscu
C 293	114	6.9	178338	3	AC023675	AC023675 Drosophil	C 366	108	6.5	1320	4	AF529268	AF529268 Ovis arie
C 294	114	6.9	192662	10	AC134397	AC134397 Mus muscu	367	108	6.5	1433	10	AY262757	AY262757 Mus muscu
295	114	6.9	272888	2	AC139198	AC139198 Mus muscu	368	108	6.5	1492	9	HSCRTL115	X78076 H.sapiens C
C 296	114	6.9	284442	3	AE003558	AE003558 Drosophil	369	108	6.5	1492	9	HSLINKC	X17405 Human mRNA

297	113.5	6.8	4634	5	AF116856	AF116856 Gallus ga
C 298	113.5	6.8	64675	2	BX322628_3	Continuation (4 of
C 299	113.5	6.8	110000	2	BX322628_2	Continuation (3 of
300	113.5	6.8	170883	9	AC067805	AC067805 Homo sapi
301	113.5	6.8	218103	5	BX465199	BX465199 Zebrafish
302	113.5	6.8	271812	2	BX530095	BX530095 Danio rer
303	113	6.8	1925	9	BC050524	BC050524 Homo sapi
304	113	6.8	2087	6	AX338947	AX338947 Sequence
305	113	6.8	2087	9	HUMPGH3A	D32039 Human pgH3
306	113	6.8	2809	5	XELDLR2A	M62978 X.laervis lo
307	113	6.8	8224	6	CQ728127	CQ728127 Sequence
308	113	6.8	8224	6	AR362654	AR362654 Sequence
309	113	6.8	8224	6	AX658277	AX658277 Sequence
310	113	6.8	8224	9	HSVERS	X15998 H.sapiens m
311	113	6.8	138091	2	AC113583	AC113583 Tetraodon
C 312	113	6.8	199942	2	AC150038	AC150038 Gallus ga
313	112	6.8	340	6	CQ704239	CQ704239 Sequence
314	112	6.8	1173	14	AJ626532	AJ626532 Human her
315	112	6.8	1173	14	AJ626542	AJ626542 Human her
316	112	6.8	1173	14	AJ626547	AJ626547 Human her
317	112	6.8	1190	6	I67656	I67656 Sequence 1
318	112	6.8	2026	5	BC068325	BC068325 Danio rer
C 319	112	6.8	3070	8	AK110196	AK110196 Oryza sat
320	112	6.8	12979	14	HEHSV1SU	X02138 Herpes simp
C 321	112	6.8	26245	14	HS1US	L00036 Human herpe
C 322	112	6.8	79444	2	AC150153	AC150153 Gallus ga
C 323	112	6.8	143178	2	AC150117	AC150117 Gallus ga
324	112	6.8	152261	14	HE1CG	X14112 Human herpe
325	112	6.8	166863	2	AC150140	AC150140 Gallus ga
326	112	6.8	176022	2	BX294110	BX294110 Danio rer
327	112	6.8	208621	2	AC150078	AC150078 Gallus ga
C 328	112	6.8	232749	2	CR354535	CR354535 Danio rer
C 329	111.5	6.7	15515	1	AE000044	AE000044 Mycoplasm
330	111	6.7	1478	4	ECRTL1G	X78077 Equus cabal
331	111	6.7	1720	6	BD195591	BD195591 70 human
332	111	6.7	1720	6	CQ775636	CQ775636 Sequence
333	111	6.7	1720	6	AR352646	AR352646 Sequence
C 334	111	6.7	184365	2	AC079639	AC079639 Mus muscu
C 335	110.5	6.7	193188	10	AL844155	AL844155 Mouse DNA
C 336	110.5	6.7	229628	2	BX908768	BX908768 Mus muscu
C 337	110.5	6.7	300299	1	AE017288	AE017288 Leptospir
338	110	6.6	1308	6	BD231671	BD231671 31 human
339	110	6.6	110000	2	BX322628_0	BX322628 Danio rer
C 340	110	6.6	110000	2	BX322628_1	Continuation (2 of
341	110	6.6	140093	8	AP005091	AP005091 Oryza sat
342	110	6.6	147748	8	AP005704	AP005704 Oryza sat
C 343	110	6.6	183682	9	AL133330	AL133330 Human DNA
C 344	110	6.6	271812	2	BX530095	BX530095 Danio rer
C 345	110	6.6	292007	2	AC128762	AC128762 Rattus no
346	109.5	6.6	1335	4	SSLINK	Y00165 Sus scrofa
347	109.5	6.6	103201	2	AC149525	AC149525 Xenopus t
348	109	6.6	2447	10	AF060879	AF060879 Rattus no
349	109	6.6	6310	9	AF026547	AF026547 Homo sapi
350	109	6.6	6312	6	CQ727544	CQ727544 Sequence
351	109	6.6	110000	2	AC096220_0	AC096220 Rattus no
C 352	109	6.6	232127	2	AC113724_	AC113724 Rattus no
353	109	6.6	235684	2	AC129422	AC129422 Rattus no
354	109	6.6	272258	2	AC123370	AC123370 Rattus no
355	108.5	6.5	1194	14	AJ626543	AJ626543 Human her
C 356	108.5	6.5	1378	1	AY127887	AY127887 Anaplasma
C 357	108.5	6.5	1399	1	AY127894	AY127894 Anaplasma
C 358	108.5	6.5	4128	1	AF527423	AF527423 Anaplasma
C 359	108.5	6.5	4185	1	AMU60779	U60779 Anaplasma m
360	108.5	6.5	37711	3	CEZK896	Z82288 Caenorhabdi
C 361	108.5	6.5	110000	8	CR382129_31	Continuation (32 o
362	108.5	6.5	189608	5	AL929208	AL929208 Zebrafish
363	108	6.5	317	10	RATLNKP4	M22339 Rat link pr
364	108	6.5	685	4	AY226857S06	AY226862 Bos tauru
365	108	6.5	1319	10	AY269788	AY269788 Mus muscu
C 366	108	6.5	1320	4	AF529268	AF529268 Ovis arie
367	108	6.5	1433	10	AY262757	AY262757 Mus muscu
C 368	108	6.5	1492	9	HSCTRL115	X78076 H.sapiens C
369	108	6.5	1492	9	HSLINKC	X17405 Human mRNA

370	108	6.5	1493	6	CQ728128	CQ728128 Sequence	443	104	6.3	6926	3	AF239611	AF239611 Drosophil
371	108	6.5	1721	9	BC057808	BC057808 Homo sapi	444	104	6.3	53580	5	AC096866	AC096866 Takifugu
372	108	6.5	1759	9	HSU43328	U43328 Human link	c	445	6.3	161126	8	NC80A10	BX294012 Neurospor
c 373	108	6.5	1790	6	AX344529	AX344529 Sequence		446	6.3	198756	2	AC135657	AC135657 Rattus no
c 374	108	6.5	1790	6	AX347277	AX347277 Sequence	447	104	6.3	346301	1	BX640432	BX640432 Bordetell
375	108	6.5	68574	2	AC113212	AC113212 Homo sapi	448	103.5	6.2	1042	10	MMU37531	U37531 Mus musculu
c 376	108	6.5	164286	9	AC020899	AC020899 Homo sapi	449	103.5	6.2	1099	3	AF436624	AF436624 Macronema
377	108	6.5	167872	2	AC007554	AC007554 Homo sapi	c	450	6.2	1310	3	AK173560	AK173560 Ciona int
378	108	6.5	226416	2	AC103519	AC103519 Rattus no	c	451	6.2	8433	6	CQ610163	CQ610163 Sequence
379	108	6.5	247266	2	AC110520	AC110520 Mus muscu	452	103.5	6.2	30630	3	AC116032	AC116032 Dictyoste
380	107.5	6.5	6279	6	CQ580641	CQ580641 Sequence	453	103.5	6.2	54309	2	AC017353	AC017353 Drosophil
c 381	107.5	6.5	12371	1	AE011224	AE011224 Leptospir	454	103.5	6.2	157482	3	AC092227	AC092227 Drosophil
382	107.5	6.5	77928	2	AC149263	AC149263 Sphoeroid	455	103.5	6.2	175058	2	CR753843	CR753843 Danio rer
383	107	6.5	427	5	CHKLNKPA3	M35037 Chicken car	c	456	6.2	177426	2	CR339044	CR339044 Danio rer
384	107	6.5	1400	6	AR036272	AR036272 Sequence	457	103.5	6.2	186803	3	AC092225	AC092225 Drosophil
385	107	6.5	1400	6	AR087156	AR087156 Sequence	c	458	6.2	225861	2	CR628381	CR628381 Danio rer
386	107	6.5	1520	6	I44674	I44674 Sequence 1	c	459	6.2	276521	3	AE003642	AE003642 Drosophil
387	107	6.5	1520	10	RNBEHAB	Z28366 R.norvegicu	c	460	6.2	305502	3	DROSADH03	AE003409 Drosophil
388	107	6.5	1851	6	AX302626	AX302626 Sequence	461	103.5	6.2	348551	8	BX649606	BX649606 Aspergill
389	107	6.5	2011	6	AX149447	AX149447 Sequence	462	103	6.2	402	6	AX778505	AX778505 Sequence
390	107	6.5	2589	6	I32212	I32212 Sequence 3	463	103	6.2	1296	6	AR549679	AR549679 Sequence
391	107	6.5	2685	6	A39780	A39780 Sequence 14	464	103	6.2	1519	4	FDBEHAB	Z28367 F.domesticu
392	107	6.5	2685	6	A74265	A74265 Sequence 21	465	103	6.2	1519	6	I44675	I44675 Sequence 2
393	107	6.5	4544	8	AK119845	AK119845 Oryza sat	c	466	6.2	1962	6	BD195649	BD195649 70 human
394	107	6.5	4614	6	BD271910	BD271910 Process f	c	467	6.2	1962	6	CQ775694	CQ775694 Sequence
395	107	6.5	4614	6	I32211	I32211 Sequence 1	c	468	6.2	1962	6	AR352704	AR352704 Sequence
396	107	6.5	5259	10	MNNEUROCM	X84727 M.musculus	469	103	6.2	2019	10	BC063758	BC063758 Mus muscu
397	107	6.5	5388	6	CQ608451	CQ608451 Sequence	470	103	6.2	2168	3	BT001711	BT001711 Drosophil
398	107	6.5	5743	8	SCFL01	X78160 S.cerevisia	c	471	6.2	10126	1	AE012547	AE012547 Xanthomon
399	107	6.5	7147	10	BC065118	BC065118 Mus muscu	472	103	6.2	224000	2	AC128599	AC128599 Rattus no
c 400	107	6.5	7782	6	CQ608450	CQ608450 Sequence	473	103	6.2	232110	2	AC096893	AC096893 Rattus no
c 401	107	6.5	8340	11	BV178350	BV178350 sqnm10003	c	474	6.2	267287	2	AC096702	AC096702 Rattus no
c 402	107	6.5	8426	2	AC013966	AC013966 Drosophil	475	102.5	6.2	1341	6	AX657611	AX657611 Sequence
c 403	107	6.5	24492	3	DMC56G7	AL031028 Drosophil	476	102.5	6.2	1372	6	CQ596994	CQ596994 Sequence
404	107	6.5	54812	8	YSCCHR1RAA	L28920 Saccharomyc	477	102.5	6.2	1491	14	AF343059	AF343059 Eyach vir
405	107	6.5	74610	8	AP006175	AP006175 Oryza sat	478	102.5	6.2	2178	14	AF282472	AF282472 Eyach vir
c 406	107	6.5	112830	2	AC151678	AC151678 Gallus ga	479	102.5	6.2	3421	3	AY060306	AY060306 Drosophil
407	107	6.5	164512	9	AL365181	AL365181 Human DNA	c	480	6.2	4492	6	CQ596993	CQ596993 Sequence
c 408	107	6.5	177096	3	AC107326	AC107326 Drosophil	481	102.5	6.2	7868	14	HPU37537	U37537 Human papil
c 409	107	6.5	202968	2	AC137422	AC137422 Rattus no	c	482	6.2	110000	1	AE016822_19	Continuation (20 o
c 410	107	6.5	304204	3	AE003421	AE003421 Drosophil	c	483	6.2	174801	2	AC014376	AC014376 Drosophil
411	106.5	6.4	1482	6	AR269667	AR269667 Sequence	c	484	6.2	179838	3	AC091220	AC091220 Drosophil
c 412	106.5	6.4	1571	8	SCYOR383C	Z75291 S.cerevisia	485	102.5	6.2	181063	3	AC010107	AC010107 Drosophil
413	106.5	6.4	2455	3	TNAF000605	AF000605 Trichoplu	c	486	6.2	285860	3	AE003551	AE003551 Drosophil
414	106.5	6.4	2455	6	AR129835	AR129835 Sequence	487	102	6.2	1215	14	AJ626536	AJ626536 Human her
415	106.5	6.4	2455	6	AR565046	AR565046 Sequence	488	102	6.2	1215	14	AJ626549	AJ626549 Human her
416	106.5	6.4	2821	3	TNAF000606	AF000606 Trichoplu	489	102	6.2	1458	3	AF167710	AF167710 Toxocara
417	106.5	6.4	2821	6	AR129836	AR129836 Sequence	490	102	6.2	8246	1	AE014770	AE014770 Bifidobac
418	106.5	6.4	2821	6	AR565047	AR565047 Sequence	491	102	6.2	26339	3	CBRG17K04	AC084514 Caenorhab
c 419	106.5	6.4	163528	10	AC121951	AC121951 Mus muscu	c	492	6.2	110000	1	AP006618_49	Continuation (50 o
c 420	106	6.4	203159	10	AC137525	AC137525 Mus muscu	c	493	6.2	110000	2	LMFLCHR36_21	Continuation (22 o
c 421	106	6.4	346406	10	BX883045	BX883045 Rattus no	494	102	6.2	110000	8	AE016819_10	Continuation (11 o
422	105.5	6.4	614	9	AB049062S7	AB049061 Homo sapi	c	495	6.2	170450	2	AC105379	AC105379 Trypanoso
423	105.5	6.4	1720	10	AF094071	AF094071 Rattus no	c	496	6.2	216015	2	AC113751	AC113751 Rattus no
424	105.5	6.4	1747	10	AF093673	AF093673 Cricetulu	497	102	6.2	272147	2	AC095648	AC095648 Rattus no
c 425	105.5	6.4	144588	2	AC012239	AC012239 Homo sapi	498	102	6.2	349980	6	AX492786	AX492786 Sequence
c 426	105.5	6.4	257513	2	AC127093	AY226866 Bos tauru	499	102	6.2	349980	6	AX553953	AX553953 Sequence
427	105	6.3	723	4	AY226857S10	U02292 Bos taurus	500	101.5	6.1	1144	8	TTU537508	AJ537508 Triticum
428	105	6.3	1941	4	BTU02292	AY530877 Simian ad	c	501	6.1	1378	1	AY127885	AY127885 Anaplasma
429	105	6.3	36604	14	AY530877	AC003110 Human DNA	502	101.5	6.1	2407	8	LTE532549	AJ532549 Lolium te
430	105	6.3	36800	9	AC003110	AC138430 Homo sapi	503	101.5	6.1	2586	10	MUSEGFREPD	L02613 Mus musculu
c 431	105	6.3	43185	9	AC138430	Continuation (6 of	504	101.5	6.1	2607	6	BD274942	BD274942 POLYNUCLE
c 432	105	6.3	110000	8	CR382129_05	AP003335 Oryza sat	505	101.5	6.1	2607	6	AR474071	AR474071 Sequence
433	105	6.3	194459	8	AP003335	AC110520 Mus muscu	506	101.5	6.1	3319	8	AK119879	AK119879 Oryza sat
c 434	105	6.3	247266	2	AC110520	AC096230 Rattus no	507	101.5	6.1	5005	9	AB011099	AB011099 Homo sapi
435	105	6.3	248817	3	LMFL2426	AL358712 Leishmani	c	508	6.1	6112	6	AX347419	AX347419 Sequence
436	104.5	6.3	35424	2	AC127426	AC127426 Magnaport	c	509	6.1	6112	6	AX657789	AX657789 Sequence
437	104.5	6.3	106586	2	AC127426	S73720 aggregcan=ag	c	510	6.1	6112	6	AX657789	AX659063 Sequence
438	104	6.3	231	10	S73719S2	S73722 aggregcan=ag	511	101.5	6.1	39737	2	AY714855	AY714855 Unculture
439	104	6.3	231	10	S73721S2	AF098641 Homo sapi	512	101.5	6.1	53178	6	CQ363755	CQ363755 Sequence
440	104	6.3	484	9	AF098641	BC008735 Homo sapi	513	101.5	6.1	117099	8	AP003572	AP003572 Oryza sat
441	104	6.3	3014	9	BC008735	AY051490 Drosophil	c	514	6.1	117099	8	AP003572	AP003572 Oryza sat
442	104	6.3	5916	3	AY051490		c	515	6.1	146874	8	AP004868	AP004868 Oryza sat

516	101.5	6.1	147640	2	AP003542	Oryza sat	589	100	6.0	110000	8	CR382132_06	Continuation (7 of
c 517	101.5	6.1	176022	2	BX294110	Danio rer	c 590	100	6.0	135850	2	AC135931	Rattus no
c 518	101.5	6.1	290850	1	SCO939127	Streptomy	c 591	100	6.0	180995	9	AC117500	Homo sapi
519	101	6.1	2421	6	CQ722898	Sequence	c 592	100	6.0	184091	2	BX294393	Mus muscu
520	101	6.1	2493	8	AB055432	Aspergill	593	100	6.0	195246	10	AC122266	Mus muscu
521	101	6.1	3118	6	BD156554	Primer fo	c 594	100	6.0	218311	2	CR749741	Danio rer
522	101	6.1	3118	6	AX877234	Sequence	595	100	6.0	230817	2	AC106909	Rattus no
523	101	6.1	3118	9	AK027692	Homo sapi	c 596	100	6.0	239696	2	AC097086	Rattus no
524	101	6.1	3175	6	AX747807	Sequence	597	100	6.0	254278	2	AC023836	Mus muscu
525	101	6.1	3175	9	AK092919	Homo sapi	598	100	6.0	308750	1	AP005216	Corynebac
526	101	6.1	3499	6	BD156002	Primer fo	c 599	100	6.0	349028	1	BX640413	Bordetell
527	101	6.1	3499	6	AX876196	Sequence	600	99.5	6.0	1008	5	AB167511	Danio rer
528	101	6.1	3499	9	AK027440	Homo sapi	601	99.5	6.0	1434	6	AR552751	Sequence
529	101	6.1	4098	9	HSA459424	Homo sapi	602	99.5	6.0	3814	5	XELNCAMA	M76710 Xenopus lae
530	101	6.1	5131	6	CQ850217	Homo sapi	603	99.5	6.0	13684	1	AE014787	AE014787 Bifidobac
531	101	6.1	5131	9	AK127328	Homo sapi	604	99.5	6.0	16114	3	AB062881	Mytilus g
c 532	101	6.1	24413	3	AC117272	Leishmani	c 605	99.5	6.0	162296	9	AL161774	Human DNA
c 533	101	6.1	72675	9	BX322573	Human DNA	c 606	99.5	6.0	197404	10	AL672124	Mouse DNA
534	101	6.1	79748	2	AC044890	Homo sapi	607	99.5	6.0	202314	2	AC132694	Rattus no
535	101	6.1	96560	9	AC090582	Homo sapi	608	99.5	6.0	220851	5	BX649335	Zebrafish
536	101	6.1	110000	8	AE016819_02	Homo sapi	609	99.5	6.0	225000	2	AC129674	Rattus no
537	101	6.1	112830	2	AC151678	Continuation (3 of	610	99.5	6.0	263891	2	AC096166	Rattus no
c 538	101	6.1	125623	3	AC115599	Dictyoste	611	99.5	6.0	268651	2	BX005198	Danio rer
c 539	101	6.1	147024	9	AC018410	Homo sapi	612	99.5	6.0	322497	2	AC112109	Rattus no
540	101	6.1	154612	2	AC093739	Homo sapi	613	99.5	6.0	349980	6	AX492787	Sequence
541	101	6.1	160625	9	AC009311	Homo sapi	614	99.5	6.0	349980	6	AX553954	Sequence
542	101	6.1	168624	9	AC092131	Homo sapi	615	99	6.0	438	6	CQ662211	Sequence
543	101	6.1	173189	9	AC092323	Homo sapi	616	99	6.0	1374	6	A91700	Sequence 4
c 544	101	6.1	178400	5	BX294376	Zebrafish	617	99	6.0	1374	6	BD023443	U89915 Mus musculu
545	101	6.1	183556	2	AC019059	Homo sapi	618	99	6.0	2029	10	MMU89915	Mus muscu
546	101	6.1	192177	5	BX005242	Zebrafish	619	99	6.0	2899	10	BC020004	BC020004 Mus muscu
c 547	101	6.1	197461	2	AC134814	Rattus no	620	99	6.0	4287	6	CQ610164	CQ610164 Sequence
548	100.5	6.1	1161	10	MMNOTA	X68278 M.musculus	621	99	6.0	4488	10	AF378831	AF378831 Mus muscu
549	100.5	6.1	1209	9	AB107883	Homo sapi	622	99	6.0	8546	1	AY512465	AY512465 Listeria
550	100.5	6.1	1236	14	AJ626540	Human her	623	99	6.0	16381	10	MMU97068	U97068 Mus musculu
551	100.5	6.1	1475	6	AX392229	Sequence	624	99	6.0	110000	6	BD430793_01	Continuation (2 of
552	100.5	6.1	1712	8	AK120901	Oryza sat	625	99	6.0	110000	8	CR382128_25	Continuation (26 o
553	100.5	6.1	1714	8	AK119612	Oryza sat	626	99	6.0	110000	8	CR382129_11	Continuation (12 o
554	100.5	6.1	1780	8	AK103182	Oryza sat	627	99	6.0	143089	5	CR388386_	CR388386 Zebrafish
555	100.5	6.1	1881	8	AK061650	Oryza sat	c 628	99	6.0	153749	5	BX649585	BX649585 Zebrafish
556	100.5	6.1	1904	8	AK101618	Oryza sat	c 629	99	6.0	166165	8	AP004753	AP004753 Oryza sat
557	100.5	6.1	1944	3	AY061148	AY061148 Drosophil	c 630	99	6.0	175124	2	AC135035	AC135035 Rattus no
558	100.5	6.1	3383	9	AY262756	AY262756 Homo sapi	c 631	99	6.0	176113	2	AC132574	AC132574 Mus muscu
559	100.5	6.1	3677	8	AF414112	Candida a	632	99	6.0	184357	2	AC073728	AC073728 Mus muscu
560	100.5	6.1	4140	6	CQ605853	Sequence	633	99	6.0	207161	2	AC120651	AC120651 Rattus no
561	100.5	6.1	5409	6	BD183451	Novel gen	634	99	6.0	224197	2	AC144404	AC144404 Medicago
562	100.5	6.1	5409	9	AB067513	Homo sapi	635	99	6.0	240525	2	AC096895	AC096895 Rattus no
563	100.5	6.1	7596	6	AX695382	Sequence	c 636	99	6.0	242063	2	AC126964	AC126964 Rattus no
564	100.5	6.1	8064	6	AX695381	Sequence	637	99	6.0	307150	1	CNSPAX01	AJ248283 Pyrococcu
565	100.5	6.1	8064	10	MMNOTCHA	Z11886 M.musculus	638	99	6.0	349980	6	AX041106	AX041106 Sequence
566	100.5	6.1	9193	10	AF508809	AF508809 Mus muscu	639	98.5	5.9	1194	14	AJ626548	AJ626548 Human her
c 567	100.5	6.1	15900	2	AC017311	Drosophil	640	98.5	5.9	1194	14	AJ626552	AJ626552 Human her
568	100.5	6.1	16256	1	AF289050	Bacteroid	641	98.5	5.9	1278	14	AJ626556	AJ626556 Human her
c 569	100.5	6.1	22029	9	AC003967	AC003967 Homo sapi	c 642	98.5	5.9	1719	8	AK176661	AK176661 Arabidops
570	100.5	6.1	43185	9	AC138430	Homo sapi	643	98.5	5.9	1898	3	AB092978	AB092978 Haliotis
571	100.5	6.1	94779	2	AC151672	AC151672 Gallus ga	644	98.5	5.9	2039	10	BC082777	BC082777 Mus muscu
c 572	100.5	6.1	110000	2	LMFLCHR31_02	Continuation (3 of	645	98.5	5.9	2790	3	DDI301670	AJ301670 Dictyoste
573	100.5	6.1	137033	8	AC107224	Oryza sat	646	98.5	5.9	3381	6	CQ608193	CQ608193 Sequence
574	100.5	6.1	154865	8	OSJN00071	AL606640 Oryza sat	647	98.5	5.9	5152	5	AY144591	AY144591 Cyprinus
575	100.5	6.1	232749	2	CR354535	CR354535 Danio rer	c 648	98.5	5.9	5283	1	AF373807	AF373807 Sinorhizo
576	100.5	6.1	236907	2	AC103254	AC103254 Rattus no	649	98.5	5.9	5381	6	CQ608192	CQ608192 Sequence
c 577	100.5	6.1	300330	1	AP005222	AP005222 Corynebac	650	98.5	5.9	6141	1	MELOSVM11	AF049242 Mesorhizo
c 578	100.5	6.1	300950	1	AP005940	AP005940 Bradyrhiz	651	98.5	5.9	79116	8	AP006373	AP006373 Lotus cor
c 579	100.5	6.1	316050	1	BX321859	BX321859 Nitrosomo	c 652	98.5	5.9	82972	8	NCB24H17	AL356815 Neurospor
580	100	6.0	983	5	BC061275	BC061275 Xenopus t	c 653	98.5	5.9	99967	8	NCB23B10	BX284752 Neurospor
581	100	6.0	1214	14	AJ626551	AJ626551 Human her	c 654	98.5	5.9	110000	8	CR382125_01	Continuation (2 of
582	100	6.0	1215	14	AJ626527	AJ626527 Human her	655	98.5	5.9	117273	2	AC015138	AC015138 Drosophil
583	100	6.0	1215	14	AJ626539	AJ626539 Human her	656	98.5	5.9	124191	9	AC005153	AC005153 Homo sapi
584	100	6.0	1215	14	AJ626553	AJ626553 Human her	657	98.5	5.9	146137	2	AC148795	AC148795 Otolemur
585	100	6.0	33706	3	CEC25G4	Z70680 Caenorhabdi	658	98.5	5.9	150050	1	MLO672112	AL672112 Mesorhizo
c 586	100	6.0	93889	2	AC105432	AC105432 Magnaport	659	98.5	5.9	170324	3	AC007805	AC007805 Drosophil
587	100	6.0	100984	10	AL929138	AL929138 Mouse DNA	c 660	98.5	5.9	174527	9	AP001183	AP001183 Homo sapi
c 588	100	6.0	107352	9	HS474A14	AL023285 Human DNA	661	98.5	5.9	182736	2	AC021672	AC021672 Homo sapi

c 662	98.5	5.9	190314	9	AC019227	AC019227 Homo sapi	c 735	97.5	5.9	170475	10	AL844546	AL844546 Mouse DNA
663	98.5	5.9	191041	9	AC091742	AC091742 Homo sapi	c 736	97.5	5.9	175152	2	AC074195	AC074195 Homo sapi
664	98.5	5.9	202555	2	AC148141	AC148141 Bos taurus	c 737	97.5	5.9	188553	2	AC151534	AC151534 Mus muscu
c 665	98.5	5.9	204018	2	AC116890	AC116890 Mus muscu	738	97.5	5.9	225989	2	AC135294	AC135294 Rattus no
666	98.5	5.9	227847	3	AE003692	AE003692 Drosophil	739	97.5	5.9	227555	10	AC108416	AC108416 Mus muscu
667	98.5	5.9	243185	2	AC094948	AC094948 Rattus no	c 740	97.5	5.9	243299	2	AC133800	AC133800 Rattus no
668	98.5	5.9	243899	5	BX510919	BX510919 Zebrafish	c 741	97.5	5.9	304500	1	AP005953	AP005953 Bradyrhiz
669	98.5	5.9	267156	6	AX336388	AX336388 Sequence	c 742	97.5	5.9	349980	6	AX044030	AX044030 Sequence
670	98.5	5.9	267156	9	U66059	U66059 Human germ	c 743	97.5	5.9	349980	6	AX044031	AX044031 Sequence
c 671	98.5	5.9	299350	1	SME591786	AL591786 Sinorhizo	744	97	5.9	304	6	CQ673468	CQ673468 Sequence
672	98	5.9	1173	14	AJ626537	AJ626537 Human her	745	97	5.9	789	6	CQ749879	CQ749879 Sequence
673	98	5.9	1173	14	AJ626555	AJ626555 Human her	746	97	5.9	1030	10	BC042902	BC042902 Mus muscu
674	98	5.9	1815	1	AF497174	AF497174 Listeria	747	97	5.9	1215	14	AJ626533	AJ626533 Human her
675	98	5.9	1815	1	AF497181	AF497181 Listeria	748	97	5.9	1231	6	AR508054	AR508054 Sequence
c 676	98	5.9	2346	3	TCCF69GNA	Z22557 T.congolens	c 749	97	5.9	2293	8	AK102226	AK102226 Oryza sat
677	98	5.9	2717	8	YLTSR1	Z69781 Y.lipolytic	750	97	5.9	2751	6	AX713940	AX713940 Sequence
678	98	5.9	6353	6	CQ580242	CQ580242 Sequence	751	97	5.9	2751	9	AK055882	AK055882 Homo sapi
679	98	5.9	8429	6	CQ580241	CQ580241 Sequence	c 752	97	5.9	2901	3	BT014661	BT014661 Drosophil
680	98	5.9	8546	1	AY512394	AY512394 Listeria	c 753	97	5.9	2908	10	BC021506	BC021506 Mus muscu
681	98	5.9	8546	1	AY512406	AY512406 Listeria	c 754	97	5.9	3058	10	BC027844	BC027844 Mus muscu
682	98	5.9	8546	1	AY512408	AY512408 Listeria	c 755	97	5.9	3374	10	BC078642	BC078642 Mus muscu
683	98	5.9	8546	1	AY512414	AY512414 Listeria	c 756	97	5.9	3629	8	AK069483	AK069483 Oryza sat
684	98	5.9	8546	1	AY512416	AY512416 Listeria	757	97	5.9	3720	5	XELNCAM	M25696 X.laevis ne
685	98	5.9	8546	1	AY512420	AY512420 Listeria	758	97	5.9	8546	1	AY512395	AY512395 Listeria
686	98	5.9	8546	1	AY512423	AY512423 Listeria	759	97	5.9	8546	1	AY512429	AY512429 Listeria
687	98	5.9	8546	1	AY512424	AY512424 Listeria	760	97	5.9	8546	1	AY512431	AY512431 Listeria
688	98	5.9	8546	1	AY512435	AY512435 Listeria	761	97	5.9	8546	1	AY512432	AY512432 Listeria
689	98	5.9	8546	1	AY512437	AY512437 Listeria	762	97	5.9	8546	1	AY512450	AY512450 Listeria
690	98	5.9	8546	1	AY512445	AY512445 Listeria	763	97	5.9	11083	1	AE001680	AE001680 Chlamydia
691	98	5.9	8546	1	AY512449	AY512449 Listeria	c 764	97	5.9	11322	1	AE002244	AE002244 Chlamydrop
692	98	5.9	8546	1	AY512455	AY512455 Listeria	765	97	5.9	110000	6	AR310754_11	Continuation (12 o
693	98	5.9	8546	1	AY512461	AY512461 Listeria	766	97	5.9	110000	8	CR382123_11	Continuation (12 o
694	98	5.9	8546	1	AY512463	AY512463 Listeria	767	97	5.9	171307	9	AC104020	AC104020 Homo sapi
695	98	5.9	8546	1	AY512466	AY512466 Listeria	c 768	97	5.9	176099	9	AC108201	AC108201 Homo sapi
696	98	5.9	8546	1	AY512491	AY512491 Listeria	769	97	5.9	190790	8	AP005802	AP005802 Oryza sat
c 697	98	5.9	13443	2	AC013070	AC013070 Drosophil	c 770	97	5.9	191462	2	AP005781	AP005781 Oryza sat
c 698	98	5.9	98521	10	AC094507	AC094507 Rattus no	c 771	97	5.9	195859	14	AF281817	AF281817 Tupaia he
c 699	98	5.9	103362	8	CR382132_39	Continuation (40 o	772	97	5.9	324746	1	AE017160	AE017160 Chlamydrop
700	98	5.9	103809	1	AE008921	AE008921 Unculture	773	97	5.9	325865	1	AP002548	AP002548 Chlamydrop
c 701	98	5.9	103995	2	AC096695	AC096695 Rattus no	774	97	5.9	349442	1	BX640447	BX640447 Bordetell
c 702	98	5.9	110000	8	CR380947_0	CR380947 Candida g	775	96.5	5.8	840	8	WHTGMPA	D78183 Triticum ae
703	98	5.9	110000	8	CR382129_28	Continuation (29 o	776	96.5	5.8	900	6	A91702	A91702 Sequence 6
704	98	5.9	119743	2	AC134515	AC134515 Rattus no	777	96.5	5.8	900	6	BD023445	BD023445 Junction
705	98	5.9	120000	2	AC127673	AC127673 Leishmani	778	96.5	5.8	1194	14	AJ626531	AJ626531 Human her
c 706	98	5.9	121478	9	AL365229	AL365229 Human DNA	779	96.5	5.8	1194	14	AJ626534	AJ626534 Human her
707	98	5.9	144167	2	AC148140	AC148140 Bos taurus	780	96.5	5.8	1194	14	AJ626538	AJ626538 Human her
c 708	98	5.9	152177	5	AL935114	AL935114 Zebrafish	781	96.5	5.8	1492	10	BC024403	BC024403 Mus muscu
c 709	98	5.9	159547	2	AC073674	AC073674 Mus muscu	782	96.5	5.8	1815	1	AF497170	AF497170 Listeria
c 710	98	5.9	159816	2	AC136044	AC136044 Rattus no	c 783	96.5	5.8	1859	8	AK106807	AK106807 Oryza sat
711	98	5.9	161264	1	AY456696	AY456696 Arthrobac	c 784	96.5	5.8	3161	6	CQ611375	CQ611375 Sequence
c 712	98	5.9	172674	3	AC007807	AC007807 Drosophil	785	96.5	5.8	3491	10	AF319949	AF319949 Mus muscu
c 713	98	5.9	174108	5	BX323078	BX323078 Zebrafish	786	96.5	5.8	3628	8	AK110169	AK110169 Oryza sat
c 714	98	5.9	190866	3	AC007824	AC007824 Drosophil	787	96.5	5.8	3691	8	D87895	D87895 Aspergillus
c 715	98	5.9	215436	2	AC123237	AC123237 Rattus no	788	96.5	5.8	3959	10	BC050817	BC050817 Mus muscu
c 716	98	5.9	220035	3	AE003716	AE003716 Drosophil	789	96.5	5.8	4501	1	ATU39263	U39263 Agrobacteri
717	98	5.9	220710	2	AC125304	AC125304 Rattus no	790	96.5	5.8	17317	8	AY421966	AY421966 Cryptococ
c 718	98	5.9	230138	14	AF232689	AF232689 Rat cytom	791	96.5	5.8	39057	8	YSCH9666	U10397 Saccharomyc
c 719	98	5.9	256879	3	AC116982	AC116982 Dictyoste	c 792	96.5	5.8	40289	2	AC151929	AC151929 Phaeodact
c 720	98	5.9	260271	1	AE017258	AE017258 Wolbachia	793	96.5	5.8	48626	2	AC013119	AC013119 Drosophil
721	98	5.9	305225	2	AC130763	AC130763 Rattus no	794	96.5	5.8	110000	8	AE016818_09	Continuation (10 o
722	97.5	5.9	1200	10	RNO010750	AJ010750 Rattus no	c 795	96.5	5.8	125673	9	AL356796	AL356796 Human DNA
723	97.5	5.9	1767	6	AR310497	AR310497 Sequence	c 796	96.5	5.8	154365	2	AC091753	AC091753 Rattus no
724	97.5	5.9	1767	6	AX000158	AX000158 Sequence	c 797	96.5	5.8	160986	3	AC108481	AC108481 Drosophil
725	97.5	5.9	2110	4	BTU10039	U10039 Bos taurus	c 798	96.5	5.8	166250	2	AC150711	AC150711 Bos tauru
726	97.5	5.9	2603	8	AF156269	AF156269 Aspergill	799	96.5	5.8	167333	2	AC147856	AC147856 Atelerix
727	97.5	5.9	2884	5	XELDLR1A	M62976 X.laevis lo	800	96.5	5.8	173740	2	AC020964	AC020964 Mus muscu
c 728	97.5	5.9	56374	9	AC074092	AC074092 Homo sapi	801	96.5	5.8	181179	9	AL161725	AL161725 Human DNA
c 729	97.5	5.9	109672	8	AP004119	AP004119 Oryza sat	802	96.5	5.8	186055	4	AC150569	AC150569 Bos tauru
730	97.5	5.9	110000	3	AC116957_2	Continuation (3 of	803	96.5	5.8	192662	10	AC134397	AC134397 Mus muscu
731	97.5	5.9	110000	8	CR382132_35	Continuation (36 o	804	96.5	5.8	211664	8	AF521177	AF521177 Hordeum v
732	97.5	5.9	110000	8	CR382132_36	Continuation (37 o	c 805	96.5	5.8	232049	2	AC127108	AC127108 Rattus no
733	97.5	5.9	130451	10	AC121877	AC121877 Mus muscu	c 806	96.5	5.8	242121	2	AC096371	AC096371 Rattus no
c 734	97.5	5.9	150401	2	AC079980	AC079980 Homo sapi	c 807	96.5	5.8	248550	1	SCO939120	AL939120 Streptomy

C	808	96.5	5.8	272888	2	AC139198	AC139198 Mus muscu	C	881	95.5	5.8	12781	6	AX825931	Sequence
C	809	96.5	5.8	295177	3	AE003430	AE003430 Drosophil		882	95.5	5.8	37728	8	YSC18543	Saccharomyc
C	810	96.5	5.8	297050	1	AP006569	AP006569 Gloeobact	C	883	95.5	5.8	53957	8	NCB2G14	Neurospor
C	811	96.5	5.8	348050	1	AP003581	AP003581 Nostoc sp		884	95.5	5.8	65140	6	AX211705	Sequence
C	812	96	5.8	206	9	HUMSCG02	L05407 Human cell		885	95.5	5.8	104241	10	AY046056	Mus muscu
C	813	96	5.8	1436	9	HSM804685	AL833372 Homo sapi		886	95.5	5.8	123580	1	AF263912	Streptomy
C	814	96	5.8	1455	5	AY288986	AY288986 Gallus ga	C	887	95.5	5.8	124605	8	CNS07YPW	Oryza sat
C	815	96	5.8	1851	10	BC021876	BC021876 Mus muscu		888	95.5	5.8	125401	6	AX211739	Sequence
C	816	96	5.8	1995	6	CQ782648	CQ782648 Sequence		889	95.5	5.8	126544	8	AP005106	Oryza sat
C	817	96	5.8	1995	6	BD127244	BD127244 Primer fo		890	95.5	5.8	140414	2	AC136548	Rattus no
C	818	96	5.8	1995	9	AK074718	AK074718 Homo sapi		891	95.5	5.8	140475	8	AP005558	Oryza sat
C	819	96	5.8	2610	5	BC077104	BC077104 Danio rer		892	95.5	5.8	143668	8	AP004268	Oryza sat
C	820	96	5.8	4562	6	AX416781	AX416781 Sequence		893	95.5	5.8	145590	8	AC109601	Oryza sat
C	821	96	5.8	5789	3	D82024	D82024 Dictyosteli	C	894	95.5	5.8	157397	8	AC133860	Oryza sat
C	822	96	5.8	7137	6	CQ726893	CQ726893 Sequence	C	895	95.5	5.8	166126	2	AC149096	Mus muscu
C	823	96	5.8	8533	1	AY512399	AY512399 Listeria		896	95.5	5.8	169184	2	AC144112	Macaca mu
C	824	96	5.8	8542	1	AY512500	AY512500 Listeria		897	95.5	5.8	174893	3	AC104608	Drosophil
C	825	96	5.8	8543	1	AY512393	AY512393 Listeria	C	898	95.5	5.8	176502	2	AC134706	Rattus no
C	826	96	5.8	8543	1	AY512400	AY512400 Listeria		899	95.5	5.8	201404	2	AC113679	Rattus no
C	827	96	5.8	8543	1	AY512425	AY512425 Listeria		900	95.5	5.8	203595	2	CR385054	Danio rer
C	828	96	5.8	8543	1	AY512427	AY512427 Listeria	C	901	95.5	5.8	234922	2	AC107585	Rattus no
C	829	96	5.8	8543	1	AY512434	AY512434 Listeria	C	902	95.5	5.8	255745	2	AC148018	Mus muscu
C	830	96	5.8	8543	1	AY512440	AY512440 Listeria	C	903	95.5	5.8	285950	3	AE003441	Drosophil
C	831	96	5.8	8543	1	AY512447	AY512447 Listeria		904	95.5	5.8	296820	10	AF312033	Mus muscu
C	832	96	5.8	8543	1	AY512448	AY512448 Listeria		905	95.5	5.8	349061	1	NMA222491	Neisseria
C	833	96	5.8	8543	1	AY512451	AY512451 Listeria		906	95.5	5.8	349535	1	BX248357	Corynebac
C	834	96	5.8	8543	1	AY512456	AY512456 Listeria		907	95	5.7	623	4	AY226857S08	Bos tauru
C	835	96	5.8	8543	1	AY512458	AY512458 Listeria		908	95	5.7	1173	14	AJ626550	Human her
C	836	96	5.8	8543	1	AY512464	AY512464 Listeria		909	95	5.7	1440	9	AF043724	Homo sapi
C	837	96	5.8	8546	1	AY512436	AY512436 Listeria		910	95	5.7	1574	8	TDY14104	Triticum du
C	838	96	5.8	8546	1	AY512441	AY512441 Listeria		911	95	5.7	1613	1	D88257	Listeria mo
C	839	96	5.8	8546	1	AY512467	AY512467 Listeria		912	95	5.7	1920	1	AF497180	Listeria
C	840	96	5.8	8546	1	AY512492	AY512492 Listeria		913	95	5.7	2041	1	AF103807	Listeria
C	841	96	5.8	11106	1	AE005891	AE005891 Caulobact	C	914	95	5.7	2211	6	CQ588543	Sequence
C	842	96	5.8	11297	1	AY230750	AY230750 Photorhab		915	95	5.7	2304	6	AX748227	Sequence
C	843	96	5.8	11659	1	AE005131	AE005131 Halobacte		916	95	5.7	2304	9	AK093619	Homo sapi
C	844	96	5.8	99890	3	AC084464	AC084464 Caenorhab		917	95	5.7	2373	5	BC057473	Danio rer
C	845	96	5.8	110000	1	AE017283_17	Continuation (18 o		918	95	5.7	2803	6	AX714680	Sequence
C	846	96	5.8	110000	1	AP006840_31	Continuation (32 o	C	919	95	5.7	2803	9	AK057241	Homo sapi
C	847	96	5.8	110000	2	LMFLCHR31_15	Continuation (16 o	C	920	95	5.7	2810	3	BT010024	Drosophil
C	848	96	5.8	110000	8	CR380953_00	CR380953 Candida g		921	95	5.7	3331	10	MMU70674	Mus musculu
C	849	96	5.8	137297	8	AC090714	AC090714 Oryza sat		922	95	5.7	3495	10	BC033459	Mus muscu
C	850	96	5.8	155548	2	CR848047	CR848047 Danio rer		923	95	5.7	3813	5	AJ720073	Gallus ga
C	851	96	5.8	163580	8	AC084767	AC084767 Oryza sat		924	95	5.7	4498	10	MMU91922	Mus musculu
C	852	96	5.8	168365	10	AC131653	AC131653 Mus muscu		925	95	5.7	4678	6	CQ588542	Sequence
C	853	96	5.8	179737	2	AC121552	AC121552 Mus muscu	C	926	95	5.7	5018	3	AC006797	Caenorhab
C	854	96	5.8	189286	9	AC008125	AC008125 Homo sapi	C	927	95	5.7	5018	8	AB023040	Arabidops
C	855	96	5.8	197845	2	BX950198	BX950198 Danio rer		928	95	5.7	8504	1	AY512403	Listeria
C	856	96	5.8	211720	2	AC121145	AC121145 Mus muscu		929	95	5.7	8643	1	AY512442	Listeria
C	857	96	5.8	239030	10	AC131323	AC131323 Mus muscu		930	95	5.7	8644	1	AY512484	Listeria
C	858	96	5.8	251756	10	AC119801	AC119801 Mus muscu		931	95	5.7	8650	1	AY512452	Listeria
C	859	96	5.8	290841	1	AE017322	AE017322 Listeria		932	95	5.7	8650	1	AY512471	Listeria
C	860	96	5.8	300800	1	AP005036	AP005036 Streptomy	C	933	95	5.7	8650	1	AE012376	Listeria
C	861	96	5.8	311000	1	SCO939122	AL939122 Streptomy		934	95	5.7	10101	1	AE012376	Xanthomon
C	862	95.5	5.8	1173	8	PRA315701	AJ315701 Phlebia r		935	95	5.7	33359	3	CEF55B11	Z83318 Caenorhabdi
C	863	95.5	5.8	1434	8	YSCSMS1	D29964 Saccharomyc	C	936	95	5.7	89992	9	AL135794	Human DNA
C	864	95.5	5.8	1491	14	AF343058	AF343058 Eyaach vir		937	95	5.7	109519	6	AX195929	Sequence
C	865	95.5	5.8	1693	8	AK061142	AK061142 Oryza sat	C	938	95	5.7	114020	10	AC127596	Mus muscu
C	866	95.5	5.8	1706	9	AK075503	AK075503 Homo sapi		939	95	5.7	136955	2	AC011910	Drosophil
C	867	95.5	5.8	1853	8	AK109612	AK109612 Oryza sat		940	95	5.7	144263	2	AP005054	Oryza sat
C	868	95.5	5.8	2012	8	AK071956	AK071956 Oryza sat		941	95	5.7	149505	2	AC126927	Felis cat
C	869	95.5	5.8	2220	8	YSCMID2P	D29945 Yeast MID2		942	95	5.7	160118	10	AC132954	Mus muscu
C	870	95.5	5.8	2246	3	AY113653	AY113653 Drosophil		943	95	5.7	162929	5	BX323842	Zebrafish
C	871	95.5	5.8	2517	8	AK105749	AK105749 Oryza sat		944	95	5.7	167475	10	AC090881	Mus Muscu
C	872	95.5	5.8	2947	1	SLI18818	Y18818 Streptomyce	C	945	95	5.7	169427	3	AC007416	Drosophil
C	873	95.5	5.8	3005	8	AK111157	AK111157 Oryza sat	C	946	95	5.7	173369	10	AL928966	Mouse DNA
C	874	95.5	5.8	4435	6	AR428567	AR428567 Sequence		947	95	5.7	195349	2	AC006705	Caenorhab
C	875	95.5	5.8	4435	6	BD078018	BD078018 Chlamydia		948	95	5.7	197913	2	BX572087	Danio rer
C	876	95.5	5.8	5894	3	ACMHC	Y00624 Acanthamoeb		949	95	5.7	199152	2	CR382297	Danio rer
C	877	95.5	5.8	11422	3	AF190405	AF190405 Drosophil	C	950	95	5.7	217807	2	AC117034	Rattus no
C	878	95.5	5.8	12781	6	AX251139	AX251139 Sequence		951	95	5.7	254733	3	AC117075	Dictyoste
C	879	95.5	5.8	12781	6	AX356403	AX356403 Sequence		952	95	5.7	256307	2	AC130125	Rattus no
C	880	95.5	5.8	12781	6	AX822291	AX822291 Sequence		953	95	5.7	258181	2	AC096936	Rattus no

954	95	5.7	263879	2	AC096060	AC096060 Rattus no
955	95	5.7	268333	2	AC098998	AC098998 Rattus no
c 956	95	5.7	289516	3	AE003619	AE003619 Drosophil
957	95	5.7	302550	1	AP006581	AP006581 Gloebact
958	95	5.7	340806	1	NMA122491	AL162752 Neisseria
c 959	95	5.7	341553	1	BX248355	BX248355 Corynebac
c 960	95	5.7	349607	1	BX957222	BX957222 Methanoco
961	94.5	5.7	907	1	GVI7274	AJ007724 Gloebact
962	94.5	5.7	948	1	AY331318	AY331318 Pseudomon
963	94.5	5.7	948	1	AY331321	AY331321 Pseudomon
964	94.5	5.7	948	1	AY331322	AY331322 Pseudomon
965	94.5	5.7	948	1	AY331323	AY331323 Pseudomon
966	94.5	5.7	948	1	AY331324	AY331324 Pseudomon
967	94.5	5.7	1152	14	AJ626535	AJ626535 Human her
968	94.5	5.7	1152	14	AJ626544	AJ626544 Human her
969	94.5	5.7	1188	14	AJ626529	AJ626529 Human her
970	94.5	5.7	1203	6	CQ751744	CQ751744 Sequence
971	94.5	5.7	1507	9	BC013325	BC013325 Homo sapi
972	94.5	5.7	1608	6	BD228728	BD228728 Novel der
c 973	94.5	5.7	1608	6	BD228729	BD228729 Novel der
974	94.5	5.7	1608	6	AR232707	AR232707 Sequence
c 975	94.5	5.7	1608	6	AR232708	AR232708 Sequence
976	94.5	5.7	1608	6	AX411859	AX411859 Sequence
c 977	94.5	5.7	1608	6	AX411861	AX411861 Sequence
978	94.5	5.7	1665	6	BD228726	BD228726 Novel der
c 979	94.5	5.7	1665	6	BD228727	BD228727 Novel der
980	94.5	5.7	1665	6	AR232705	AR232705 Sequence
c 981	94.5	5.7	1665	6	AR232706	AR232706 Sequence
982	94.5	5.7	1665	6	AX411856	AX411856 Sequence
c 983	94.5	5.7	1665	6	AX411858	AX411858 Sequence
984	94.5	5.7	1752	3	AF178772	AF178772 Dermatoph
985	94.5	5.7	1752	6	BD228724	BD228724 Novel der
c 986	94.5	5.7	1752	6	BD228725	BD228725 Novel der
987	94.5	5.7	1752	6	AR232703	AR232703 Sequence
c 988	94.5	5.7	1752	6	AR232704	AR232704 Sequence
989	94.5	5.7	1752	6	AX411853	AX411853 Sequence
c 990	94.5	5.7	1752	6	AX411855	AX411855 Sequence
991	94.5	5.7	1994	5	BC059200	BC059200 Danio rer
992	94.5	5.7	2155	9	S52488	S52488 CSPG2=versi
993	94.5	5.7	2438	6	CQ843471	CQ843471 Sequence
994	94.5	5.7	2438	9	AK126455	AK126455 Homo sapi
995	94.5	5.7	2690	3	DPU20332	U20332 Drosophila
c 996	94.5	5.7	2784	6	AX654208	AX654208 Sequence
997	94.5	5.7	2967	1	AY184164	AY184164 Chlamydia
998	94.5	5.7	2967	1	AY184165	AY184165 Chlamydia
999	94.5	5.7	2967	1	AY184166	AY184166 Chlamydia
1000	94.5	5.7	3401	6	AX536450	AX536450 Sequence
1001	94.5	5.7	3958	8	YSCSN6A	M17826 Yeast (S.ce
1002	94.5	5.7	4041	5	GGNEUFASC	X65224 G.gallus mR
1003	94.5	5.7	4866	8	YSCCYC8	M23440 Yeast (S.ce
c1004	94.5	5.7	5374	8	SCYBR112C	Z35981 S.cerevisia
1005	94.5	5.7	6674	1	LDE512946	AJ512946 Lactobaci
c1006	94.5	5.7	8664	3	LMFL6823	AL139796 Leishmani
c1007	94.5	5.7	8949	8	SCCMDLYS	X66247 S.cerevisia
c1008	94.5	5.7	11613	1	AE015347	AE015347 Shigella
c1009	94.5	5.7	15509	3	CEC03D6	Z75525 Caenorhabdi
1010	94.5	5.7	26356	3	AF077538	AF077538 Caenorhab
1011	94.5	5.7	50709	1	AY034092	AY034092 Micrococc
1012	94.5	5.7	68702	9	AL445193	AL445193 Human DNA
c1013	94.5	5.7	69748	8	SCRACII	X78993 S.cerevisia
c1014	94.5	5.7	86761	10	AL663044	AL663044 Mouse DNA
c1015	94.5	5.7	92294	1	AY117439	AY117439 Streptomy
1016	94.5	5.7	102311	9	AC005377	AC005377 Homo sapi
1017	94.5	5.7	103419	2	AL139221	AL139221 Homo sapi
1018	94.5	5.7	107379	1	SHGCP1R	X86780 S.hygroscop
1019	94.5	5.7	110000	2	AC102349_1	Continuation (2 of
1020	94.5	5.7	110000	2	AC102349_2	Continuation (3 of
c1021	94.5	5.7	110000	2	LMFLCHR36_01	Continuation (2 of
1022	94.5	5.7	121705	9	AC006452	AC006452 Homo sapi
1023	94.5	5.7	125862	9	AC026696	AC026696 Homo sapi
c1024	94.5	5.7	132151	8	AC144491	AC144491 Oryza sat
1025	94.5	5.7	139275	2	BX323887	BX323887 Danio rer
1026	94.5	5.7	144695	8	AP005451	AP005451 Oryza sat

94.5	5.7	159802	8	AP005447	AP005447 Oryza sat
94.5	5.7	160738	8	AC073556	AC073556 Oryza sat
94.5	5.7	160871	5	AL954145	AL954145 Zebrafish
94.5	5.7	164223	10	AC127228	AC127228 Mus muscu
94.5	5.7	166138	9	AC099684	AC099684 Homo sapi
94.5	5.7	168131	2	AC135937	AC135937 Rattus no
94.5	5.7	182122	2	AC104194	AC104194 Mus muscu
94.5	5.7	198222	2	AC092429	AC092429 Homo sapi
94.5	5.7	202269	9	AC130689	AC130689 Homo sapi
94.5	5.7	216860	10	AC134793	AC134793 Mus muscu
94.5	5.7	226307	10	AC119851	AC119851 Mus muscu
94.5	5.7	232292	2	AC126517	AC126517 Rattus no
94.5	5.7	242875	2	AC096494	AC096494 Rattus no
94.5	5.7	246913	10	AC109542	AC109542 Rattus no
94.5	5.7	247306	2	AC131445	AC131445 Rattus no
94.5	5.7	252509	2	AC098338	AC098338 Rattus no
94.5	5.7	253360	2	AC096943	AC096943 Rattus no
94.5	5.7	289816	1	AE016992	AE016992 Shigella
94.5	5.7	292550	1	AP001513	AP001513 Bacillus
94.5	5.7	349751	3	PFMAL4P3	AL035476 Plasmodiu
94	5.7	700	9	S72412	S72412 proteoglyca
94	5.7	942	8	AK060999	AK060999 Oryza sat
94	5.7	1566	6	CQ716121	CQ716121 Sequence
94	5.7	1810	5	CR761800	CR761800 Xenopus t
94	5.7	1920	1	AF497173	AF497173 Listeria
94	5.7	1946	6	CQ588132	CQ588132 Sequence
94	5.7	1946	6	AX254510	AX254510 Sequence
94	5.7	2023	8	CSMCPN601	X70867 Cucurbita s
94	5.7	2398	8	AF190462	AF190462 Phaseolus
94	5.7	2461	8	MSY428052	AJ428052 Malassezi
94	5.7	2713	10	MMZFY	X14382 Mouse zinc
94	5.7	2990	3	AY122212	AY122212 Drosophil
94	5.7	3774	2	AC019365	AC019365 Drosophil
94	5.7	3946	6	CQ588131	CQ588131 Sequence
94	5.7	3946	6	AX254509	AX254509 Sequence
94	5.7	4849	3	AK113070	AK113070 Ciona int
94	5.7	6047	6	AX346361	AX346361 Sequence
94	5.7	6313	6	CQ604274	CQ604274 Sequence
94	5.7	6530	1	AB017438	AB017438 Streptomy
94	5.7	7056	1	AF042494	AF042494 Sulfolobu
94	5.7	7823	14	HPV27	X74473 Human papil
94	5.7	8643	1	AY512405	AY512405 Listeria
94	5.7	8643	1	AY512421	AY512421 Listeria
94	5.7	8643	1	AY512422	AY512422 Listeria
94	5.7	8643	1	AY512444	AY512444 Listeria
94	5.7	8643	1	AY512468	AY512468 Listeria
94	5.7	8643	1	AY512469	AY512469 Listeria
94	5.7	8643	1	AY512490	AY512490 Listeria
94	5.7	8649	1	AY512481	AY512481 Listeria
94	5.7	8651	1	AY512391	AY512391 Listeria
94	5.7	8651	1	AY512398	AY512398 Listeria
94	5.7	8651	1	AY512401	AY512401 Listeria
94	5.7	8651	1	AY512415	AY512415 Listeria
94	5.7	8651	1	AY512426	AY512426 Listeria
94	5.7	8651	1	AY512457	AY512457 Listeria
94	5.7	8651	1	AY512459	AY512459 Listeria
94	5.7	8651	1	AY512460	AY512460 Listeria
94	5.7	9642	10	AF187873	AF187873 Cavia por
94	5.7	10029	1	AE011851	AE011851 Xanthomon
94	5.7	11085	1	AE006896	AE006896 Sulfolobu
94	5.7	11106	1	AE012183	AE012183 Xanthomon
94	5.7	14198	1	AE011967	AE011967 Xanthomon
94	5.7	80167	2	AC020038	AC020038 Drosophil
94	5.7	110000	1	AP006618_28	Continuation (29 o
94	5.7	121377	8	AP004038	AP004038 Oryza sat
94	5.7	123010	2	AC009746	AC009746 Drosophil
94	5.7	127405	10	AL645599	AL645599 Mouse DNA
94	5.7	137046	8	AP004775	AP004775 Oryza sat
94	5.7	138994	2	AC141046	AC141046 Rattus no
94	5.7	146123	2	AC147458	AC147458 Felis cat
94	5.7	169138	3	AC010571	AC010571 Drosophil
94	5.7	184887	3	AC008207	AC008207 Drosophil
94	5.7	192187	3	AC117072	AC117072 Dictyoste

c1100	94	5.7	199271	2	AC142243	AC142243 Mus muscu	c1173	93.5	5.6	349980	6	AX492786	AX492786 Sequence
c1101	94	5.7	212159	2	AC113023	AC113023 Mus muscu	c1174	93.5	5.6	349980	6	AX553953	AX553953 Sequence
c1102	94	5.7	214256	10	AC118007	AC118007 Mus muscu	1175	93	5.6	712	3	AK174897	AK174897 Ciona int
1103	94	5.7	227219	3	AE003750	AE003750 Drosophil	1176	93	5.6	786	3	AJ586552	AJ586552 Elimeria t
1104	94	5.7	241592	2	AC111683	AC111683 Rattus no	1177	93	5.6	1050	3	AY466439	AY466439 Caenorhab
1105	94	5.7	246566	2	AC097926	AC097926 Rattus no	1178	93	5.6	1095	9	CR457114	CR457114 Homo sapi
c1106	94	5.7	263297	2	AC127631	AC127631 Rattus no	c1179	93	5.6	1200	14	AF395734	AF395734 Human ast
c1107	94	5.7	292100	1	SCO939121	AL939121 Streptomy	1180	93	5.6	1268	3	AF250045	AF250045 Caenorhab
c1108	94	5.7	294272	3	AE003595	AE003595 Drosophil	1181	93	5.6	1321	6	AR097540	AR097540 Sequence
1109	94	5.7	297950	1	AP006582	AP006582 Gloeobact	1182	93	5.6	1815	10	AF170709	AF170709 Mus muscu
1110	94	5.7	302040	1	AE017317	AE017317 Desulfovi	1183	93	5.6	1920	1	AF497175	AF497175 Listeria
1111	94	5.7	303550	1	SCO939131	AL939131 Streptomy	1184	93	5.6	1920	1	AF497177	AF497177 Listeria
c1112	94	5.7	329861	1	NMA522491	AL162756 Neisseria	1185	93	5.6	1929	10	AF169191	AF169191 Mus muscu
1113	93.5	5.6	757	10	BC021401	BC021401 Mus muscu	1186	93	5.6	1962	10	AF169192	AF169192 Mus muscu
1114	93.5	5.6	826	5	CHKLNKPA4	M35038 Chicken car	1187	93	5.6	2032	3	DMU17693	UI7693 Drosophila
1115	93.5	5.6	981	9	BC041179	BC041179 Homo sapi	1188	93	5.6	2032	6	AR195309	AR195309 Sequence
1116	93.5	5.6	1070	8	AK061303	AK061303 Oryza sat	1189	93	5.6	2032	6	AR222274	AR222274 Sequence
1117	93.5	5.6	1152	14	AJ626554	AJ626554 Human her	1190	93	5.6	2051	4	CFGPCR1	X14048 Canis famil
1118	93.5	5.6	1172	8	AK104138	AK104138 Oryza sat	1191	93	5.6	2105	5	BC081615	BC081615 Danio rer
1119	93.5	5.6	1175	8	AK104400	AK104400 Oryza sat	1192	93	5.6	2806	10	AF299345	AF299345 Mus muscu
1120	93.5	5.6	1216	10	BC060539	BC060539 Rattus no	1193	93	5.6	2833	10	BC005414	BC005414 Mus muscu
1121	93.5	5.6	1245	8	AK073355	AK073355 Oryza sat	1194	93	5.6	2841	10	AB028895	AB028895 Mus muscu
1122	93.5	5.6	1785	3	AB162804	AB162804 Haliotis	c1195	93	5.6	3004	6	CQ593711	CQ593711 Sequence
1123	93.5	5.6	1824	1	AF497171	AF497171 Listeria	1196	93	5.6	3036	3	AY245772	AY245772 Monosiga
1124	93.5	5.6	1881	3	AF164027	AF164027 Leishmani	1197	93	5.6	4047	9	HSA298318	AJ298318 Homo sapi
1125	93.5	5.6	1943	3	AK116624	AK116624 Ciona int	1198	93	5.6	4977	1	CDCMANA	L01257 Caldocellum
c1126	93.5	5.6	2176	6	CQ841674	CQ841674 Sequence	1199	93	5.6	5931	6	CQ607290	CQ607290 Sequence
c1127	93.5	5.6	2176	9	AK123334	AK123334 Homo sapi	1200	93	5.6	7396	3	TGU62660	U62660 Toxoplasma
1128	93.5	5.6	2900	8	HVBIHORG	X03103 Barley gene	c1201	93	5.6	7931	6	CQ607289	CQ607289 Sequence
c1129	93.5	5.6	6108	3	CETRA3S1	U12516 Caenorhabdi	1202	93	5.6	8651	1	AY512410	AY512410 Listeria
1130	93.5	5.6	6166	6	AX699575	AX699575 Sequence	1203	93	5.6	8651	1	AY512489	AY512489 Listeria
c1131	93.5	5.6	7348	6	AX251090	AX251090 Sequence	1204	93	5.6	22045	2	AC020403	AC020403 Drosophil
c1132	93.5	5.6	8146	6	AR448064	AR448064 Sequence	1205	93	5.6	29176	8	AP001312	AP001312 Arabidops
c1133	93.5	5.6	9169	6	CQ413012	CQ413012 Sequence	1206	93	5.6	35307	2	AC014905	AC014905 Drosophil
c1134	93.5	5.6	9220	6	CQ492536	CQ492536 Sequence	c1207	93	5.6	78419	3	AC004639	AC004639 Drosophil
c1135	93.5	5.6	9220	6	CQ493387	CQ493387 Sequence	1208	93	5.6	82441	2	AC014491	AC014491 Drosophil
c1136	93.5	5.6	9416	9	HUMSEOX	L06237 Human micro	1209	93	5.6	86677	2	AC005646	AC005646 Drosophil
c1137	93.5	5.6	11474	1	AE014763	AE014763 Bifidobac	1210	93	5.6	107480	9	AL596094	AL596094 Human DNA
c1138	93.5	5.6	11917	6	AR454559	AR454559 Sequence	1211	93	5.6	110000	2	AL732359_06	Continuation (7 of
c1139	93.5	5.6	34570	6	AX695782	AX695782 Sequence	1212	93	5.6	125111	2	AC147938	AC147938 Ornithorh
c1140	93.5	5.6	34571	6	CQ868601	CQ868601 Sequence	1213	93	5.6	129037	8	OSJN00198	AL662296 Oryza sat
1141	93.5	5.6	35920	3	CELLC1	Z82277 Caenorhabdi	1214	93	5.6	131417	8	AP006050	AP006050 Oryza sat
c1142	93.5	5.6	60101	9	AL672207	AL672207 Human DNA	1215	93	5.6	139653	2	AP005890	AP005890 Oryza sat
1143	93.5	5.6	98771	2	AC025044	AC025044 Oryza sat	1216	93	5.6	145911	1	AP003014	AP003014 Mesorhizo
c1144	93.5	5.6	107252	8	AP004182	AP004182 Oryza sat	1217	93	5.6	160920	3	AC007580	AC007580 Drosophil
1145	93.5	5.6	110000	8	CR380949_3	Continuation (4 of	1218	93	5.6	161865	8	AP005912	AP005912 Oryza sat
c1146	93.5	5.6	113170	8	AP003804	AP003804 Oryza sat	c1219	93	5.6	162200	8	CNS08CCI	AL935066 Oryza sat
1147	93.5	5.6	119638	9	AC024575	AC024575 Homo sapi	1220	93	5.6	162329	2	CR381583	CR381583 Danio rer
1148	93.5	5.6	124162	2	AC141121	AC141121 Rattus no	1221	93	5.6	169689	3	AC008306	AC008306 Drosophil
c1149	93.5	5.6	124394	8	AC144645	AC144645 Medicago	c1222	93	5.6	176644	5	AL824708	AL824708 Zebrafish
1150	93.5	5.6	133475	9	AC006254	AC006254 Homo sapi	c1223	93	5.6	180498	3	AC009847	AC009847 Drosophil
c1151	93.5	5.6	142233	10	AC125129	AC125129 Mus muscu	1224	93	5.6	181244	2	AC146968	AC146968 Sus scrof
1152	93.5	5.6	145153	1	AY458649	AY458649 Unculture	c1225	93	5.6	198162	5	BX323985	BX323985 Zebrafish
1153	93.5	5.6	148433	9	AC012609	AC012609 Homo sapi	c1226	93	5.6	203042	2	AC116261	AC116261 Rattus no
1154	93.5	5.6	152397	8	AC027660	AC027660 Oryza sat	1227	93	5.6	208145	2	AC053504	AC053504 Homo sapi
1155	93.5	5.6	156897	2	AC018782	AC018782 Homo sapi	1228	93	5.6	209672	2	AL773584	AL773584 Danio rer
1156	93.5	5.6	173597	2	AC025749	AC025749 Homo sapi	c1229	93	5.6	235915	10	AC129606	AC129606 Mus muscu
c1157	93.5	5.6	190339	2	AC113876	AC113876 Rattus no	c1230	93	5.6	244978	2	AC128734	AC128734 Rattus no
1158	93.5	5.6	195982	2	AC121281	AC121281 Mus muscu	c1231	93	5.6	251021	2	AC129763	AC129763 Rattus no
c1159	93.5	5.6	203844	9	AC099667	AC099667 Homo sapi	c1232	93	5.6	251700	1	AP000062	AP000062 Aeropyrum
c1160	93.5	5.6	211624	10	AC114817	AC114817 Mus muscu	c1233	93	5.6	260045	2	AC116843	AC116843 Mus muscu
c1161	93.5	5.6	214146	2	AC096822	AC096822 Rattus no	1234	93	5.6	260091	2	AC134021	AC134021 Rattus no
1162	93.5	5.6	215895	2	AC121688	AC121688 Rattus no	c1235	93	5.6	265602	2	AC107184	AC107184 Rattus no
1163	93.5	5.6	217668	2	AC020561	AC020561 Homo sapi	1236	93	5.6	301129	3	AE003785	AE003785 Drosophil
1164	93.5	5.6	232406	2	AC146898	AC146898 Pongo pyg	c1237	93	5.6	301400	1	AP006578	AP006578 Gloeobact
1165	93.5	5.6	233830	2	AC073731	AC073731 Mus muscu	1238	92.5	5.6	926	3	AK116944	AK116944 Ciona int
1166	93.5	5.6	245476	2	AC098496	AC098496 Rattus no	1239	92.5	5.6	1185	6	AX534833	AX534833 Sequence
1167	93.5	5.6	277106	2	AC120959	AC120959 Rattus no	1240	92.5	5.6	1247	10	AY262758	AY262758 Mus muscu
1168	93.5	5.6	300029	8	AE017094	AE017094 Oryza sat	1241	92.5	5.6	1275	6	AX720123	AX720123 Sequence
c1169	93.5	5.6	305520	1	AE016780	AE016780 Pseudomon	1242	92.5	5.6	1572	6	AR548321	AR548321 Sequence
c1170	93.5	5.6	313800	1	SCO939114	AL939114 Streptomy	1243	92.5	5.6	1695	8	AK110525	AK110525 Oryza sat
1171	93.5	5.6	321250	1	SCO939111	AL939111 Streptomy	1244	92.5	5.6	1709	6	BD157677	BD157677 Primer fo
1172	93.5	5.6	346294	1	AP002999	AP002999 Mesorhizo	1245	92.5	5.6	1709	6	AX879145	AX879145 Sequence

1246	92.5	5.6	1709	9	AK0222463	AK022463 Homo sapi	1319	92	5.6	1500	4	BTA550060	AJ550060 Bos tauru
1247	92.5	5.6	1710	1	AF282221	AF282221 Listeria	1320	92	5.6	1542	3	AY071278	AY071278 Drosophil
1248	92.5	5.6	1872	5	IPJ00267	AJ000267 Ictalurus	c1321	92	5.6	1695	8	AK110525	AK110525 Oryza sat
1249	92.5	5.6	1990	8	AK107421	AK107421 Oryza sat	1322	92	5.6	1812	1	AF241531	AF241531 Listeria
1250	92.5	5.6	2101	10	BC006604	BC006604 Mus muscu	c1323	92	5.6	1986	8	AK068129	AK068129 Oryza sat
1251	92.5	5.6	2556	10	AY269789	AY269789 Mus muscu	1324	92	5.6	2044	8	AK070083	AK070083 Oryza sat
c1252	92.5	5.6	3548	8	AK119882	AK119882 Oryza sat	c1325	92	5.6	3175	3	BT001762	BT001762 Drosophil
1253	92.5	5.6	3606	10	AB107882	AB107882 Mus muscu	1326	92	5.6	3177	8	AB001030	AB001030 Humicola
c1254	92.5	5.6	3776	1	AF318069	AF318069 Nostoc pu	c1327	92	5.6	3425	8	AK073220	AK073220 Oryza sat
1255	92.5	5.6	4104	6	AR527843	AR527843 Sequence	1328	92	5.6	4138	5	XSMTK	X16891 Xiphophorus
1256	92.5	5.6	5500	4	AY212921	AY212921 Oryctolag	c1329	92	5.6	5087	6	CQ807144	CQ807144 Sequence
1257	92.5	5.6	5877	8	SCU17580	U17580 Saccharomyc	c1330	92	5.6	5087	6	CQ807204	CQ807204 Sequence
c1258	92.5	5.6	6113	6	AX344580	AX344580 Sequence	1331	92	5.6	5269	6	CQ579591	CQ579591 Sequence
1259	92.5	5.6	6551	1	LM0012345	AJ012345 Listeria	c1332	92	5.6	7740	6	CQ579590	CQ579590 Sequence
1260	92.5	5.6	8536	1	AY512402	AY512402 Listeria	1333	92	5.6	8490	5	XLU64442	U64442 Xenopus lae
c1261	92.5	5.6	9917	1	AE004558	AE004558 Pseudomon	1334	92	5.6	8651	1	AY512411	AY512411 Listeria
1262	92.5	5.6	22753	2	AC017598	AC017598 Drosophil	1335	92	5.6	9248	8	SCAF000227	AF000227 Secale ce
1263	92.5	5.6	29246	8	AP004947	AP004947 Lotus cor	c1336	92	5.6	11251	1	AE005560	AE005560 Escherich
c1264	92.5	5.6	32481	3	U21310	U21310 Caenorhabdi	c1337	92	5.6	11460	1	AE005066	AE005066 Halobacte
c1265	92.5	5.6	38573	2	AC017717	AC017717 Drosophil	1338	92	5.6	16951	1	MSU46844	U46844 Mycobacteri
c1266	92.5	5.6	39852	9	AC006128	AC006128 Homo sapi	c1339	92	5.6	56455	2	AC020278	AC020278 Drosophil
1267	92.5	5.6	43025	3	AY190948	AY190948 Drosophil	1340	92	5.6	60019	3	AC005650	AC005650 Drosophil
c1268	92.5	5.6	55972	1	AF386507	AF386507 Streptomy	c1341	92	5.6	66518	8	BX897672	BX897672 Neurospor
1269	92.5	5.6	82064	2	AC006937	AC006937 Drosophil	1342	92	5.6	80767	9	HS745E8	AL020998 Human DNA
1270	92.5	5.6	93134	8	BX908807	BX908807 Neurospor	1343	92	5.6	110000	2	AC146908_2	Continuation (3 of
1271	92.5	5.6	110000	2	BX005127_0	BX005127 Mus muscu	c1344	92	5.6	110000	2	LMFLCHR31_12	Continuation (13 o
1272	92.5	5.6	110000	8	CR382127_21	Continuation (22 o	1345	92	5.6	110000	8	CR382127_11	Continuation (12 o
c1273	92.5	5.6	110000	8	AE016817_10	Continuation (11 o	c1346	92	5.6	110000	8	CR382128_14	Continuation (15 o
1274	92.5	5.6	125596	10	AL662926	AL662926 Mouse DNA	1347	92	5.6	110000	10	AE008683_2	Continuation (3 of
1275	92.5	5.6	134006	2	AC124166	AC124166 Felis cat	c1348	92	5.6	130058	8	AC078840	AC078840 Oryza sat
c1276	92.5	5.6	134511	2	AC149927	AC149927 Strongylo	1349	92	5.6	131732	10	AF259071	AF259071 Mus muscu
c1277	92.5	5.6	145911	1	AP003014	AP003014 Mesorhizo	1350	92	5.6	143285	9	AL139423	AL139423 Human DNA
c1278	92.5	5.6	150155	8	AC097277	AC097277 Oryza sat	c1351	92	5.6	143721	9	AC117414	AC117414 Homo sapi
1279	92.5	5.6	153749	3	AC093098	AC093098 Drosophil	1352	92	5.6	147486	10	AL670276	AL670276 Mouse DNA
1280	92.5	5.6	163183	3	AC009842	AC009842 Drosophil	1353	92	5.6	155490	2	CR749749	CR749749 Danio rer
1281	92.5	5.6	170684	3	AC007578	AC007578 Drosophil	1354	92	5.6	158500	2	CR382340	CR382340 Danio rer
1282	92.5	5.6	171261	2	AC146349	AC146349 Zea mays	c1355	92	5.6	159579	8	AC106887	AC106887 Oryza sat
c1283	92.5	5.6	172988	2	AC123391	AC123391 Mus muscu	1356	92	5.6	165411	2	AC113480	AC113480 Mus muscu
1284	92.5	5.6	182897	3	AC092232	AC092232 Drosophil	1357	92	5.6	167059	10	AC124455	AC124455 Mus muscu
c1285	92.5	5.6	184357	2	AC073728	AC073728 Mus muscu	1358	92	5.6	167753	2	AC126039	AC126039 Mus muscu
c1286	92.5	5.6	197019	9	AC104435	AC104435 Homo sapi	c1359	92	5.6	170226	8	AP003450	AP003450 Oryza sat
c1287	92.5	5.6	198922	2	AC094540	AC094540 Rattus no	c1360	92	5.6	175448	3	AC099035	AC099035 Drosophil
c1288	92.5	5.6	203773	9	AC097369	AC097369 Homo sapi	1361	92	5.6	176129	10	AC141484	AC141484 Mus muscu
1289	92.5	5.6	209999	10	AL731711	AL731711 Mouse DNA	1362	92	5.6	176167	9	AC096656	AC096656 Homo sapi
1290	92.5	5.6	231676	2	AC134063	AC134063 Rattus no	c1363	92	5.6	177539	2	CR388413	CR388413 Danio rer
c1291	92.5	5.6	246199	2	AC119558	AC119558 Rattus no	c1364	92	5.6	179749	2	CR392354	CR392354 Danio rer
c1292	92.5	5.6	248871	2	AC094352	AC094352 Rattus no	c1365	92	5.6	184395	2	AC118475	AC118475 Mus muscu
c1293	92.5	5.6	259834	2	AC128503	AC128503 Rattus no	c1366	92	5.6	187323	10	AC123055	AC123055 Mus muscu
c1294	92.5	5.6	270050	1	AL591977	AL591977 Listeria	c1367	92	5.6	191438	3	AC008351	AC008351 Drosophil
c1295	92.5	5.6	272258	2	AC123370	AC123370 Rattus no	1368	92	5.6	203784	2	AC116498	AC116498 Mus muscu
c1296	92.5	5.6	289893	3	AE003576	AE003576 Drosophil	1369	92	5.6	211336	10	AC139886	AC139886 Mus muscu
c1297	92.5	5.6	295050	1	AL591982	AL591982 Listeria	1370	92	5.6	215168	2	AC124589	AC124589 Mus muscu
c1298	92.5	5.6	299175	1	AP005023	AP005023 Streptomy	c1371	92	5.6	219827	2	AC127357	AC127357 Mus muscu
c1299	92.5	5.6	300029	1	AE017178	AE017178 Porphyrom	c1372	92	5.6	227442	2	AC111515	AC111515 Rattus no
c1300	92.5	5.6	300658	1	AE017313	AE017313 Desulfovi	c1373	92	5.6	231008	2	AC129166	AC129166 Rattus no
1301	92.5	5.6	300704	1	AE017316	AE017316 Desulfovi	1374	92	5.6	231989	10	AL805897	AL805897 Mouse DNA
c1302	92.5	5.6	301150	1	AP004602	AP004602 Oceanobac	c1375	92	5.6	235407	2	AC094280	AC094280 Rattus no
c1296	92.5	5.6	289893	3	AE003576	AE003576 Drosophil	1376	92	5.6	236907	2	AC103254	AC103254 Rattus no
c1297	92.5	5.6	295050	1	AL591982	AL591982 Listeria	c1376	92	5.6	261476	2	AC129130	AC129130 Rattus no
c1298	92.5	5.6	299175	1	AP005023	AP005023 Streptomy	c1371	92	5.6	219827	2	AC127357	AC127357 Mus muscu
c1299	92.5	5.6	300029	1	AE017178	AE017178 Porphyrom	c1372	92	5.6	227442	2	AC111515	AC111515 Rattus no
c1300	92.5	5.6	300658	1	AE017313	AE017313 Desulfovi	c1373	92	5.6	231008	2	AC129166	AC129166 Rattus no
1301	92.5	5.6	300704	1	AE017316	AE017316 Desulfovi	1374	92	5.6	231989	10	AL805897	AL805897 Mouse DNA
c1302	92.5	5.6	301150	1	AP004602	AP004602 Oceanobac	c1375	92	5.6	235407	2	AC094280	AC094280 Rattus no
c1296	92.5	5.6	289893	3	AE003576	AE003576 Drosophil	1376	92	5.6	236907	2	AC103254	AC103254 Rattus no
c1297	92.5	5.6	295050	1	AL591982	AL591982 Listeria	c1376	92	5.6	261476	2	AC129130	AC129130 Rattus no
c1298	92.5	5.6	299175	1	AP005023	AP005023 Streptomy	c1371	92	5.6	219827	2	AC127357	AC127357 Mus muscu
c1299	92.5	5.6	300029	1	AE017178	AE017178 Porphyrom	c1372	92	5.6	227442	2	AC111515	AC111515 Rattus no
c1300	92.5	5.6	300658	1	AE017313	AE017313 Desulfovi	c1373	92	5.6	231008	2	AC129166	AC129166 Rattus no
1301	92.5	5.6	300704	1	AE017316	AE017316 Desulfovi	1374	92	5.6	231989	10	AL805897	AL805897 Mouse DNA
c1302	92.5	5.6	301150	1	AP004602	AP004602 Oceanobac	c1375	92	5.6	235407	2	AC094280	AC094280 Rattus no
c1296	92.5	5.6	289893	3	AE003576	AE003576 Drosophil	1376	92	5.6	236907	2	AC103254	AC103254 Rattus no
c1297	92.5	5.6	295050	1	AL591982	AL591982 Listeria	c1376	92	5.6	261476	2	AC129130	AC129130 Rattus no
c1298	92.5	5.6	299175	1	AP005023	AP005023 Streptomy	c1371	92	5.6	219827	2	AC127357	AC127357 Mus muscu
c1299	92.5	5.6	300029	1	AE017178	AE017178 Porphyrom	c1372	92	5.6	227442	2	AC111515	AC111515 Rattus no
c1300	92.5	5.6	300658	1	AE017313	AE017313 Desulfovi	c1373	92	5.6	231008	2	AC129166	AC129166 Rattus no
1301	92.5	5.6	300704	1	AE017316	AE017316 Desulfovi	1374	92	5.6	231989	10	AL805897	AL805897 Mouse DNA
c1302	92.5	5.6	301150	1	AP004602	AP004602 Oceanobac	c1375	92	5.6	235407	2	AC094280	AC094280 Rattus no
c1296	92.5	5.6	289893	3	AE003576	AE003576 Drosophil	1376	92	5.6	236907	2	AC103254	AC103254 Rattus no
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c1299	92.5	5.6	300029	1	AE017178	AE017178 Porphyrom	c1372	92	5.6	227442	2	AC111515	AC111515 Rattus no
c1300	92.5	5.6	300658	1	AE017313	AE017313 Desulfovi	c1373	92	5.6	231008	2	AC129166	AC129166 Rattus no
1301	92.5	5.6	300704	1	AE017316	AE017316 Desulfovi	1374	92	5.6	231989	10	AL805897	AL805897 Mouse DNA
c1302	92.5	5.6	301150	1	AP004602	AP004602 Oceanobac	c1375	92	5.6	235407	2	AC094280	AC094280 Rattus no
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1402	1402	91.5	5.5	1736	1	AB102689	D88258 Listeria mo
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1418	1418	91.5	5.5	2377	5	AJ719666	AF005735 Marburg v
1419	1419	91.5	5.5	2438	3	DROTROIIN	L02115 Frog integu
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C1478	91.5	5.5	129231	9	AC092265	AC092265 Homo sapi
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1489	91.5	5.5	188555	10	AC122417	AC122417 Mus muscu
C1490	91.5	5.5	188655	2	BX324137	BX324137 Danio rer
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1492	91.5	5.5	193714	10	AC007518	AC007518 Mus muscu
C1493	91.5	5.5	197698	8	BX908809	BX908809 Neurospor
1494	91.5	5.5	200219	2	AC117312	AC117312 Rattus no
1495	91.5	5.5	202881	2	AC115947	AC115947 Mus muscu
1496	91.5	5.5	204278	10	AC124507	AC124507 Mus muscu
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ALIGNMENTS

RESULT 1	AF127670	AF127670	1285 bp	mRNA	linear	PRI 13-OCT-2000
LOCUS	Homo sapiens	hyaluronic acid receptor (HAR)	mrna	complete cds.		
DEFINITION	AF127670	AF127670	1285 bp	mRNA	linear	PRI 13-OCT-2000
ACCESSION	AF127670	AF127670	1285 bp	mRNA	linear	PRI 13-OCT-2000
VERSION	AF127670.2	GI:10800121				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 1285)					
TITLE	Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.					
JOURNAL	HAR: a novel homolog of CD44 and putative hyaluronic acid receptor encoded by a gene on human chromosome 11p15					
REFERENCE	Unpublished					
AUTHORS	2 (bases 1 to 1009)					
TITLE	Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.					
JOURNAL	Direct Submission					
REFERENCE	Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA					
AUTHORS	3 (bases 1 to 1285)					
TITLE	Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.					
JOURNAL	Direct Submission					
REFERENCE	Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA					
AUTHORS	Sequence update by submitter					
TITLE	On Oct 13, 2000 this sequence version replaced gi:5732667.					
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ORIGIN

Alignment Scores:
Pred. No.: 2.8e-127 Length: 1285
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AF127670 (1-1285)

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Db 181 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGTGTCTATGCAGAATTATGGGG 240
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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RESULT 2
AX136227 1755 bp DNA linear PAT 30-MAY-2001
LOCUS AX136227
DEFINITION Sequence 149 from Patent EP1067182.
ACCESSION AX136227
VERSION AX136227.1 GI:14272635
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 149 10-JAN-2001;
Helix Research Institute (JP)
FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 4.17e-127 Length: 1755
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x AX136227 (1-1755)

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Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	921	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	980
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	981	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAAGGAAATGATCGAAACC	1040
Qy	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1041	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1100
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1101	GATAAAAACCCAGAGAGTCCAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT	1160
Qy	321	GluVal	322
Db	1161	GAAGTT	1166
RESULT	3		
BD123566			
LOCUS	BD123566	1755 bp	DNA linear PAT 18-SEP-2002
DEFINITION	Secretory protein or membrane protein.		
ACCESSION	BD123566		
VERSION	BD123566.1	GI:23218511	
KEYWORDS	JP 2002017376-A/75.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1755) Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: JP 2002017376-A 75 22-JAN-2002; HELIX RESEARCH INSTITUTE		
COMMENT	OS Homo sapiens (human) PN JP 2002017376-A/75 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253173 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU PI SUGIYAMA, PI KOJI HAYASHI PC		
FEATURES	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10, PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC Secretory protein or membrane protein FH Key Location/Qualifiers FT CDS (201)..(1166).		
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Score:	1657.00	Matches:	322
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Best Local Similarity:	100.00%	Mismatches:	0
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Db	201	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG	260
Qy	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	261	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	320
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	321	ATCACCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	380
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	381	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	440
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	441	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT	500
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	501	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG	560
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	561	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT	620
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	621	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	680
Qy	161	GlupheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180


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Db      681 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC 740
Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
Db      741 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 800
Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db      801 TGTGTCACAGAAGTTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 860
Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||
Db      861 GAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGTCTG 920
Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db      921 CTAGTGCTTGCTCTCCTCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 980
Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Qy      321 GluVal 322
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Db      1161 GAAGTT 1166

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AK075443
LOCUS
DEFINITION
Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar
to Homo sapiens lymphatic endothelium-specific hyaluronan receptor
LYVE-1 mRNA.
ACCESSION
AK075443
VERSION
AK075443.1 GI:22761535
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
HRI human cDNA sequencing project
2
Unpublished
2 (bases 1 to 1755)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library consturction: Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
FEATURES
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Pred. No.: 4.17e-127 Length: 1755
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AK075443 (1-1755)
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Db      261 GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 320
Qy      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Qy      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db      381 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGAGCT 440
Qy      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db      441 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGGTCATCTCTAGGATT 500
Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Qy      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db      561 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 620
Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
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Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||
Db      681 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 740
Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db      741 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 800
Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db      801 TGTGTCACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 860
Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||
Db      861 GAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 920
Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||
Db      921 CTAGTGCTTGCTCTCCTCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 980
Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Qy 321 GluVal 322

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RESULT 5

BD222718

LOCUS BD222718 2029 bp DNA linear PAT 17-JUL-2003

DEFINITION Human signal peptide-containing protein.

ACCESSION BD222718

VERSION BD222718.1 GI:33032488

KEYWORDS JP 2002519030-A/64.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2029)

REFERENCE Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.

AUTHORS Human signal peptide-containing protein

TITLE Patent: JP 2002519030-A 64 02-JUL-2002;

JOURNAL INCYTE PHARMACEUTICALS INC

COMMENT OS Homo sapiens (human)

PN JP 2002519030-A/64

PD 02-JUL-2002

PF 25-JUN-1999 JP 2000557363

PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER, PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE, PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00, PC A61P25/00, PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19, PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC C12N15/00, PC A61K37/02,C12N5/00

CC Incyte Clone No: 3044710

FH Key Location/Qualifiers

FT source 1..2029

FT /organism='Homo sapiens (human)'

FEATURES

source Location/Qualifiers

1..2029

/organism="Homo sapiens"

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ORIGIN

Alignment Scores:

Pred. No.: 5.03e-127 Length: 2029

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x BD222718 (1-2029)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 183 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTCGACACGAGGCTCCTG 242

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 243 GTCCAAGGCTCTTTCGTCGAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 302

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 303 ATCACCCCTGTGAGCAAAAAGGGCAACACGACGAGCTGAATTTACAGAAAGCTAAGGAGCC 362

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 363 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgile 100

Db 423 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCACTCTTAGGATT 482

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 483 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTTGGAAGGTTCCAGTG 542

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140

Db 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 602

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 603 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAAACTGCAACAACA 662

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 663 GAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722

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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 843 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG 902

Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 903 CTAGTGCTTGCTCTCTCTCTCTTCTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 962

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACC 1022

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1023 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT 1082

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Db 1083 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1142

Qy 321 GluVal 322

Db 1143 GAAGTT 1148

RESULT 6

AR204700

LOCUS AR204700 2029 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 13 from patent US 6368794.

ACCESSION AR204700

VERSION AR204700.1 GI:21502094

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2029)

AUTHORS Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.

TITLE Detection of altered expression of genes regulating cell proliferation

JOURNAL Patent: US 6368794-A 13 09-APR-2002;

FEATURES Location/Qualifiers

[illegible]

Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
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Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	572	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	631
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	632	CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT	691
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPPropheVal	220
Db	692	TGtGTACAGAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	751
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	752	GAATAATAAGCAGCATTCAAGATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG	811
Qy	241	LeuValIleuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	812	CTAGTGTCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGATTTTGTATGTCAA	871
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	872	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	931
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	932	AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT	991
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
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LOCUS			
DEFINITION	BD172392	2372 bp DNA linear	PAT 18-FEB-2003
		Secreted and transmembrane polypeptides and nucleic acids encoding	
		the same.	
ACCESSION	BD172392		
VERSION	BD172392.1	GI:28413692	
KEYWORDS	JP 2002223786-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	1	(bases 1 to 2372)	
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002223786-A 165 13-AUG-2002;		
COMMENT	GENENTECH INC		
	OS Homo sapiens (human)		
	PN JP 2002223786-A/165		
	PD 13-AUG-2002		
	PF 18-DEC-2001	JP 2001385135	
	PR 17-SEP-1997	US 60/059115,17-SEP-1997	US 60/059184 PR
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	17-SEP-1997	US 60/059119,18-SEP-1997	US 60/059263 PR
	18-SEP-1997	US 60/059266,15-OCT-1997	US 60/062125 PR
	17-OCT-1997	US 60/062287,17-OCT-1997	US 60/062285 PR
	21-OCT-1997	US 60/063486,24-OCT-1997	US 60/062816 PR
	24-OCT-1997	US 60/062814,24-OCT-1997	US 60/063127 PR
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	24-OCT-1997	US 60/063045,24-OCT-1997	US 60/063128 PR

27-OCT-1997	US	60/063329,27-OCT-1997	US	60/063327	PR
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29-OCT-1997	US	60/063734,29-OCT-1997	US	60/063738	PR
29-OCT-1997	US	60/063704,29-OCT-1997	US	60/063435	PR
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29-OCT-1997	US	60/063732,31-OCT-1997	US	60/064103	PR
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24-NOV-1997	US	60/066770,24-NOV-1997	US	60/066511	PR
24-NOV-1997	US	60/066453,25-NOV-1997	US	60/066840	PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI JIAN ZHENG,					
PI JEAN YUAN					
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,					
PC					
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Db	160	ATGCCCAGGTGCTTCAGCCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG	219		
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40		
Db	220	GTCCAAGGCTCTTTGCGIGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279		
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60		
Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	339		
Qy	61	CysArgLeuLeuGlyLeuSerLysAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80		
Db	340	TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAAGTGAACAGCCTTGAAAGCT	399		
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100		
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGTCATCTCTAGGATT	459		
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120		
Db	460	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTG	519		
Qy	121	SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140		
Db	520	AGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACTTGGACTTAACCTCGTGCA	579		

Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
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Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
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Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCystyrVallLys	260
Db	880	CTAGTGCTTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939
Qy	261	ArgTyrVallLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
Qy	281	LysValVallLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAGACT	1119
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LOCUS	BD172711	2372 bp	DNA linear PAT 18-FEB-2003
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD172711		
VERSION	BD172711.1	GI:28414015	
KEYWORDS	JP 2002238586-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238586-A 165 27-AUG-2002; GENENTECH INC		
COMMENT	OS Homo sapiens (human)		
	PN JP 2002238586-A/165		
	PD 27-AUG-2002		
	PF 18-DEC-2001	JP 2001385205	
	PR 17-SEP-1997	US 60/059115,17-SEP-1997	US 60/059184 PR
	17-SEP-1997	US 60/059122,17-SEP-1997	US 60/059117 PR
	17-SEP-1997	US 60/059113,17-SEP-1997	US 60/059121 PR
	17-SEP-1997	US 60/059119,18-SEP-1997	US 60/059263 PR
	18-SEP-1997	US 60/059266,15-OCT-1997	US 60/062125 PR
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI					
JIAN ZHENG,					
PI JEAN YUAN					
PC	C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,				
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CC	Secreted and transmembrane polypeptides and nucleic CC acids encoding the same				
FH	Key	Location/Qualifiers			
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ORIGIN					
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Score:	1657.00	Matches:	322		
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Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60		
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Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100		
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTAGGATT	459		
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120		
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTGATTTTGGAAGGTTCCAGTG	519		
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140		

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACCTGGACTAACTCGTGCAAT 579

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LOCUS

DEFINITION BD173030 2372 bp DNA linear PAT 18-FEB-2003

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD173030

VERSION BD173030.1 GI:28414336

KEYWORDS JP 2002238587-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002238587-A 165 27-AUG-2002;

COMMENT GENENTECH INC

OS Homo sapiens (human)

PN JP 2002238587-A/165

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385248

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

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27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC

C12N15/02,

PC

C12P21/02,C12P21/08// (C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC

(C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted

and transmembrane polypeptides and nucleic CC acids encoding the

same

FEATURES

source

FT

Key Location/Qualifiers

1. .2372

/organism='Homo sapiens (human)'.
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ORIGIN

Alignment Scores:

Pred. No.: 6.14e-127 Length: 2372

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x BD173030 (1-2372)

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Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAAGCTAAGGAGGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
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Db 400 ACCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGTCATCTCTAGGATT 459

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValleulleTrpLysValProVal 120
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Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 519

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Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACA 639

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Db 700 CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 820 GAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGTCTG 879

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Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 1060 GATAAAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCGTGGAAAGCT 1119

Qy 321 GluVal 322
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Db 1120 GAAGTT 1125

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BD173349

LOCUS BD173349 2372 bp DNA linear PAT 18-FEB-2003

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD173349

VERSION BD173349.1 GI:284114660

KEYWORDS JP 2002238588-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002238588-A 165 27-AUG-2002; GENENTECH INC

COMMENT OS Homo sapiens (human)
PN JP 2002238588-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/435,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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PC (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
Secreted and transmembrane polypeptides and nucleic CC acids
encoding the same
FH Key Location/Qualifiers
FT source 1..2372 /organism='Homo sapiens (human)'.
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source 1..2372 /organism="Homo sapiens"
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/db_xref="taxon:9606"

FEATURES

ORIGIN

Alignment Scores:
Pred. No.: 6.14e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x BD173349 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 160 ATGCCCAGGTGCTTCAGCTGGTGTGCTTCTCACITTCATCTGGACCACGAGGCTCCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db 220 GTCCAAGGCTCTTTGGCTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db 280 ATCACCCCTTGTGAGCAAAAAGGGCGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 340 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 399

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGAGATTCTGTGTCATCTCTAGGATT 459

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 460 AGCCCAACCCCAAGTGTGGAAAAAATGGGGTGGGTGCTGATTTTGAAGGTTCCAGTG 519

Qy 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
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Db 520 ACCCGACAGTTTGCAGCCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 579

Db 1120 GAAGTT 1125

RESULT 14
AR439125

LOCUS AR439125 2372 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 200 from patent US 6664376.

ACCESSION AR439125

VERSION AR439125.1 GI:42664974

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6664376-A 200 16-DEC-2003;

FEATURES Location/Qualifiers

source 1. .2372

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 6.14e-127 Length: 2372

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x AR439125 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGCC 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCTGTGAGCAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATGGATTCTGTGATCTCTAGGATT 459

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 519

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTGGACTAACTCGTGCAAT 579

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAATTATCACCCAAAGATCCATATTCACACTCAAACTGCAACACAAACAACA 639

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

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Db 700 CCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACAGAGAAGTTTTTATGAAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

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Db 1120 GAAGTT 1125

RESULT 15

AR473145

LOCUS AR473145 2372 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 200 from patent US 6686451.

ACCESSION AR473145

VERSION AR473145.1 GI:42708520

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Mather,J.P., Williams,P.M. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6686451-A 200 03-FEB-2004;

FEATURES Location/Qualifiers

source 1. .2372

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 6.14e-127 Length: 2372

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DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x AR473145 (1-2372)

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Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTATGAGGAGGCTGAGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

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Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTGGACTAACTCGTGCAAT 579

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

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QY	81	SerpheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValileSerArgIle	100
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Db	760	TGTGTACAGAAAGTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTTGTCTCTCTCTTTGGTGCTGCAGTGGTCTTTGGATTTTGTCTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 19:02:58 ; Search time 3740.72 Seconds
 (without alignments)
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 Xgapop 10.0 , Xgapext 0.5
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
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U52179 Rattus norv							
U46957 Rattus norv							
AF065147 Rattus no							
BC061531 Rattus no							
AF332869 Anas plat							
M27129 Mouse CD44							
M30655 Mouse phago							
X66081 M.musculus							
X66082 M.musculus							
AY029553 Anas plat							
X66084 M.musculus							
M33827 Hamster hya							
U10881 Mesocricetu							
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AF045939 Ceratothe							
AR365492 Sequence							
M22452 Baboon lymph							
AX939196 Sequence							
BD077623 5'EST of							
CQ875295 Sequence							
AJ251595 Homo sapi							
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CQ766842 Sequence							
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91	197	17.5	1794	9	HUMCD44B	M59040 Human cell	164	127.5	11.3	1985	6	AR439135	AR439135 Sequence
92	197	17.5	2035	5	AF153205	AF153205 Gallus ga	165	127.5	11.3	1985	6	AR473155	AR473155 Sequence
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96	196.5	17.5	2097	6	AX824989	AX824989 Sequence	169	127.5	11.3	1985	6	AX697621	AX697621 Sequence
97	196.5	17.5	2100	6	AX056982	AX056982 Sequence	170	127.5	11.3	1985	6	BD075542	BD075542 Secretory
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101	196	17.4	1083	6	AX824985	AX824985 Sequence	174	127.5	11.3	2558	9	AF229053	AF229053 Homo sapi
102	196	17.4	1339	9	AY101193	AY101193 Homo sapi	175	127.5	11.3	2868	10	RNALPBRE	X79881 R.norvegicu
103	196	17.4	1356	9	BC067348	BC067348 Homo sapi	176	127.5	11.3	3077	9	AF228710	AF228710 Homo sapi
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106	196	17.4	5165	6	CQ413028	CQ413028 Sequence	179	127.5	11.3	3275	9	BC009117	BC009117 Homo sapi
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124	145.5	12.9	834	9	HSA419936	AJ419936 Homo sapi	196	125.5	11.2	2160	6	AX748299	AX748299 Sequence
125	145.5	12.9	1430	9	BC030205	BC030205 Homo sapi	197	125.5	11.2	2160	9	AK093774	AK093774 Homo sapi
126	145.5	12.9	1481	4	AF314813	AF314813 Sus scrof	198	125.5	11.2	2780	10	AF098460	AF098460 Mus muscu
127	145.5	12.9	12307	5	CHKPRL	D13542 Chicken mRN	199	125.5	11.2	4738	10	BC066853	BC066853 Mus muscu
128	145	12.9	466	6	CQ713460	CQ713460 Sequence	200	125.5	11.2	7870	9	BSA275213	AJ275213 Homo sapi
129	145	12.9	834	9	HSA421518	AJ421518 Homo sapi	201	125	11.1	201	11	BV206501	BV206501 sqnm22108
130	145	12.9	1414	6	AR063905	AR063905 Sequence	202	125	11.1	1414	6	AX336169	AX336169 Sequence
131	145	12.9	1414	6	AR144434	AR144434 Sequence	203	125	11.1	1414	9	HUMTSG6A	M31165 Human tumor
132	145	12.9	1414	6	AR281307	AR281307 Sequence	204	124.5	11.1	2430	10	AF139572	AF139572 Mus muscu
133	144	12.8	1605	10	MMU83903	U83903 Mus musculu	205	124.5	11.1	7136	6	CQ716466	CQ716466 Sequence
134	144	12.8	1616	10	BC021155	BC021155 Mus muscu	206	124.5	11.1	7909	9	D87433	D87433 Homo sapien
135	143	12.7	6452	5	CHKSPCP	L21913 Chicken cho	207	124.5	11.1	7916	9	AB052956	AB052956 Homo sapi
136	143	12.7	6477	5	CHKAGGRECA	M88101 White legho	208	124	11.0	1682	5	CR762351	CR762351 Xenopus t
137	140	12.4	3911	10	BC031166	BC031166 Mus muscu	209	124	11.0	249541	2	AC095672	AC095672 Rattus no
138	140	12.4	7931	10	AF290914	AF290914 Mus muscu	210	124	11.0	249774	2	AC126196	AC126196 Rattus no
c 139	140	12.4	208621	2	AC150078	AC150078 Gallus ga	211	123	10.9	2116	4	AF060459	AF060459 Bos tauru
140	139.5	12.4	7104	4	CFU65989	U65989 Canis famil	212	123	10.9	4040	5	AF325324	AF325324 Xenopus l
141	139	12.4	1608	9	AKI29808	AKI29808 Homo sapi	213	123	10.9	5077	4	AF060458	AF060458 Bos tauru
142	139	12.4	6597	5	GGU78555	U78555 Gallus gall	214	123	10.9	7330	4	AF060457	AF060457 Bos tauru
143	138.5	12.3	1411	6	AX202114	AX202114 Sequence	215	123	10.9	10291	4	AF060456	AF060456 Bos tauru
144	137	12.2	1406	4	RABFS4EA	M86381 Oryctolagus	216	122	10.8	1183	4	RABAGGRECA	L38480 Oryctolagus
145	137	12.2	6939	10	RATPGCA	J03485 Rat alterna	217	121.5	10.8	959	6	CQ723845	CQ723845 Sequence
146	135.5	12.0	3076	10	BC052032	BC052032 Mus muscu	218	121	10.8	1587	6	AR432563	AR432563 Sequence
147	135.5	12.0	3153	10	MMBREVGEN	X87096 M.musculus	219	121	10.8	1587	6	BD078622	BD078622 Human pro
148	135	12.0	7382	10	MUSAGGRECA	L07049 Mus musculu	220	121	10.8	1704	9	AY007241	AY007241 Homo sapi
149	133.5	11.9	1734	6	AR220822	AR220822 Sequence	c 221	121	10.8	155548	2	CR848047	CR848047 Danio rer
150	133	11.8	1683	10	RNU46958	U46958 Rattus norv	222	120.5	10.7	3259	4	BTBREV	X75887 B.taurus Br
							223	120.5	10.7	5614	5	AB119257	AB119257 Danio rer

224	120	10.7	2954	5	BC046259	BC046259 Xenopus l	110	9.8	271812	2	BX530095	BX530095 Danio rer
225	120	10.7	4069	5	BC078043	BC078043 Xenopus l	110	9.8	292007	2	AC128762	AC128762 Rattus no
c 226	119.5	10.6	221762	2	BX908731	BX908731 Danio rer	299	9.7	1406	10	AB049056	AB049056 Rattus no
227	119	10.6	480	10	MMLINK4	AF137277 Mus muscu	300	9.7	5191	6	I56080	I56080 Sequence 1
228	118.5	10.5	5923	9	HSU26555	U26555 Human versi	301	9.7	5191	10	RATNCAN	M97161 Rattus norv
229	118.5	10.5	11185	6	CQ776629	CQ776629 Sequence	302	9.7	6310	9	AF026547	AF026547 Homo sapi
230	118.5	10.5	11185	6	AX330530	AX330530 Sequence	303	9.7	6312	6	CQ727544	CQ727544 Sequence
231	118.5	10.5	11185	6	AX410665	AX410665 Sequence	304	9.7	110000	2	AC096220_0	AC096220 Rattus no
232	118.5	10.5	11185	9	HSU16306	U16306 Human chond	305	9.7	183682	9	AL133330_	AL133330 Human DNA
233	118.5	10.5	12319	6	AX281831	AX281831 Sequence	306	9.7	232127	2	AC113724	AC113724 Rattus no
234	118.5	10.5	164846	2	AC107727	AC107727 Mus muscu	307	9.7	235684	2	AC129422	AC129422 Rattus no
235	118	10.5	2318	10	MUSPGM3B	D32040 Mouse pgM3	308	9.7	272258	2	AC123370	AC123370 Rattus no
236	118	10.5	7375	6	CQ777492	CQ777492 Sequence	309	9.6	103201	2	AC149525	AC149525 Xenopus t
237	118	10.5	7375	10	MUSPGMV	D16263 Mus musculu	310	9.6	317	10	RATLNKP4	M22339 Rat link pr
238	117	10.5	10427	10	MUSPGM	D28599 Mouse mRNA	311	9.6	685	4	AY226857S06	AY226862 Bos tauru
239	117	10.4	209852	2	AC151363	AC151363 Gasterost	312	9.6	1319	10	AY269788	AY269788 Mus muscu
240	116	10.3	1910	5	CHKLNKPA	M13212 Chicken car	313	9.6	1320	4	AF529268	AF529268 Ovis arie
241	116	10.3	8444	6	AX686192	AX686192 Sequence	314	9.6	1433	10	AY262757	AY262757 Mus muscu
242	115.5	10.3	1626	9	AK090712	AK090712 Homo sapi	315	9.6	1492	9	HSCRTL115	X78076 H.sapiens C
243	115.5	10.3	1630	9	BC029864	BC029864 Homo sapi	316	9.6	1492	9	HSLINKC	X17405 Human mRNA
244	115.5	10.3	8069	9	AK160380	AK160380 Homo sapi	317	9.6	1493	6	CQ728128	CQ728128 Sequence
245	115.5	10.3	197370	9	AC103982	AC103982 Homo sapi	318	9.6	1721	9	BC057808	BC057808 Homo sapi
246	115	10.2	1249	10	BC022136	BC022136 Mus muscu	319	9.6	1759	9	HSU43328	U43328 Human link
247	114.5	10.2	1736	10	AB049055	AB049055 Mus muscu	320	9.6	68574	2	AC113212	AC113212 Homo sapi
248	114	10.1	1794	9	AB049054	AB049054 Homo sapi	321	9.6	164286	9	AC020899	AC020899 Homo sapi
c 249	114	10.1	192662	10	AC134397	AC134397 Mus muscu	322	9.6	167872	2	AC007554	AC007554 Homo sapi
250	114	10.1	272888	2	AC139198	AC139198 Mus muscu	323	9.6	226416	2	AC103519	AC103519 Rattus no
c 251	113.5	10.1	64675	2	BX322628_3	Continuation (4 of	324	9.6	247266	2	AC110520	AC110520 Mus muscu
c 252	113.5	10.1	110000	2	BX322628_2	Continuation (3 of	325	9.6	1335	4	SSLINK	Y00165 Sus scrofa
253	113.5	10.1	170883	9	AC067805	AC067805 Homo sapi	326	9.5	427	5	CHKLNKPA3	M35037 Chicken car
254	113.5	10.1	218103	5	BX465199	BX465199 Zebrafish	327	9.5	1400	6	AR036272	AR036272 Sequence
255	113.5	10.1	271812	2	BX530095	BX530095 Danio rer	328	9.5	1400	6	AR087156	AR087156 Sequence
256	113	10.0	1925	9	BC050524	BC050524 Homo sapi	329	9.5	1520	6	I44674	I44674 Sequence 1
257	113	10.0	2087	6	AX338947	AX338947 Sequence	330	9.5	1520	10	RNBEHAB	Z28366 R.norvegicu
258	113	10.0	2087	9	HUMPGH3A	D32039 Human pgH3	331	9.5	1851	6	AX302626	AX302626 Sequence
259	113	10.0	8224	6	CQ728127	CQ728127 Sequence	332	9.5	2011	6	AX149447	AX149447 Sequence
260	113	10.0	8224	6	AR362654	AR362654 Sequence	333	9.5	5259	10	MMNEUROCM	X84727 M.musculus
261	113	10.0	8224	6	AX658277	AX658277 Sequence	334	9.5	7147	10	BC065118	BC065118 Mus muscu
262	113	10.0	8224	9	HSVERS	X15998 H.sapiens m	335	9.5	8340	11	BV178350	BV178350 sgnml0003
263	113	10.0	136886	2	AC149262	AC149262 Sphoeroid	336	9.5	112830	2	AC151678	AC151678 Gallus ga
264	113	10.0	138091	2	AC113583	AC113583 Tetradon	337	9.5	164512	9	AL365181	AL365181 Human DNA
c 265	113	10.0	199942	2	AC150038	AC150038 Gallus ga	338	9.5	2447	10	AF060879	AF060879 Rattus no
266	112.5	10.0	3260	6	AX686401	AX686401 Sequence	339	9.5	77928	2	AC149263	AC149263 Sphoeroid
267	112.5	10.0	3260	9	AF160476	AF160476 Homo sapi	340	9.5	150209	2	CR759744	CR759744 Danio rer
268	112.5	10.0	3591	6	CQ719622	CQ719622 Sequence	341	9.4	203159	10	AC137525	AC137525 Mus muscu
269	112.5	10.0	4492	9	AY227444	AY227444 Homo sapi	342	9.4	346406	10	BX883045	BX883045 Rattus no
270	112.5	10.0	4575	9	AK024503	AK024503 Homo sapi	343	9.4	614	9	AB049062S7	AB049061 Homo sapi
271	112.5	10.0	5604	9	AK074051	AK074051 Homo sapi	344	9.4	1308	6	BD231671	BD231671 31 human
272	112.5	10.0	8214	9	AB052958	AB052958 Homo sapi	345	9.4	193188	10	AL844155	AL844155 Mouse DNA
273	112.5	10.0	8251	9	AY311388	AY311388 Homo sapi	346	9.4	229628	2	BX908768	BX908768 Mus muscu
274	112.5	10.0	8266	9	HSA295695	AJ295695 Homo sapi	347	9.3	723	4	AY226857S10	AY226866 Bos tauru
275	112	10.0	340	6	CQ704239	CQ704239 Sequence	348	9.3	1941	4	BTU02292	U02292 Bos taurus
276	112	10.0	2026	5	BC068325	BC068325 Danio rer	349	9.3	36800	9	AC003110	AC003110 Human DNA
c 277	112	10.0	79444	2	AC150153	AC150153 Gallus ga	350	9.3	43185	9	AC138430	AC138430 Homo sapi
c 278	112	10.0	143178	2	AC150117	AC150117 Gallus ga	351	9.3	247266	2	AC110520	AC110520 Mus muscu
279	112	10.0	166863	2	AC150140	AC150140 Gallus ga	352	9.3	248817	2	AC096230	AC096230 Rattus no
280	112	10.0	176022	2	BX294110	BX294110 Danio rer	353	9.3	189608	5	AL929208	AL929208 Zebrafish
281	112	10.0	208621	2	AC150078	AC150078 Gallus ga	354	9.2	231	10	S73719S2	S73720 aggregcan=ag
c 282	112	10.0	232749	2	CR354535	CR354535 Danio rer	355	9.2	231	10	S73721S2	S73722 aggregcan=ag
c 283	111.5	9.9	226416	2	AC103519	AC103519 Rattus no	356	9.2	484	9	AF098641	AF098641 Homo sapi
c 284	111.5	9.9	230817	2	AC106909	AC106909 Rattus no	357	9.2	53580	5	AC096866	AC096866 Takifugu
285	111	9.9	1478	4	ECCRTLIG	X78077 Equus cabal	358	9.2	1310	3	AK173560	AK173560 Ciona int
286	111	9.9	1720	6	BD195591	BD195591 70 human	359	9.2	8433	6	CQ610163	CQ610163 Sequence
287	111	9.9	1720	6	CQ775636	CQ775636 Sequence	360	9.2	54309	2	AC017353	AC017353 Drosophil
288	111	9.9	1720	6	AR352646	AR352646 Sequence	361	9.2	157482	3	AC092227	AC092227 Drosophil
289	111	9.9	3625	6	AX149461	AX149461 Sequence	362	9.2	17426	2	CR339044	CR339044 Danio rer
290	111	9.9	8495	6	AX686194	AX686194 Sequence	363	9.2	186803	3	AC092225	AC092225 Drosophil
c 291	111	9.9	184365	2	AC079639	AC079639 Mus muscu	364	9.2	276521	3	AE003642	AE003642 Drosophil
c 292	110.5	9.8	207418	2	AC109112	AC109112 Rattus no	365	9.2	305502	3	DROSADH03	AE003409 Drosophil
293	110.5	9.8	246369	2	AC125707	AC125707 Gallus no	366	9.2	402	6	AX778505	AX778505 Sequence
294	110	9.8	4634	5	AF116856	AF116856 Gallus ga	367	9.2	1099	3	AF436624	AF436624 Macronema
295	110	9.8	110000	2	BX322628_0	BX322628 Danio rer	368	9.2	1519	4	FDBEHAB	Z28367 F.domesticu
c 296	110	9.8	110000	2	BX322628_1	Continuation (2 of	369	9.2	1519	6	I44675	I44675 Sequence 2

370	103	9.2	1785	9	BC052287	BC052287 Homo sapi
C 371	103	9.2	267287	2	AC096702	Rattus no
372	102.5	9.1	1482	6	AR269667	Sequence
C 373	102.5	9.1	1962	6	BD195649	BD195649 70 human
C 374	102.5	9.1	1962	6	CQ775694	Sequence
C 375	102.5	9.1	1962	6	AR352704	AR352704 Sequence
376	102.5	9.1	198756	2	AC135657	AC135657 Rattus no
C 377	102	9.1	216015	2	AC113751	AC113751 Rattus no
378	102	9.1	272147	2	AC095648	AC095648 Rattus no
379	101.5	9.0	1236	14	AJ626545	AJ626545 Human her
380	101.5	9.0	2586	10	MUSEGFREPD	L02613 Mus musculu
381	101.5	9.0	3319	8	AK119879	AK119879 Oryza sat
C 382	101.5	9.0	110000	1	AP006618_49	Continuation (50 o
C 383	101.5	9.0	202968	2	AC137422	Rattus no
384	101	9.0	3014	9	BC008735	BC008735 Homo sapi
C 385	101	9.0	72675	9	BX322573	BX322573 Human DNA
386	101	9.0	79748	2	AC044890	AC044890 Homo sapi
387	101	9.0	110000	8	AE016819_02	Continuation (3 of
388	101	9.0	154612	2	AC093739	AC093739 Homo sapi
389	101	9.0	160625	9	AC009311	AC009311 Homo sapi
C 390	101	9.0	178400	5	BX294376	BX294376 Zebrafish
391	101	9.0	192177	5	BX005242	BX005242 Zebrafish
392	100.5	8.9	1161	10	MMMOTA	X68278 M.musculus
393	100.5	8.9	1209	9	AB107883	AB107883 Homo sapi
394	100.5	8.9	1475	6	AX392229	AX392229 Sequence
395	100.5	8.9	1712	8	AK120901	AK120901 Oryza sat
396	100.5	8.9	1714	8	AK119612	AK119612 Oryza sat
397	100.5	8.9	1780	8	AK103182	AK103182 Oryza sat
398	100.5	8.9	1881	8	AK061650	AK061650 Oryza sat
399	100.5	8.9	1904	8	AK101618	AK101618 Oryza sat
400	100.5	8.9	3383	9	AY262756	AY262756 Homo sapi
401	100.5	8.9	5409	6	BD183451	BD183451 Novel gen
402	100.5	8.9	5409	9	AB067513	AB067513 Homo sapi
403	100.5	8.9	7596	6	AX695382	AX695382 Sequence
404	100.5	8.9	8064	6	AX695381	AX695381 Sequence
405	100.5	8.9	8064	10	MMNOTCHA	Z11886 M.musculus
406	100.5	8.9	9193	10	AF508809	AF508809 Mus muscu
C 407	100.5	8.9	22029	9	AC003967	AC003967 Homo sapi
408	100.5	8.9	43185	9	AC138430	AC138430 Homo sapi
409	100.5	8.9	112830	2	AC151678	AC151678 Gallus ga
410	100.5	8.9	154865	8	OSJN00071	AL606640 Oryza sat
C 411	100.5	8.9	300330	1	AP005222	AP005222 Corynebac
412	100	8.9	33706	3	CEC25G4	Z70680 Caenorhabdi
413	100	8.9	100984	10	AL929138	AL929138 Mouse DNA
C 414	100	8.9	107352	9	HS474A14	AL023285 Human DNA
C 415	100	8.9	135850	2	AC135931	AC135931 Rattus no
C 416	100	8.9	180995	9	AC117500	AC117500 Homo sapi
C 417	100	8.9	184091	2	BX294393	BX294393 Mus muscu
C 418	100	8.9	218311	2	CR749741	CR749741 Danio rer
C 419	100	8.9	230817	2	AC106909	AC106909 Rattus no
C 420	100	8.9	239696	2	AC097086	AC097086 Rattus no
421	99.5	8.8	1008	5	AB167511	AB167511 Danio rer
422	99.5	8.8	1194	14	AJ626546	AJ626546 Human her
423	99.5	8.8	37711	3	CEZK896	Z82288 Caenorhabdi
C 424	99.5	8.8	162296	9	AL161774	AL161774 Human DNA
C 425	99.5	8.8	176022	2	BX294110	BX294110 Danio rer
426	99.5	8.8	225000	2	AC129674	AC129674 Rattus no
427	99.5	8.8	232749	2	CR354535	CR354535 Danio rer
428	99.5	8.8	236907	2	AC103254	AC103254 Rattus no
429	99	8.8	438	6	CQ662211	CQ662211 Sequence
430	99	8.8	4287	6	CQ610164	CQ610164 Sequence
C 431	99	8.8	110000	2	LMFLCHR36_21	Continuation (22 o
432	99	8.8	110000	6	BD430793_01	Continuation (2 of
433	99	8.8	143089	5	CR388386_	CR388386 Zebrafish
C 434	99	8.8	153749	5	BX649585	BX649585 Zebrafish
435	99	8.8	307150	1	CNSPAX01	AJ248283 Pyrococcu
436	99	8.8	349980	6	AX041106	AX041106 Sequence
C 437	98.5	8.8	1719	8	AK176661	AK176661 Arabidops
438	98.5	8.8	1720	10	AB094071	AB094071 Rattus no
439	98.5	8.8	1898	3	AB092978	AB092978 Haliotis
440	98.5	8.8	5152	5	AY144591	AY144591 Cyprinus
C 441	98.5	8.8	5283	1	AF373807	AF373807 Sinorhizo
442	98.5	8.8	7868	14	HPU37537	U37537 Human papil

C 443	98.5	8.8	82972	8	NCB24H17	AL356815 Neurospor
444	98.5	8.8	124191	9	AC005153	AC005153 Homo sapi
445	98.5	8.8	146137	2	AC148795	AC148795 Otlemur
446	98.5	8.8	184357	2	AC073728	AC073728 Mus muscu
C 447	98.5	8.8	299350	1	SME591786	AL591786 Sinorhizo
448	98	8.7	1341	6	AX657611	AX657611 Sequence
C 449	98	8.7	1378	1	AY127887	AY127887 Anaplasma
450	98	8.7	2421	6	CQ722898	CQ722898 Sequence
451	98	8.7	3118	6	BD156554	BD156554 Primer fo
452	98	8.7	3118	6	AX877234	AX877234 Sequence
453	98	8.7	3118	9	AK027692	AK027692 Homo sapi
454	98	8.7	3499	6	BD156002	BD156002 Primer fo
455	98	8.7	3499	6	AX876196	AX876196 Sequence
456	98	8.7	3499	9	AK027440	AK027440 Homo sapi
457	98	8.7	4098	9	HSA459424	AJ459424 Homo sapi
C 458	98	8.7	4128	1	AF527423	AF527423 Anaplasma
C 459	98	8.7	4185	1	AMU60779	U60779 Anaplasma m
460	98	8.7	5131	6	CQ850217	CQ850217 Sequence
461	98	8.7	5131	9	AK127328	AK127328 Homo sapi
462	98	8.7	6353	6	CQ580242	CQ580242 Sequence
463	98	8.7	8429	6	CQ580241	CQ580241 Sequence
C 464	98	8.7	13443	2	AC013070	AC013070 Drosophil
C 465	98	8.7	103995	2	AC096695	AC096695 Rattus no
C 466	98	8.7	121478	9	AL365229	AL365229 Human DNA
C 467	98	8.7	144588	2	AC012239	AC012239 Homo sapi
C 468	98	8.7	172674	3	AC007807	AC007807 Drosophil
C 469	98	8.7	190866	3	AC007824	AC007824 Drosophil
C 470	98	8.7	220035	3	AE003716	AE003716 Drosophil
471	98	8.7	220710	2	AC125304	AC125304 Rattus no
472	98	8.7	305225	2	AC130763	AC130763 Rattus no
473	98	8.7	346301	1	BX640432	BX640432 Bordetell
474	97.5	8.7	1144	8	TTU537508	AJ537508 Triticum
C 475	97.5	8.7	1399	1	AY127894	AY127894 Anaplasma
C 476	97.5	8.7	56374	9	AC074092	AC074092 Homo sapi
477	97.5	8.7	144167	2	AC148140	AC148140 Bos tauru
C 478	97.5	8.7	150401	2	AC079980	AC079980 Homo sapi
C 479	97.5	8.7	174527	9	AP001183	AP001183 Homo sapi
480	97.5	8.7	182736	2	AC021672	AC021672 Homo sapi
C 481	97.5	8.7	190314	9	AC019227	AC019227 Homo sapi
482	97.5	8.7	202555	2	AC148141	AC148141 Bos tauru
C 483	97.5	8.7	304500	1	AP005953	AP005953 Bradyrhiz
484	97	8.6	304	6	CQ673468	CQ673468 Sequence
485	97	8.6	789	6	CQ749879	CQ749879 Sequence
486	97	8.6	1173	14	AJ626532	AJ626532 Human her
487	97	8.6	1173	14	AJ626542	AJ626542 Human her
488	97	8.6	1173	14	AJ626547	AJ626547 Human her
489	97	8.6	1190	6	I67656	I67656 Sequence 1
C 490	97	8.6	2293	8	AK102226	AK102226 Oryza sat
491	97	8.6	12979	14	HEHSV1SU	X02138 Herpes simp
C 492	97	8.6	26245	14	HS1US	L00036 Human herpe
493	97	8.6	152261	14	HE1CG	X14112 Human herpe
494	97	8.6	171307	9	AC104020	AC104020 Homo sapi
495	97	8.6	263891	2	AC096166	AC096166 Rattus no
496	97	8.6	349442	1	BX640447	BX640447 Bordetell
497	96.5	8.6	840	8	WHTGMPA	D78183 Triticum ae
C 498	96.5	8.6	1859	8	AK106807	AK106807 Oryza sat
499	96.5	8.6	4501	1	ATU39263	U39263 Agrobacteri
C 500	96.5	8.6	24413	3	AC117272	AC117272 Leishmani
C 501	96.5	8.6	110000	1	AE016822_19	Continuation (20 o
C 502	96.5	8.6	125673	9	AL356796_	AL356796 Human DNA
503	96.5	8.6	181179	9	AL161725	AL161725 Human DNA
504	96.5	8.6	192662	10	AC134397	AC134397 Mus muscu
505	96.5	8.6	224197	2	AC144404	AC144404 Medicago
506	96.5	8.6	225989	2	AC135294	AC135294 Rattus no
C 507	96.5	8.6	272888	2	AC139198	AC139198 Mus muscu
508	96	8.5	206	9	HUMSCG02	L05407 Human cell
509	96	8.5	1458	3	AF167710	AF167710 Toxocara
510	96	8.5	1767	6	AR310497	AR310497 Sequence
511	96	8.5	1767	6	AX000158	AX000158 Sequence
512	96	8.5	2603	8	AF156269	AF156269 Aspergill
513	96	8.5	11659	1	AE005131	AE005131 Halobacte
514	96	8.5	110000	2	LMFLCHR31_15	Continuation (16 o
515	96	8.5	155548	2	CR848047	CR848047 Danio rer

C 516	96	8.5	174108	5	BX323078	BX323078 Zebrafish
517	96	8.5	300800	1	AP005036	AP005036 Streptomy
518	95.5	8.5	1693	8	AK061142	AK061142 Oryza sat
519	95.5	8.5	2012	8	AK071956	AK071956 Oryza sat
520	95.5	8.5	2517	8	AK105749	AK105749 Oryza sat
521	95.5	8.5	5894	3	ACMHC	Y00624 Acanthamoeb
522	95.5	8.5	65140	6	AX211705	AX211705 Sequence
523	95.5	8.5	123580	1	AF263912	AF263912 Streptomy
524	95.5	8.5	125401	6	AX211739	AX211739 Sequence
525	95.5	8.5	140475	8	AP005558	AP005558 Oryza sat
526	95.5	8.5	145590	8	AC109601	AC109601 Oryza sat
C 527	95.5	8.5	157397	8	AC133860	AC133860 Oryza sat
528	95.5	8.5	169184	2	AC144112	AC144112 Macaca mu
529	95.5	8.5	243899	5	BX510919	BX510919 Zebrafish
530	95	8.4	623	4	AY226857	AY226864 Bos tauru
C 531	95	8.4	4498	10	MMU91922	U91922 Mus musculu
C 532	95	8.4	5018	3	AC006797	AC006797 Caenorhab
C 533	95	8.4	6478	8	AB023040	AB023040 Arabidops
C 534	95	8.4	10101	1	AE012376	AE012376 Xanthomon
C 535	95	8.4	114020	10	AC127596	AC127596 Mus muscu
C 536	95	8.4	159547	2	AC073674	AC073674 Mus muscu
C 537	95	8.4	173369	10	AL928966	AL928966 Mouse DNA
538	95	8.4	258181	2	AC096936	AC096936 Rattus no
539	95	8.4	302550	1	AP006581	AP006581 Gloeobact
C 540	95	8.4	349607	1	BX957222	BX957222 Methanoco
541	94.5	8.4	907	1	GVI7274	AJ007274 Gloeobact
542	94.5	8.4	948	1	AY331318	AY331318 Pseudomon
543	94.5	8.4	948	1	AY331321	AY331321 Pseudomon
544	94.5	8.4	948	1	AY331322	AY331322 Pseudomon
545	94.5	8.4	948	1	AY331323	AY331323 Pseudomon
546	94.5	8.4	948	1	AY331324	AY331324 Pseudomon
547	94.5	8.4	1372	6	CQ596994	CQ596994 Sequence
548	94.5	8.4	2155	9	S52488	S52488 CSPG2=versi
549	94.5	8.4	2168	3	BT001711	BT001711 Drosophil
550	94.5	8.4	2407	8	LTE532549	AJ532549 Lolium te
551	94.5	8.4	2690	3	DFU20332	U20332 Drosophila
552	94.5	8.4	3421	3	AY060306	AY060306 Drosophil
C 553	94.5	8.4	4492	6	CQ596993	CQ596993 Sequence
554	94.5	8.4	5388	6	CQ608451	CQ608451 Sequence
C 555	94.5	8.4	7782	6	CQ608450	CQ608450 Sequence
C 556	94.5	8.4	8426	2	AC013966	AC013966 Drosophil
C 557	94.5	8.4	8664	3	LMFL6823	AL139796 Leishmani
C 558	94.5	8.4	24492	3	DMC55G7	AL031028 Drosophil
C 559	94.5	8.4	110000	2	LMFLCHR36_01	Continuation (2 of
560	94.5	8.4	121705	9	AC006452	AC006452 Homo sapi
561	94.5	8.4	125862	9	AC026696	AC026696 Homo sapi
C 562	94.5	8.4	132151	8	AC144491	AC144491 Oryza sat
563	94.5	8.4	160738	8	AC073556	AC073556 Oryza sat
C 564	94.5	8.4	174801	2	AC014376	AC014376 Drosophil
C 565	94.5	8.4	177096	3	AC107326	AC107326 Drosophil
566	94.5	8.4	179838	3	AC091220	AC091220 Drosophil
C 567	94.5	8.4	181063	3	AC010107	AC010107 Drosophil
C 568	94.5	8.4	198222	2	AC092429	AC092429 Homo sapi
569	94.5	8.4	216860	10	AC134793	AC134793 Mus muscu
570	94.5	8.4	285860	3	AE003551	AE003551 Drosophil
571	94.5	8.4	297050	1	AP006569	AP006569 Gloeobact
C 572	94.5	8.4	304204	3	AE003421	AE003421 Drosophil
573	94	8.4	700	9	S72412	S72412 proteoglyca
C 574	94	8.4	2346	3	TCCP69GNA	Z22557 T.congolens
C 575	94	8.4	110000	1	AP006618_28	Continuation (29 o
576	94	8.4	121377	8	AP004038	AP004038 Oryza sat
577	94	8.4	137046	8	AP004775	AP004775 Oryza sat
C 578	94	8.4	212159	2	AC113023	AC113023 Mus muscu
C 579	94	8.4	292100	1	SCO939121	AL939121 Streptomy
580	94	8.4	297950	1	AP006582	AP006582 Gloeobact
581	94	8.4	302040	1	AE017317	AE017317 Desulfovi
C 582	94	8.4	349028	1	BX640413	BX640413 Bordetell
583	93.5	8.3	757	10	BC021401	BC021401 Mus muscu
584	93.5	8.3	826	5	CHKLNKPA4	M35038 Chicken car
585	93.5	8.3	1070	8	AK061303	AK061303 Oryza sat
586	93.5	8.3	1172	8	AK104138	AK104138 Oryza sat
587	93.5	8.3	1175	8	AK104400	AK104400 Oryza sat
588	93.5	8.3	1194	14	AJ626543	AJ626543 Human her

589	93.5	8.3	1231	6	AR508054	AR508054 Sequence
590	93.5	8.3	1245	8	AK073355	AK073355 Oryza sat
591	93.5	8.3	1574	8	TDY14104	Y14104 Triticum du
592	93.5	8.3	1785	3	AB162804	AB162804 Hallotis
593	93.5	8.3	1943	3	AK116624	AK116624 Ciona int
C 594	93.5	8.3	7137	6	CQ726893	CQ726893 Sequence
C 595	93.5	8.3	8146	6	AR448064	AR448064 Sequence
C 596	93.5	8.3	9169	6	CQ413012	CQ413012 Sequence
C 597	93.5	8.3	9220	6	CQ492536	CQ492536 Sequence
C 598	93.5	8.3	9220	6	CQ493387	CQ493387 Sequence
C 599	93.5	8.3	9416	9	HUMSEQX	L06237 Human micro
C 600	93.5	8.3	11474	1	AE014763	AE014763 Bifidobac
C 601	93.5	8.3	11917	6	AR454559	AR454559 Sequence
602	93.5	8.3	138994	2	AC141046	AC141046 Rattus no
603	93.5	8.3	148433	9	AC012609	AC012609 Homo sapi
C 604	93.5	8.3	152177	5	AL935114	AL935114 Zebrafish
C 605	93.5	8.3	166138	9	AC099684	AC099684 Homo sapi
606	93.5	8.3	202269	9	AC130689	AC130689 Homo sapi
C 607	93.5	8.3	214146	2	AC096822	AC096822 Rattus no
608	93.5	8.3	246566	2	AC097926	AC097926 Rattus no
609	93.5	8.3	254733	3	AC117075	AC117075 Dictyoste
C 610	93.5	8.3	263297	2	AC127631	AC127631 Rattus no
C 611	93.5	8.3	313800	1	SCO939114	AL939114 Streptomy
612	93.5	8.3	321250	1	SCO939111	AL939111 Streptomy
C 613	93.5	8.3	349980	6	AX492786	AX492786 Sequence
C 614	93.5	8.3	349980	6	AX553953	AX553953 Sequence
615	93	8.3	1321	6	AR097540	AR097540 Sequence
C 616	93	8.3	1378	1	AY127885	AY127885 Anaplasma
617	93	8.3	1995	6	CQ782648	CQ782648 Sequence
618	93	8.3	1995	6	BD127244	BD127244 Primer fo
619	93	8.3	1995	9	AK074718	AK074718 Homo sapi
620	93	8.3	2105	5	BC081615	BC081615 Danio rer
621	93	8.3	3036	3	AY245772	AY245772 Monosiga
622	93	8.3	4849	3	AK113070	AK113070 Ciona int
623	93	8.3	4977	1	CDCMANA	L01257 Caldocellum
624	93	8.3	5931	6	CQ607290	CQ607290 Sequence
C 625	93	8.3	7931	6	CQ607289	CQ607289 Sequence
C 626	93	8.3	15900	2	AC017311	AC017311 Drosophil
627	93	8.3	35307	2	AC014905	AC014905 Drosophil
628	93	8.3	107480	9	AL596094	AL596094 Human DNA
629	93	8.3	110000	2	AL732359_06	Continuation (7 of
630	93	8.3	162329	2	CR381583	CR381583 Danio rer
C 631	93	8.3	164223	10	AC127228	AC127228 Mus muscu
C 632	93	8.3	180498	3	AC009847	AC009847 Drosophil
C 633	93	8.3	198162	5	BX323985	BX323985 Zebrafish
634	93	8.3	208145	2	AC053504	AC053504 Homo sapi
C 635	93	8.3	226307	10	AC119851	AC119851 Mus muscu
C 636	93	8.3	244978	2	AC128734	AC128734 Rattus no
637	93	8.3	260091	2	AC134021	AC134021 Rattus no
C 638	93	8.3	265602	2	AC107184	AC107184 Rattus no
639	93	8.3	301129	3	AE003785	AE003785 Drosophil
640	92.5	8.2	1247	10	AY262758	AY262758 Mus muscu
641	92.5	8.2	2556	10	AY269789	AY269789 Mus muscu
642	92.5	8.2	2589	6	I32212	I32212 Sequence 3
643	92.5	8.2	2685	6	A39780	A39780 Sequence 14
644	92.5	8.2	2685	6	A74265	A74265 Sequence 21
645	92.5	8.2	2967	1	AY184164	AY184164 Chlamydia
646	92.5	8.2	2967	1	AY184165	AY184165 Chlamydia
647	92.5	8.2	2967	1	AY184166	AY184166 Chlamydia
648	92.5	8.2	3606	10	AB107882	AB107882 Mus muscu
649	92.5	8.2	4614	6	BD271910	BD271910 Process f
650	92.5	8.2	4614	6	I32211	I32211 Sequence 1
651	92.5	8.2	5500	4	AY212921	AY212921 Oryctolag
652	92.5	8.2	5743	8	SCFL01	X78160 S.cerevisia
653	92.5	8.2	22753	2	AC017598	AC017598 Drosophil
C 654	92.5	8.2	32481	3	U21310	U21310 Caenorhabdi
655	92.5	8.2	33359	3	CEP55B11	Z83318 Caenorhabdi
656	92.5	8.2	36604	14	AY530877	AY530877 Simian ad
C 657	92.5	8.2	38573	2	AC017717	AC017717 Drosophil
658	92.5	8.2	54812	8	YSCCHR1RAA	L28920 Saccharomyc
659	92.5	8.2	82064	2	AC006937	AC006937 Drosophil
660	92.5	8.2	93134	8	BX908807	BX908807 Neurospor
C 661	92.5	8.2	134511	2	AC149927	AC149927 Strongylo

C 662	92.5	8.2	145911	1	AP003014	AP003014 Mesorhizo	C 735	91.5	8.1	161126	8	NC80A10	BX294012 Neurospor
663	92.5	8.2	153749	3	AC093098	AC093098 Drosophil	736	91.5	8.1	162538	2	BX649414	BX649414 Homo sapi
664	92.5	8.2	163183	3	AC009842	AC009842 Drosophil	737	91.5	8.1	162929	5	BX323842	BX323842 Zebrafish
665	92.5	8.2	170684	3	AC007578	AC007578 Drosophil	738	91.5	8.1	170324	3	AC007805	AC007805 Drosophil
666	92.5	8.2	182897	3	AC092232	AC092232 Drosophil	739	91.5	8.1	188555	10	AC122417	AC122417 Mus muscu
C 667	92.5	8.2	184357	2	AC073728	AC073728 Mus muscu	740	91.5	8.1	197913	2	BX572087	BX572087 Danio rer
668	92.5	8.2	191041	9	AC091742	AC091742 Homo sapi	741	91.5	8.1	203595	2	CR385054	CR385054 Danio rer
669	92.5	8.2	195349	2	AC006705	AC006705 Caenorhab	742	91.5	8.1	204278	10	AC124507	AC124507 Mus muscu
670	92.5	8.2	197845	2	BX950198	BX950198 Danio rer	C 743	91.5	8.1	218236	2	AC108828	AC108828 Mus muscu
671	92.5	8.2	231676	2	AC134063	AC134063 Rattus no	744	91.5	8.1	227847	3	AE003692	AE003692 Drosophil
672	92.5	8.2	267156	6	AX336388	AX336388 Sequence	745	91.5	8.1	246913	10	AC109542	AC109542 Rattus no
673	92.5	8.2	267156	9	U66059	U66059 Human germ	C 746	91.5	8.1	299991	1	AE016776	AE016776 Pseudomon
C 674	92.5	8.2	272258	2	AC123370	AC123370 Rattus no	747	91	8.1	1005	6	AR555393	AR555393 Sequence
C 675	92.5	8.2	289893	3	AE003576	AE003576 Drosophil	748	91	8.1	1793	3	AK174570	AK174570 Ciona int
C 676	92.5	8.2	299175	1	AP005023	AP005023 Streptomy	749	91	8.1	1828	8	AK100900	AK100900 Oryza sat
C 677	92.5	8.2	310092	3	AE003826	AE003826 Drosophil	750	91	8.1	2110	4	BTU10039	U10039 Bos taurus
678	92	8.2	154	9	HUMSCG03	L05408 Human cell	751	91	8.1	2636	10	RNU89744	U89744 Rattus norv
679	92	8.2	1042	10	MMU37531	U37531 Mus musculu	C 752	91	8.1	5280	1	STYCYSA	M64606 S.typhimuri
680	92	8.2	1144	8	TAE17845	Y17845 Triticum ae	C 753	91	8.1	23069	1	AE008859	AE008859 Salmonell
681	92	8.2	1342	8	SCSEC1A	X60294 S.cereale S	754	91	8.1	26154	3	CEF33E2	Z84574 Caenorhabdi
682	92	8.2	1434	6	ARS52751	ARS52751 Sequence	755	91	8.1	50709	1	AY034092	AY034092 Micrococc
683	92	8.2	1500	4	BTA550060	AJ550060 Bos tauru	C 756	91	8.1	55173	2	AC132816	AC132816 Homo sapi
684	92	8.2	1542	3	AY071278	AY071278 Drosophil	757	91	8.1	77572	2	OSIG00032	AL732333 Oryza sat
C 685	92	8.2	1986	8	AK068129	AK068129 Oryza sat	C 758	91	8.1	78419	3	AC004639	AC004639 Drosophil
686	92	8.2	2044	8	AK070083	AK070083 Oryza sat	759	91	8.1	110000	1	AP006618_35	Continuation (36 o
C 687	92	8.2	3425	8	AK073220	AK073220 Oryza sat	760	91	8.1	110000	2	AC098456_0	AC098456 Rattus no
688	92	8.2	3677	8	AF414112	AF414112 Candida a	761	91	8.1	137001	9	AP001005	AP001005 Homo sapi
689	92	8.2	4138	5	XSMTK	X16891 Xiphophorus	C 762	91	8.1	143298	8	OSJN00114	AL606994 Oryza sat
C 690	92	8.2	6108	3	CETRA3S1	U12516 Caenorhabdi	763	91	8.1	145153	1	AY458649	AY458649 Unculture
691	92	8.2	9248	8	SCAF000227	AF000227 Secale ce	764	91	8.1	147258	2	AC141400	AC141400 Rattus no
692	92	8.2	10029	1	AE011851	AE011851 Xanthomon	765	91	8.1	160429	5	BX004784	BX004784 Zebrafish
C 693	92	8.2	11251	1	AE005560	AE005560 Escherich	766	91	8.1	173317	2	AC119924	AC119924 Mus muscu
C 694	92	8.2	11613	1	AE015347	AE015347 Shigella	C 767	91	8.1	175949	4	AC107065	AC107065 Bos tauru
695	92	8.2	35920	3	CELLC1	Z82277 Caenorhabdi	C 768	91	8.1	176644	5	AL824708	AL824708 Zebrafish
C 696	92	8.2	53957	8	NCB2G14	BX284753 Neurospor	769	91	8.1	205235	2	AC151864	AC151864 Colobus g
697	92	8.2	80767	9	HS745E8	AL020998 Human DNA	C 770	91	8.1	205503	2	AC148001	AC148001 Mus muscu
698	92	8.2	107379	1	SHGCP1R	X86780 S.hygrosco	771	91	8.1	209672	2	AL773584	AL773584 Danio rer
699	92	8.2	110000	1	AP006840_31	Continuation (32 o	772	91	8.1	220191	10	AC113968	AC113968 Mus muscu
700	92	8.2	110000	2	AC146908_2	Continuation (3 of	C 773	91	8.1	231844	2	AC116068	AC116068 Rattus no
C 701	92	8.2	110000	2	LMFLCHR31_12	Continuation (13 o	774	91	8.1	234234	2	AC097194	AC097194 Rattus no
702	92	8.2	110000	8	CR382129_28	Continuation (29 o	775	91	8.1	241644	2	AC094176	AC094176 Rattus no
703	92	8.2	155490	2	CR749749_28	CR749749 Danio rer	C 776	91	8.1	248158	2	AC111483	AC111483 Rattus no
704	92	8.2	158500	2	CR382340	CR382340 Danio rer	C 777	91	8.1	292550	1	AP001513	AP001513 Bacillus
C 705	92	8.2	159579	8	AC106887	AC106887 Oryza sat	C 778	91	8.1	308015	1	AE016783	AE016783 Pseudomon
C 706	92	8.2	170226	8	AP003450	AP003450 Oryza sat	779	91	8.1	333321	3	AC116986	AC116986 Dictyoste
707	92	8.2	215895	2	AC121688	AC121688 Rattus no	C 780	91	8.1	349323	1	BX572096	BX572096 Prochloro
C 708	92	8.2	232292	2	AC126517	AC126517 Rattus no	C 781	91	8.1	349737	1	BX572597	BX572597 Rhodopseu
709	92	8.2	247306	2	AC131445	AC131445 Rattus no	C 782	90.5	8.0	1075	6	CQ056637	CQ056637 Sequence
710	92	8.2	289816	1	AE016992	AE016992 Shigella	C 783	90.5	8.0	1075	6	CQ075914	CQ075914 Sequence
711	92	8.2	306650	1	AP005221	AP005221 Corynebac	C 784	90.5	8.0	1075	6	CQ106891	CQ106891 Sequence
C 712	92	8.2	307962	1	AP002564	AP002564 Escherich	C 785	90.5	8.0	1075	6	CQ145546	CQ145546 Sequence
C 713	92	8.2	345012	1	BX572607	BX572607 Rhodopseu	C 786	90.5	8.0	1075	6	CQ180991	CQ180991 Sequence
714	91.5	8.1	768	8	ASP389719	AJ389719 Aegilops	C 787	90.5	8.0	1075	6	CQ205355	CQ205355 Sequence
C 715	91.5	8.1	999	1	AF456032	AF456032 Burkholde	C 788	90.5	8.0	1075	6	CQ228754	CQ228754 Sequence
C 716	91.5	8.1	999	1	AF456047	AF456047 Burkholde	C 789	90.5	8.0	1075	6	CQ266896	CQ266896 Sequence
C 717	91.5	8.1	1041	1	AY099312	AY099312 Burkholde	C 790	90.5	8.0	1075	6	CQ303869	CQ303869 Sequence
718	91.5	8.1	1770	10	BC061990	BC061990 Rattus no	C 791	90.5	8.0	1075	6	CQ341185	CQ341185 Sequence
719	91.5	8.1	2493	8	AB055432	AB055432 Aspergill	C 792	90.5	8.0	1293	8	BT006583	BT006583 Arabidops
720	91.5	8.1	3381	6	CQ608193	CQ608193 Sequence	C 793	90.5	8.0	1403	6	CQ051669	CQ051669 Sequence
721	91.5	8.1	3502	6	A22122	A22122 ILTV gp60 g	C 794	90.5	8.0	1403	6	CQ066726	CQ066726 Sequence
722	91.5	8.1	3916	8	YLI549517	AJ549517 Yarrowia	C 795	90.5	8.0	1403	6	CQ093768	CQ093768 Sequence
723	91.5	8.1	5381	6	CQ608192	CQ608192 Sequence	C 796	90.5	8.0	1403	6	CQ132545	CQ132545 Sequence
724	91.5	8.1	8692	3	LVU34823	U34823 Lytechinus	C 797	90.5	8.0	1403	6	CQ171117	CQ171117 Sequence
725	91.5	8.1	16256	1	AF289050	AF289050 Bacteroid	C 798	90.5	8.0	1403	6	CQ200252	CQ200252 Sequence
726	91.5	8.1	35424	3	LMFL2185	AL358712 Leishmani	C 799	90.5	8.0	1403	6	CQ215756	CQ215756 Sequence
727	91.5	8.1	82584	8	NCB13B3	BX284762 Neurospor	C 800	90.5	8.0	1403	6	CQ254334	CQ254334 Sequence
C 728	91.5	8.1	110000	8	CR382131_09	Continuation (10 o	C 801	90.5	8.0	1403	6	CQ291368	CQ291368 Sequence
729	91.5	8.1	111731	2	BX323063	BX323063 Homo sapi	C 802	90.5	8.0	1403	6	CQ328471	CQ328471 Sequence
730	91.5	8.1	114793	9	AF217796	AF217796 Homo sapi	803	90.5	8.0	1491	14	AF343059	AF343059 Eyach vir
731	91.5	8.1	117273	2	AC015138	AC015138 Drosophil	804	90.5	8.0	1548	10	RATLGP96	D90211 Rattus sp.
C 732	91.5	8.1	129231	9	AC092265	AC092265 Homo sapi	C 805	90.5	8.0	1609	8	AK176622	AK176622 Arabidops
C 733	91.5	8.1	138203	1	AY310323	AY310323 Streptomy	C 806	90.5	8.0	1660	8	AY140063	AY140063 Arabidops
734	91.5	8.1	155490	2	AC015478	AC015478 Homo sapi	807	90.5	8.0	2178	14	AF282472	AF282472 Eyach vir

C 808	90.5	8.0	3262	1	AF008569	AF008569 Streptomy	881	90	8.0	139653	2	AP005890	AP005890 Oryza sat
C 809	90.5	8.0	41278	3	CBRG30E10	AC084545 Caenorhab	882	90	8.0	143285	9	AL139423	AL139423 Human DNA
810	90.5	8.0	44552	2	AC014809	AC014809 Drosophil	883	90	8.0	161865	8	AP005912	AP005912 Oryza sat
811	90.5	8.0	92970	9	AC108467	AC108467 Homo sapi	C 884	90	8.0	166485	9	AC123900	AC123900 Homo sapi
812	90.5	8.0	96642	8	AC002291	AC002291 Arabidops	885	90	8.0	170790	2	AC025609	AC025609 Homo sapi
C 813	90.5	8.0	98521	10	AC094507	AC094507 Rattus no	C 886	90	8.0	179075	2	AC150138	AC150138 Gallus ga
C 814	90.5	8.0	110000	1	BX571856_23	Continuation (24 o	C 887	90	8.0	184139	9	AC022966	AC022966 Homo sapi
C 815	90.5	8.0	110000	3	AC116305_1	Continuation (2 of	C 888	90	8.0	197698	8	BX908809	BX908809 Neurospor
816	90.5	8.0	125111	2	AC147938	AC147938 Ornithorh	C 889	90	8.0	198922	2	AC094540	AC094540 Rattus no
C 817	90.5	8.0	125623	3	AC115599	AC115599 Dictyoste	890	90	8.0	227555	10	AC108416	AC108416 Mus muscu
C 818	90.5	8.0	139275	2	BX323887	BX323887 Danio rer	891	90	8.0	241120	2	AC123458	AC123458 Rattus no
C 819	90.5	8.0	141084	10	AC127971	AC127971 Rattus no	C 892	90	8.0	248871	2	AC094352	AC094352 Rattus no
820	90.5	8.0	151741	2	AC018609	AC018609 Mus muscu	C 893	90	8.0	256879	3	AC116982	AC116982 Dictyoste
C 821	90.5	8.0	166568	8	AP005256	AP005256 Oryza sat	C 894	90	8.0	290850	1	SCO939127	AL939127 Streptomy
822	90.5	8.0	180291	10	AC129146	AC129146 Rattus no	895	90	8.0	292100	1	SCO939121	AL939121 Streptomy
823	90.5	8.0	187000	3	AC091201	AC091201 Drosophil	896	89.5	8.0	528	8	CR377484	CR377484 Pinus pin
C 824	90.5	8.0	189774	10	AC098709	AC098709 Mus muscu	897	89.5	8.0	771	8	ASP389720	AJ389720 Aegilops
825	90.5	8.0	198115	2	AC099712	AC099712 Mus muscu	898	89.5	8.0	828	8	AY338395	AY338395 Triticum
C 826	90.5	8.0	198363	2	AC144410	AC144410 Mus muscu	899	89.5	8.0	849	8	AY338390	AY338390 Triticum
C 827	90.5	8.0	204018	2	AC116890	AC116890 Mus muscu	900	89.5	8.0	1014	6	AR081996	AR081996 Sequence
828	90.5	8.0	210648	10	AL772306	AL772306 Mouse DNA	901	89.5	8.0	1014	6	AR198392	AR198392 Sequence
C 829	90.5	8.0	226622	2	AC106843	AC106843 Mus muscu	902	89.5	8.0	1173	8	PRA315701	AJ315701 Phlebia r
830	90.5	8.0	232893	2	AC096182	AC096182 Rattus no	903	89.5	8.0	1252	8	AB062852	AB062852 Triticum
C 831	90.5	8.0	238965	2	AC126647	AC126647 Rattus no	904	89.5	8.0	1275	6	AX720123	AX720123 Sequence
832	90.5	8.0	241592	2	AC111683	AC111683 Rattus no	905	89.5	8.0	1280	8	AB062866	AB062866 Triticum
833	90.5	8.0	243185	2	AC094948	AC094948 Rattus no	C 906	89.5	8.0	1406	4	SHPKDP	L11343 Ovis aries
834	90.5	8.0	251457	3	AE003566	AE003566 Drosophil	C 907	89.5	8.0	1423	4	OAU00165	U00165 Ovis aries
835	90.5	8.0	251664	2	AC008908	AC008908 Homo sapi	908	89.5	8.0	1595	10	RATLGPB	M32016 Rat lysosom
C 836	90.5	8.0	252140	2	AC094898	AC094898 Rattus no	909	89.5	8.0	1731	1	RLNHASE	X64360 R.rhodochro
C 837	90.5	8.0	255654	2	AC107481	AC107481 Rattus no	910	89.5	8.0	1731	6	AR008340	AR008340 Sequence
838	90.5	8.0	256307	2	AC130125	AC130125 Rattus no	911	89.5	8.0	1731	6	E03848	E03848 DNA encodin
839	90.5	8.0	271417	2	AC097826	AC097826 Rattus no	912	89.5	8.0	1731	6	I93631	I93631 Sequence 15
C 840	90.5	8.0	349980	6	AX044030	AX044030 Sequence	C 913	89.5	8.0	1768	8	AY188532	AY188532 Larix pot
C 841	90.5	8.0	349980	6	AX044031	AX044031 Sequence	914	89.5	8.0	2198	6	CQ605618	CQ605618 Sequence
842	90	8.0	9983	5	BC061275	BC061275 Xenopus t	915	89.5	8.0	2723	3	DFU20331	U20331 Drosophila
843	90	8.0	1030	6	CQ727556	CQ727556 Sequence	916	89.5	8.0	2780	3	AK112792	AK112792 Ciona int
844	90	8.0	1098	3	AF436604	AF436604 Taschorem	917	89.5	8.0	4047	9	HTA298318	AJ298318 Homo sapi
C 845	90	8.0	1344	6	CQ606222	CQ606222 Sequence	918	89.5	8.0	6443	8	AF234649	AF234649 Triticum
846	90	8.0	1608	6	BD228728	BD228728 Novel der	919	89.5	8.0	9917	1	AE004558	AE004558 Pseudomon
C 847	90	8.0	1608	6	BD228729	BD228729 Novel der	C 920	89.5	8.0	10013	1	AE002558	AE002558 Neisseria
848	90	8.0	1608	6	AR232707	AR232707 Sequence	921	89.5	8.0	27551	10	AL807812	AL807812 Mouse DNA
C 849	90	8.0	1608	6	AR232708	AR232708 Sequence	922	89.5	8.0	39502	1	AY534910	AY534910 Unculture
850	90	8.0	1608	6	AX411859	AX411859 Sequence	923	89.5	8.0	66924	2	NCB9J10	AL356324 Neurospor
C 851	90	8.0	1608	6	AX411861	AX411861 Sequence	C 924	89.5	8.0	69668	2	AC131503	AC131503 Lytechinu
852	90	8.0	1665	6	BD228726	BD228726 Novel der	925	89.5	8.0	78533	9	HS278N12	AL033376 Human DNA
C 853	90	8.0	1665	6	BD228727	BD228727 Novel der	C 926	89.5	8.0	92591	2	AC110966_3	Continuation (4 of
854	90	8.0	1665	6	AR232705	AR232705 Sequence	927	89.5	8.0	109996	10	MMU311612	AJ311612 Mus muscu
C 855	90	8.0	1665	6	AR232706	AR232706 Sequence	928	89.5	8.0	110000	1	CP000011_21	Continuation (22 o
C 856	90	8.0	1665	6	AX411856	AX411856 Sequence	C 929	89.5	8.0	110000	1	CR522870_09	Continuation (10 o
C 857	90	8.0	1665	6	AX411858	AX411858 Sequence	930	89.5	8.0	113946	8	AC126222	AC126222 Oryza sat
858	90	8.0	1752	3	AF178772	AF178772 Dermatoph	931	89.5	8.0	130058	8	AC078840	AC078840 Oryza sat
859	90	8.0	1752	6	BD228724	BD228724 Novel der	932	89.5	8.0	133093	10	AC134439	AC134439 Mus muscu
C 860	90	8.0	1752	6	BD228725	BD228725 Novel der	C 933	89.5	8.0	153351	2	BX546485	BX546485 Danio rer
861	90	8.0	1752	6	AR232703	AR232703 Sequence	C 934	89.5	8.0	161403	2	BX957243	BX957243 Danio rer
C 862	90	8.0	1752	6	AR232704	AR232704 Sequence	935	89.5	8.0	167841	2	AC125767	AC125767 Rattus no
863	90	8.0	1752	6	AX411853	AX411853 Sequence	936	89.5	8.0	172325	6	AX044035	AX044035 Sequence
C 864	90	8.0	1752	6	AX411855	AX411855 Sequence	937	89.5	8.0	173723	3	AC009351	AC009351 Drosophil
865	90	8.0	1832	8	SCSECI1B	X60295 S.cereale S	938	89.5	8.0	176952	8	AC084023	AC084023 Oryza sat
866	90	8.0	1966	5	AF359429	AF359429 Danio rer	C 939	89.5	8.0	178416	10	AC140840	AC140840 Mus muscu
867	90	8.0	2900	8	HVB1HORG	X03103 Barley gene	940	89.5	8.0	181936	2	AC122156	AC122156 Sus scrof
868	90	8.0	3547	3	AB045982	AB045982 Patinopec	941	89.5	8.0	207161	2	AC120651	AC120651 Rattus no
869	90	8.0	7823	14	HPV27	X74473 Human papil	C 942	89.5	8.0	218270	2	AC079499	AC079499 Mus muscu
870	90	8.0	11775	1	AE012930	AE012930 Chlorobiu	943	89.5	8.0	238980	2	AC106296	AC106296 Rattus no
871	90	8.0	14467	1	CVU84760	U84760 Chromatium	944	89.5	8.0	240525	2	AC096895	AC096895 Rattus no
C 872	90	8.0	15515	1	AE000044	AE000044 Mycoplasm	C 945	89.5	8.0	251208	2	AC096610	AC096610 Rattus no
873	90	8.0	54441	3	AC115584	AC115584 Dictyoste	946	89.5	8.0	260673	3	AE003612	AE003612 Drosophil
C 874	90	8.0	84077	9	AL157371	AL157371 Human DNA	C 947	89.5	8.0	301675	1	AP005027	AP005027 Streptomy
875	90	8.0	103194	8	AP004026	AP004026 Oryza sat	948	89.5	8.0	301934	8	AE017110	AE017110 Oryza sat
C 876	90	8.0	110000	1	AP006618_41	Continuation (42 o	C 949	89.5	8.0	318930	2	AC073495	AC073495 Mus muscu
C 877	90	8.0	110000	8	CR382127_12	Continuation (13 o	C 950	89.5	8.0	340806	1	NMA122491	AL162752 Neisseria
C 878	90	8.0	110000	8	CR382132_20	Continuation (21 o	951	89	7.9	904	10	AF247816	AF247816 Mus muscu
C 879	90	8.0	110000	8	CR382132_21	Continuation (22 o	952	89	7.9	1110	6	CQ596670	CQ596670 Sequence
880	90	8.0	128601	10	AC118318	AC118318 Rattus no	953	89	7.9	1298	6	BD238487	BD238487 Expressio

881	90	8.0	139653	2	AP005890	AP005890 Oryza sat
882	90	8.0	143285	9	AL139423	AL139423 Human DNA
883	90	8.0	161865	8	AP005912	AP005912 Oryza sat
C 884	90	8.0	166485	9	AC123900	AC123900 Homo sapi
885	90	8.0	170790	2	AC025609	AC025609 Homo sapi
C 886	90	8.0	179075	2	AC150138	AC150138 Gallus ga
C 887	90	8.0	184139	9	AC022966	AC022966 Homo sapi
C 888	90	8.0	197698	8	BX908809	BX908809 Neurospor
C 889	90	8.0	198922	2	AC094540	AC094540 Rattus no
890	90	8.0	227555	10	AC108416	AC108416 Mus muscu
891	90	8.0	241120	2	AC123458	AC123458 Rattus no
C 892	90	8.0	248871	2	AC094352	AC094352 Rattus no
C 893	90	8.0	256879	3	AC116982	AC116982 Dictyoste
C 894	90	8.0	290850	1	SCO939127	AL939127 Streptomy
895	90	8.0	292100	1	SCO939121	AL939121 Streptomy
896	89.5	8.0	528	8	CR377484	CR377484 Pinus pin
897	89.5	8.0	771	8	ASP389720	AJ389720 Aegilops
898	89.5	8.0	828	8	AY338395	AY338395 Triticum
899	89.5	8.0	849	8	AY338390	AY338390 Triticum
900	89.5	8.0	1014	6	AR081996	AR081996 Sequence
901	89.5	8.0	1014	6	AR198392	AR198392 Sequence
902	89.5	8.0	1173	8	PRA315701	AJ315701 Phlebia r
903	89.5	8.0	1252	8	AB062852	AB062852 Triticum
904	89.5	8.0	1275	6	AX720123	AX720123 Sequence
905	89.5	8.0	1280	8	AB062866	AB062866 Triticum
C 906	89.5	8.0	1406	4	SHPKDP	L11343 Ovis aries
C 907	89.5	8.0	1423	4	OAU00165	U00165 Ovis aries
908	89.5	8.0	1595	10	RATLGPB	M32016 Rat lysosom
909	89.5	8.0	1731	1	RLNLHASE	X64360 R.rhodochro
910	89.5	8.0	1731	6	AR008340	AR008340 Sequence
911	89.5	8.0	1731	6	E03848	E03848 DNA encodin
912	89.5	8.0	1731	6	I93631	I93631 Sequence 15
C 913	89.5	8.0	1768	8	AY188532	AY188532 Larix pot
914	89.5	8.0	2198	6	CQ605618	CQ605618 Sequence
915	89.5	8.0	2723	3	DFU20331	U20331 Drosophila
916	89.5	8.0	2780	3	AK112792	AK112792 Ciona int
917	89.5	8.0	4047	9	HSA298318	AJ298318 Homo sapi
918	89.5	8.0	6443	8	AF234649	AF234649 Triticum
C 919	89.5	8.0	9917	1	AE004558	AE004558 Pseudomon
920	89.5	8.0	10013	1	AE002558	AE002558 Neisseria
921	89.5	8.0	27551	10	AL807812	AL807812 Mouse DNA
922	89.5	8.0	39502	1	AY534910	AY534910 Unculture
923	89.5	8.0	66924	8	NCB9J10	AL356324 Neurospor
C 924	89.5	8.0	69668	2	AC131503	AC131503 Lytechinu
925	89.5	8.0	78533	9	HS278N12	AL033376 Human DNA
C 926	89.5	8.0	92591	2	AC110966_3	Continuation (4 of
927	89.5	8.0	109996	10	MMU3111612	AJ311612 Mus muscu
C 928	89.5	8.0	110000	1	CP000011_21	Continuation (22 o
C 929	89.5	8.0	110000	1	CR522870_09	Continuation (10 o
930	89.5	8.0	113946	8	AC126222	AC126222 Oryza sat
931	89.5	8.0	130058	8	AC078840	AC078840 Oryza sat
932	89.5	8.0	133093	10	AC134439	AC134439 Mus muscu
C 933	89.5	8.0	153351	2	BX546485	BX546485 Danio rer
C 934	89.5	8.0	161403	2	BX957243	BX957243 Danio rer
935	89.5	8.0	167841	2	AC125767	AC125767 Rattus no
936	89.5	8.0	172325	6	AX044035	AX044035 Sequence
937	89.5	8.0	173723	3	AC009351	AC009351 Drosophil
938	89.5	8.0	176952	8	AC084023	AC084023 Oryza sat
C 939	89.5	8.0	178416	10	AC140840	AC140840 Mus muscu
940	89.5	8.0	181936	2	AC122156	AC122156 Sus scrof
941	89.5	8.0	207161	2	AC120651	AC120651 Rattus no
C 942	89.5	8.0	218270	2	AC079499	AC079499 Mus muscu
943	89.5	8.0	238980	2	AC106296	AC106296 Rattus no
944	89.5	8.0	240525	2	AC096895	AC096895 Rattus no
C 945	89.5	8.0	251208	2	AC096610	AC096610 Rattus no
946	89.5	8.0	260673	3	AE003612	AE003612 Drosophil
C 947	89.5	8.0	301675	1	AP005027	AP005027 Streptomy
948	89.5	8.0	301934	8	AE017110	AE017110 Oryza sat
C 949	89.5	8.0	318930	2	AC073495	AC073495 Mus muscu
C 950	89.5	8.0	340806	1	NMA1Z2491	AL162752 Neisseria
951	89	7.9	904	10	AF247816	AF247816 Mus muscu
952	89	7.9	1110	6	CQ596670	CQ596670 Sequence
953	89	7.9	1298	6	BD238487	BD238487 Expressio

954	89	7.9	1640	8	D17320	D17320 Candida tro	1027	89	7.9	298900	1	AP005937	AP005937 Bradyrhiz
955	89	7.9	1789	10	BC034162	BC034162 Mus muscu	c1028	89	7.9	300217	1	AE016922	AE016922 Chromobac
c 956	89	7.9	2090	4	AF529269	AF529269 Ovis arle	1029	89	7.9	341346	2	AC146873	AC146873 Xenopus t
957	89	7.9	2298	3	AF317090	AF317090 Drosophil	c1030	88.5	7.9	300	8	CR377485	CR377485 Pinus pin
958	89	7.9	2339	9	BC021288	BC021288 Homo sapi	c1031	88.5	7.9	651	3	AY515020	AY515020 Eulimnadi
959	89	7.9	2409	6	E11341	E11341 Cellulase g	1032	88.5	7.9	948	1	AY331337	AY331337 Pseudomon
960	89	7.9	2409	6	AR213262	AR213262 Sequence	1033	88.5	7.9	1216	8	AY667097	AY667097 Aegilops
961	89	7.9	2416	9	AK092398	AK092398 Homo sapi	1034	88.5	7.9	1799	5	GGNEU27	Y14350 Gallus gall
962	89	7.9	2455	6	I55036	I55036 Sequence 1	1035	88.5	7.9	1962	3	DOAMY1	X76240 D. pseudoob
963	89	7.9	2455	9	HUMLAMP1A	J04182 Homo sapien	1036	88.5	7.9	2310	6	BD263729	BD263729 Modified
964	89	7.9	2649	8	AB048710	AB048710 Humicola	1037	88.5	7.9	2310	6	AR474254	AR474254 Sequence
965	89	7.9	2712	6	E01813	E01813 cDNA encodi	1038	88.5	7.9	2535	6	BD263721	BD263721 Modified
966	89	7.9	2716	6	E02135	E02135 cDNA encodi	1039	88.5	7.9	2535	6	AR474246	AR474246 Sequence
967	89	7.9	3177	8	AB001030	AB001030 Humicola	c1040	88.5	7.9	2665	6	CQ611648	CQ611648 Sequence
c 968	89	7.9	3183	6	CQ596669	CQ596669 Sequence	1041	88.5	7.9	4068	3	AY582941	AY582941 Litomosoi
969	89	7.9	3762	3	AY052017	AY052017 Drosophil	1042	88.5	7.9	9031	9	HSA291390	AJ291390 Homo sapi
970	89	7.9	4736	2	AC014951	AC014951 Drosophil	c1043	88.5	7.9	10481	1	AE012541	AE012541 Xanthomon
c 971	89	7.9	5162	1	AF151965	AF151965 Pseudomon	c1044	88.5	7.9	18088	1	AE004447	AE004447 Pseudomon
c 972	89	7.9	5618	1	ECNIRBC	X14202 E. coli nir	1045	88.5	7.9	26449	3	U23449	U23449 Caenorhabdi
973	89	7.9	6751	3	DMSG3378	X01918 Drosophila	c1046	88.5	7.9	73005	1	BX571966_31	Continuation (32 o
c 974	89	7.9	8660	1	AF153207	AF153207 Pseudomon	c1047	88.5	7.9	110000	1	AP006618_57	Continuation (58 o
c 975	89	7.9	9677	8	AY495602	AY495602 Gibberell	c1048	88.5	7.9	110000	2	AC095209_0	AC095209 Rattus no
c 976	89	7.9	11449	1	AE005078	AE005078 Halobacte	1049	88.5	7.9	110000	2	AC095248_3	Continuation (4 of
977	89	7.9	13496	3	DAU53698	US3698 Drosophila	1050	88.5	7.9	110000	2	AP006501_08	Continuation (9 of
978	89	7.9	41782	1	AY118081	AY118081 Streptomy	1051	88.5	7.9	110000	2	LMFLCHR36_02	Continuation (3 of
c 979	89	7.9	54695	2	AC010004	AC010004 Drosophil	1052	88.5	7.9	110000	8	CR382129_25	Continuation (26 o
980	89	7.9	56127	2	AC100393	AC100393 Mus muscu	1053	88.5	7.9	110000	8	CR382132_24	Continuation (25 o
c 981	89	7.9	83340	3	AC004438	AC004438 Drosophil	c1054	88.5	7.9	133894	6	A48542	A48542 Sequence 1
982	89	7.9	98832	9	AL137127	AL137127 Human DNA	c1055	88.5	7.9	133894	14	L22858	L22858 Autographa
983	89	7.9	99890	3	AC084464	AC084464 Caenorhab	c1056	88.5	7.9	148481	2	CR548627	CR548627 Danio rer
984	89	7.9	101762	5	AL928854	AL928854 Zebrafish	c1057	88.5	7.9	151449	9	AL954244	AL954244 Pan trogl
c 985	89	7.9	110000	1	U00096_34	Continuation (35 o	1058	88.5	7.9	160173	2	AC141008	AC141008 Rattus no
c 986	89	7.9	110000	1	ECOUW67_2	Continuation (3 of	c1059	88.5	7.9	162180	9	AC124287	AC124287 Homo sapi
987	89	7.9	110000	8	CR382128_24	Continuation (25 o	c1060	88.5	7.9	166000	3	AC104511	AC104511 Drosophil
988	89	7.9	110000	8	CR382132_06	Continuation (7 of	1061	88.5	7.9	17131	8	CNS08C8L	AL731881 Oryza sat
989	89	7.9	110000	8	CR382136_03	Continuation (4 of	c1062	88.5	7.9	173299	2	AC149469	AC149469 Canis fam
990	89	7.9	125623	3	AC115599	AC115599 Dictyoste	1063	88.5	7.9	187712	2	AC120815	AC120815 Rattus no
991	89	7.9	132891	2	BX088564	BX088564 Danio rer	1064	88.5	7.9	190676	2	AC084747	AC084747 Mus muscu
992	89	7.9	136171	2	AC141946	AC141946 Rattus no	1065	88.5	7.9	199152	2	CR382297	CR382297 Danio rer
c 993	89	7.9	137477	5	BX004882	BX004882 Zebrafish	c1066	88.5	7.9	199916	3	AC008099	AC008099 Drosophil
994	89	7.9	140327	2	AP003938	AP003938 Oryza sat	c1067	88.5	7.9	206851	2	AC094583	AC094583 Rattus no
c 995	89	7.9	142000	9	AC095353	AC095353 Homo sapi	c1068	88.5	7.9	214332	2	AC120945	AC120945 Rattus no
c 996	89	7.9	150695	2	AC023576	AC023576 Homo sapi	1069	88.5	7.9	214911	2	AC098924	AC098924 Rattus no
c 997	89	7.9	157947	8	OSJN00260	AL731614 Oryza sat	1070	88.5	7.9	215566	10	AC119805	AC119805 Mus muscu
c 998	89	7.9	160982	2	CR786564	CR786564 Danio rer	c1071	88.5	7.9	216379	9	AL954243	AL954243 Pan trogl
999	89	7.9	163063	10	BX813333	BX813333 Mouse DNA	c1072	88.5	7.9	220742	2	AC105644	AC105644 Rattus no
1000	89	7.9	167076	2	AC128174	AC128174 Rattus no	1073	88.5	7.9	224500	2	AC136530	AC136530 Rattus no
1001	89	7.9	167333	2	AC147856	AC147856 Atelerix	c1074	88.5	7.9	227442	2	AC111515	AC111515 Rattus no
c1002	89	7.9	173301	8	AP003539	AP003539 Oryza sat	c1075	88.5	7.9	227769	2	AC112437	AC112437 Rattus no
1003	89	7.9	173570	2	CR457484	CR457484 Danio rer	c1076	88.5	7.9	231008	2	AC129166	AC129166 Rattus no
1004	89	7.9	174773	5	CR383662	CR383662 Zebrafish	c1077	88.5	7.9	241974	2	AC095601	AC095601 Rattus no
c1005	89	7.9	185249	2	OSJN00223	AL731585 Oryza sat	c1078	88.5	7.9	242139	2	AC095431	AC095431 Rattus no
1006	89	7.9	186474	2	AL831728	AL831728 Mus muscu	c1079	88.5	7.9	242463	2	AC095409	AC095409 Rattus no
1007	89	7.9	188653	3	AC010033	AC010033 Drosophil	c1080	88.5	7.9	246199	2	AC119558	AC119558 Rattus no
c1008	89	7.9	190948	2	AC036131	AC036131 Homo sapi	c1081	88.5	7.9	253567	2	AC113827	AC113827 Rattus no
1009	89	7.9	191512	2	BX914207	BX914207 Danio rer	1082	88.5	7.9	254175	2	AC096015	AC096015 Rattus no
1010	89	7.9	191512	2	AC068463	AC068463 Homo sapi	1083	88.5	7.9	257028	2	AC129248	AC129248 Rattus no
1011	89	7.9	193552	9	AC097511	AC097511 Homo sapi	1084	88.5	7.9	283883	2	AC126084	AC126084 Rattus no
c1012	89	7.9	211118	2	AC073752	AC073752 Mus muscu	1085	88.5	7.9	301399	1	AE017233	AE017233 Mycobacte
1013	89	7.9	218243	2	AC141505	AC141505 Rattus no	c1086	88.5	7.9	308750	1	AP005216	AP005216 Corynebac
c1014	89	7.9	222855	2	AC096703	AC096703 Rattus no	1087	88.5	7.9	313096	2	AC131879	AC131879 Rattus no
c1015	89	7.9	235435	2	AC094124	AC094124 Rattus no	1088	88.5	7.9	330401	3	AE003575	AE003575 Drosophil
c1016	89	7.9	235468	10	AC105586	AC105586 Rattus no	1089	88.5	7.9	332029	3	AE003491	AE003491 Drosophil
1017	89	7.9	237423	2	AC149593	AC149593 Mus muscu	c1090	88.5	7.9	346357	1	BX842647	BX842647 Bdellovib
1018	89	7.9	240691	2	AC115178	AC115178 Rattus no	1091	88	7.8	310	4	AF159384	AF159384 Sus scrof
c1019	89	7.9	244742	2	AC125663	AC125663 Rattus no	1092	88	7.8	1017	11	CNS06EFT	AL395055 T7 end of
c1020	89	7.9	246143	2	AC127063	AC127063 Rattus no	1093	88	7.8	1618	8	CRECPN1C	L27473 Chlamydomon
1021	89	7.9	249691	2	AC096154	AC096154 Rattus no	1094	88	7.8	1662	6	CQ733018	CQ733018 Sequence
1022	89	7.9	249994	2	AC103191	AC103191 Rattus no	1095	88	7.8	1701	6	CQ829353	CQ829353 Sequence
1023	89	7.9	261278	2	AC130742	AC130742 Rattus no	1096	88	7.8	1738	9	HS272L161	AL049688 Human gen
1024	89	7.9	267459	2	AC118927	AC118927 Mus muscu	c1097	88	7.8	1804	8	AK073372	AK073372 Oryza sat
1025	89	7.9	269572	2	AC108552	AC108552 Rattus no	c1098	88	7.8	1852	9	AK129672	AK129672 Homo sapi
1026	89	7.9	280394	3	AE003544	AE003544 Drosophil	c1099	88	7.8	1917	9	AK093489	AK093489 Homo sapi

1100	88	7.8	1946	6	CQ588132	CQ588132 Sequence	1173	88	7.8	34866	1	BX640426	BX640426 Bordetell
1101	88	7.8	1946	6	AX254510	AX254510 Sequence	1174	88	7.8	34980	6	AX492783	AX492783 Sequence
c1102	88	7.8	1955	6	AX833072	AX833072 Sequence	1175	88	7.8	34980	6	AX553950	AX553950 Sequence
c1103	88	7.8	1955	9	AK094497	AK094497 Homo sapi	1176	87.5	7.8	543	8	AF457962	AF457962 Zea mays
1104	88	7.8	2148	9	AF253321	AF253321 Homo sapi	1177	87.5	7.8	712	3	AK174897	AK174897 Ciona int
1105	88	7.8	2165	6	AR339318	AR339318 Sequence	1178	87.5	7.8	759	6	A87197	A87197 Sequence 8
1106	88	7.8	2198	6	CQ723340	CQ723340 Sequence	1179	87.5	7.8	759	6	A87580	A87580 Sequence 8
1107	88	7.8	2447	6	AX399682	AX399682 Sequence	1180	87.5	7.8	770	6	A87196	A87196 Sequence 7
1108	88	7.8	2456	8	AK107164	AK107164 Oryza sat	1181	87.5	7.8	770	6	A87579	A87579 Sequence 7
1109	88	7.8	2474	9	BC032787	BC032787 Homo sapi	1182	87.5	7.8	823	8	AK062502	AK062502 Oryza sat
1110	88	7.8	2580	8	ATH011641	AJ011641 Arabidops	1183	87.5	7.8	834	8	TAEI33613	AJ133613 Triticum
1111	88	7.8	2612	9	AK095713	AK095713 Homo sapi	1184	87.5	7.8	914	8	AK102186	AK102186 Oryza sat
1112	88	7.8	2717	8	YLTSR1	Z69781 Y.lipolytic	1185	87.5	7.8	1358	8	AY197773	AY197773 Zea mays
1113	88	7.8	2921	8	AK099800	AK099800 Oryza sat	1186	87.5	7.8	1449	3	AK116662	AK116662 Ciona int
1114	88	7.8	2990	3	AY122212	AY122212 Drosophil	1187	87.5	7.8	1539	8	AB018537	AB018537 Yarrowia
1115	88	7.8	3153	8	AK066544	AK066544 Oryza sat	1188	87.5	7.8	1611	10	MMU70651	U70651 Mus musculu
1116	88	7.8	3227	3	AB095267	AB095267 Babesia c	1189	87.5	7.8	2036	8	AF465468	AF465468 Lolium pe
c1117	88	7.8	3946	6	CQ588131	CQ588131 Sequence	1190	87.5	7.8	2298	8	AF356870	AF356870 Candida a
c1118	88	7.8	3946	6	AX254509	AX254509 Sequence	1191	87.5	7.8	2484	9	BC021557	BC021557 Homo sapi
c1119	88	7.8	4238	10	RNCNG41	AJ000496 Rattus no	c1192	87.5	7.8	2525	1	SCDNAPABD	X86475 S.coelicolo
1120	88	7.8	4971	8	AF201084	AF201084 Secale ce	1193	87.5	7.8	2561	9	AB045292	AB045292 Homo sapi
c1121	88	7.8	10006	1	AE009473	AE009473 Brucella	1194	87.5	7.8	2578	6	BD134612	BD134612 Novel mem
1122	88	7.8	10626	1	AE014464	AE014464 Brucella	c1195	87.5	7.8	2589	3	AK115983	AK115983 Ciona int
c1123	88	7.8	11106	1	AE012183	AE012183 Xanthomon	c1196	87.5	7.8	2713	10	MMZFY	X14382 Mouse zinc
1124	88	7.8	12829	1	AE014692	AE014692 Bifidobac	1197	87.5	7.8	3306	1	CFCENC	X57858 Cellulomona
1125	88	7.8	16114	3	AB062881	AB062881 Mytilus g	1198	87.5	7.8	3671	14	ADEPP	L16239 Andean pota
c1126	88	7.8	28291	3	CEF56H9	Z74473 Caenorhabdi	1199	87.5	7.8	5249	4	S67307	S67307 Ca(2+)-sens
c1127	88	7.8	31685	3	U67956	U67956 Caenorhabdi	1200	87.5	7.8	5275	6	AR012622	AR012622 Sequence
c1128	88	7.8	51531	2	AC017444	AC017444 Drosophil	1201	87.5	7.8	5275	6	AR028465	AR028465 Sequence
1129	88	7.8	69644	1	AY179507	AY179507 Streptomy	1202	87.5	7.8	5275	6	AR078217	AR078217 Sequence
c1130	88	7.8	80167	2	AC020038	AC020038 Drosophil	1203	87.5	7.8	5275	6	ARI77781	ARI77781 Sequence
1131	88	7.8	92770	2	AC138544	AC138544 Magnaport	1204	87.5	7.8	5275	6	I75051	I75051 Sequence 1
1132	88	7.8	106973	8	U89959	U89959 Arabidopsis	c1205	87.5	7.8	10280	1	AE004808	AE004808 Pseudomon
1133	88	7.8	110000	8	CR382128_04	Continuation (5 of	1206	87.5	7.8	10643	1	AE011581	AE011581 Leptospir
1134	88	7.8	110000	8	CR382128_05	Continuation (6 of	c1207	87.5	7.8	11712	1	AE011976	AE011976 Xanthomon
1135	88	7.8	110000	8	CR382130_16	Continuation (17 o	c1208	87.5	7.8	14198	1	AE011967	AE011967 Xanthomon
c1136	88	7.8	128520	8	AP004123	AP004123 Oryza sat	1209	87.5	7.8	14568	1	AE004453	AE004453 Pseudomon
c1137	88	7.8	143561	2	CR318598	CR318598 Danio rer	c1210	87.5	7.8	25821	2	AC013226	AC013226 Drosophil
c1138	88	7.8	153749	8	AP003019	AP003019 Oryza sat	c1211	87.5	7.8	92294	1	AY117439	AY117439 Streptomy
1139	88	7.8	155366	5	BX294662	BX294662 Zebrafish	c1212	87.5	7.8	94287	1	AP005645	AP005645 Streptomy
c1140	88	7.8	166093	10	AL714011	AL714011 Mouse DNA	1213	87.5	7.8	106859	9	AL512626	AL512626 Human DNA
1141	88	7.8	167475	10	AC090881	AC090881 Mus Muscu	1214	87.5	7.8	110000	1	AE017282_23	Continuation (24 o
c1142	88	7.8	168839	5	BX004999	BX004999 Zebrafish	c1215	87.5	7.8	110000	2	AC138524_0	AC138524 Homo sapi
c1143	88	7.8	168949	9	AC046134	AC046134 Homo sapi	1216	87.5	7.8	110000	2	LMFLCHR12_12	Continuation (13 o
c1144	88	7.8	169138	3	AC010571	AC010571 Drosophil	1217	87.5	7.8	110000	2	LMFLCHR12_13	Continuation (14 o
1145	88	7.8	170240	8	AP005869	AP005869 Oryza sat	1218	87.5	7.8	110000	8	CR382128_25	Continuation (26 o
c1146	88	7.8	171329	2	AC147785	AC147785 Pan trogl	c1219	87.5	7.8	110000	9	AY528719_1	Continuation (2 of
1147	88	7.8	179661	2	CR318647	CR318647 Danio rer	1220	87.5	7.8	113212	9	AL513355	AL513355 Human DNA
1148	88	7.8	184321	2	AC025890	AC025890 Homo sapi	c1221	87.5	7.8	117099	8	AP003572	AP003572 Oryza sat
c1149	88	7.8	186939	2	CR450728	CR450728 Danio rer	c1222	87.5	7.8	120138	2	AC024624	AC024624 Mus muscu
1150	88	7.8	194785	2	AC136047	AC136047 Rattus no	1223	87.5	7.8	127643	5	BX321877	BX321877 Zebrafish
c1151	88	7.8	200906	2	BX649457	BX649457 Danio rer	c1224	87.5	7.8	143178	2	BX005034	BX005034 Homo sapi
1152	88	7.8	204579	2	CR354552	CR354552 Danio rer	c1225	87.5	7.8	144386	8	AP003538	AP003538 Oryza sat
c1153	88	7.8	207091	10	AC079443	AC079443 Mus muscu	c1226	87.5	7.8	145524	2	AC016777	AC016777 Homo sapi
c1154	88	7.8	208564	2	AC093936	AC093936 Rattus no	1227	87.5	7.8	147640	2	AP003542	AP003542 Oryza sat
1155	88	7.8	209797	5	AC146541	AC146541 Gasterost	c1228	87.5	7.8	152668	9	AC142291	AC142291 Pan trogl
1156	88	7.8	214819	2	AC145079	AC145079 Mus muscu	1229	87.5	7.8	154153	9	AL445933	AL445933 Human DNA
1157	88	7.8	227319	10	AC119894	AC119894 Mus muscu	1230	87.5	7.8	156102	7	AY129337	AY129337 Mycobacte
c1158	88	7.8	227781	2	BX649554	BX649554 Danio rer	c1231	87.5	7.8	157141	3	AC016445	AC016445 Drosophil
1159	88	7.8	237193	2	AC108555	AC108555 Rattus no	1232	87.5	7.8	164342	2	AC073982	AC073982 Homo sapi
1160	88	7.8	238090	2	AC135202	AC135202 Rattus no	c1233	87.5	7.8	169247	9	AL669970	AL669970 Human DNA
c1161	88	7.8	248550	1	SC0939120	AL939120 Streptomy	1234	87.5	7.8	170507	9	AC087530	AC087530 Homo sapi
c1162	88	7.8	252352	2	BX545917	BX545917 Danio rer	c1235	87.5	7.8	173639	10	AL606921	AL606921 Mouse DNA
c1163	88	7.8	258158	2	BX957297	BX957297 Danio rer	c1236	87.5	7.8	176349	2	AC122679	AC122679 Rattus no
1164	88	7.8	262812	2	BX510345	BX510345 Danio rer	1237	87.5	7.8	176918	2	AC109613	AC109613 Bos tauru
c1165	88	7.8	294272	3	AE003595	AE003595 Drosophil	c1238	87.5	7.8	177855	3	AC010211	AC010211 Drosophil
c1166	88	7.8	300150	1	AP004598	AP004598 Oceanobac	c1239	87.5	7.8	182041	2	AC023025	AC023025 Homo sapi
c1167	88	7.8	300425	1	AP005041	AP005041 Streptomy	c1240	87.5	7.8	182916	9	AC112482	AC112482 Homo sapi
1168	88	7.8	304985	2	CR385070	CR385070 Danio rer	1241	87.5	7.8	190563	2	BX927257	BX927257 Danio rer
c1169	88	7.8	309904	1	AE016865	AE016865 Pseudomon	1242	87.5	7.8	192096	2	AC126838	AC126838 Rattus no
c1170	88	7.8	329861	1	NMA522491	AL162756 Neisseria	c1243	87.5	7.8	192410	2	AC135831	AC135831 Rattus no
1171	88	7.8	334520	1	AP003588	AP003588 Nostoc sp	1244	87.5	7.8	207439	14	AY509253	AY509253 Ostreid h
1172	88	7.8	348624	1	BX640441	BX640441 Bordetell	c1245	87.5	7.8	208978	2	AC101932	AC101932 Mus muscu

c1246	87.5	7.8	209844	9	AC0111495	AC011495 Homo sapi	1319	87	7.7	176231	3	AC008367	AC008367 Drosophil
1247	87.5	7.8	219254	2	AC122677	AC122677 Rattus no	1320	87	7.7	180139	10	AC012297	AC012297 Mus muscu
c1248	87.5	7.8	230278	14	MCU68299	U68299 Mouse cytom	c1321	87	7.7	183914	2	AC069331	AC069331 Homo sapi
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1252	87.5	7.8	244813	2	AC097868	AC097868 Rattus no	c1325	87	7.7	198318	2	BX957253	BX957253 Danio rer
c1253	87.5	7.8	251269	2	AC119030	AC119030 Rattus no	c1326	87	7.7	200274	9	AC115088	AC115088 Homo sapi
c1254	87.5	7.8	253611	2	AC111473	AC111473 Rattus no	1327	87	7.7	200771	2	AC133587	AC133587 Homo sapi
1255	87.5	7.8	292641	3	AE003600	AE003600 Drosophil	c1328	87	7.7	205825	2	AP000881	AP000881 Homo sapi
1256	87.5	7.8	299950	1	AP005963	AP005963 Bradyrhiz	1329	87	7.7	210719	2	AC087646	AC087646 Homo sapi
c1257	87.5	7.8	300800	1	SCO939112	AL939112 Streptomy	1330	87	7.7	213217	2	CR356230	CR356230 Danio rer
c1258	87.5	7.8	301925	1	AP005046	AP005046 Streptomy	c1331	87	7.7	213359	2	AC069006	AC069006 Homo sapi
c1259	87.5	7.8	343504	2	AL158031	AL158031 Homo sapi	c1332	87	7.7	218631	2	AC109532	AC109532 Rattus no
1260	87	7.7	705	10	RNMUCINR	Z29072 R.norvegicu	1333	87	7.7	219180	2	AC092251	AC092251 Mus muscu
1261	87	7.7	765	10	BC021158	BC021158 Mus muscu	c1334	87	7.7	221911	2	AC114095	AC114095 Rattus no
1262	87	7.7	790	6	AR560749	AR560749 Sequence	c1335	87	7.7	221001	2	AC130981	AC130981 Rattus no
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1264	87	7.7	867	6	AR279196	AR279196 Sequence	c1337	87	7.7	235050	2	AC106979	AC106979 Rattus no
1265	87	7.7	867	6	AR279197	AR279197 Sequence	c1338	87	7.7	241420	2	AC094501	AC094501 Rattus no
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1269	87	7.7	927	8	AF175312	AF175312 Triticum	1342	87	7.7	304713	3	AE003502	AE003502 Drosophil
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1279	87	7.7	2464	9	AF428261	AF428261 Homo sapi	1352	86.5	7.7	1368	6	AI0377	AI0377 Artificial
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c1285	87	7.7	8778	10	MMU27268	U27268 Mus musculu	c1358	86.5	7.7	2113	8	AK099094	AK099094 Oryza sat
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c1289	87	7.7	11361	1	AE011741	AE011741 Xanthomon	1362	86.5	7.7	2541	6	BD263720	BD263720 Modified
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c1292	87	7.7	16377	3	AF202180	AF202180 Plasmodiu	1365	86.5	7.7	2940	1	AY184167	AY184167 Chlamydia
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c1294	87	7.7	73424	2	AC0129508	AC0129508 Homo sapi	1367	86.5	7.7	2943	1	AY184168	AY184168 Chlamydia
1295	87	7.7	85740	2	AC014942	AC014942 Drosophil	1368	86.5	7.7	3079	9	HUMHOX13G	M26679 Homo sapien
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c1309	87	7.7	146080	5	AL9533855	AL9533855 Zebrafish	1382	86.5	7.7	10944	1	AE004771	AE004771 Pseudomon
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c1311	87	7.7	157011	2	AC140115	AC140115 Rattus no	c1384	86.5	7.7	42416	9	AC005551	AC005551 Homo sapi
c1312	87	7.7	161547	9	AP001929	AP001929 Homo sapi	c1385	86.5	7.7	45256	9	AC084035	AC084035 Homo sapi
1313	87	7.7	161996	3	AC008284	AC008284 Drosophil	1386	86.5	7.7	79554	8	NCB11B23	AL669991 Neurospor
1314	87	7.7	166007	9	H5BA425A6	AL121749 Human DNA	c1387	86.5	7.7	85109	8	ATT2J13	AL132967 Arabidops
1315	87	7.7	166935	3	AC010920	AC010920 Drosophil	1388	86.5	7.7	91436	8	NCB14A6	AL670007 Neurospor
c1316	87	7.7	167013	9	HSDJ828H9	AL121757 Human DNA	c1389	86.5	7.7	109672	8	AP004119	AP004119 Oryza sat
1317	87	7.7	173597	2	AC025749	AC025749 Homo sapi	c1390	86.5	7.7	110000	1	AE000516_37	Continuation (38 o
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ORIGIN
Alignment Scores:
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Score:          1125.00      Matches:    218
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US-10-063-670-6_COPY_17_234 (1-218) x AF127670 (1-1285)

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Db      229  AGAATTATGGGATCACCCCTGTGAGCAAAAAGGCGACCAAGCAGCTGAATTCACAGAA 288

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QY      61  AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
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DEFINITION Sequence 149 from Patent EP1067182.
ACCESSION  AX136227
VERSION     AX136227.1  GI:14272635
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
TITLE       Secretory protein or membrane protein
JOURNAL     Patent: EP 1067182-A 149 10-JAN-2001;
            Helix Research Institute (JP)
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ORIGIN
Alignment Scores:
Pred. No.:      6.08e-83      Length:      1755
Score:          1125.00      Matches:    218
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:    0
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US-10-063-670-6_COPY_17_234 (1-218) x AX136227 (1-1755)

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Db      309  AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTCACAGAA 368

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QY      101  LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
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Qy	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
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LOCUS	BD123566	1755 bp	DNA linear PAT 18-SEP-2002
DEFINITION	Secretory protein or membrane protein.		
ACCESSION	BD123566		
VERSION	BD123566.1	GI:23218511	
KEYWORDS	JP 2002017376-A/75.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 1755)	
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: JP 2002017376-A 75 22-JAN-2002;		
	HELIX RESEARCH INSTITUTE		
COMMENT	OS Homo sapiens (human)		
	PN JP 2002017376-A/75		
	PD 22-JAN-2002		
	PF 07-JUL-2000 JP 2000253173		
	PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU		
	PI SUGIYAMA,		
	PI KOJI HAYASHI		
	PC		
	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/	PC	
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FT	CDS	(201)..(1166).	
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Alignment Scores:			
Pred. No.:	6.08e-83	Length:	1755
Score:	1125.00	Matches:	218
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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Db	309	AGAATTATGGGGATCACCTTGTGAGCAAAAGCGCAACCAGCAGCTGAATTTACAGAA	368
Qy	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60

Db	369	GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA	428
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
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Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	489	ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTGG	548
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	549	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACT	608
Qy	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	609	AACTCGTGCAATCCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCA	668
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	669	ACACAAACAACAGAAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT	728
Qy	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	729	ACAATACCTGCCCTACTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	788
Qy	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	789	AAAAAATTGATTGTGTACAGAAAGTTTATTGGAACCTAGCACCATGTCTACAGAAACT	848
Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	849	GAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA	902
RESULT 4			
AK075443			
LOCUS	AK075443	1755 bp	mRNA linear PRI 03-SEP-2002
DEFINITION	Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar to Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1 mRNA.		
ACCESSION	AK075443		
VERSION	AK075443.1	GI:22761535	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.		
TITLE	HRI human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 1755)	
AUTHORS	Isogai,T. and Yamamoto,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)		
COMMENT	HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.		
FEATURES	Location/Qualifiers		
source	1..1755		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="PLACE1004850"		
	/tissue type="placenta"		
	/clone_lib="PLACE1"		

ORIGIN

Alignment Scores:
Pred. No.: 6.08e-83 Length: 1755
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AK075443 (1-1755)

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20

Db 249 ACGAGGCTCCTGGTCCAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGC 308

QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 309 AGAATTATGGGATCACCCCTGTGAGCAAAAAGCGCAACAGCAGCTGAATTCACAGAA 368

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 369 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA 428

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 429 GCCTTGAAAGCTAGCTTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTC 488

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 489 ATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGG 548

QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 549 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 608

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 609 AACTCGTGCAATTCAGAAATTATCACCACCAAGATCCCATATTC AACACTCAAAC TGCA 668

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 669 ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT 728

QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180

Db 729 ACAATACCTGCCCTACTACTACTCCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 788

QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200

Db 789 AAAAAAATTGATTTGTGTACAGAAAGTTTATTATGGAAACTAGCACCATGTCTACAGAAACT 848

QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218

Db 849 GAACCATTTGTTGAAAAATAAAGCAGCATTC AAGAATGAAGCTGCTGGGTTTGA 902

RESULT 5

BD222718

LOCUS BD222718 2029 bp DNA linear PAT 17-JUL-2003

DEFINITION Human signal peptide-containing protein.

ACCESSION BD222718

VERSION BD222718.1 GI:33032488

KEYWORDS JP 2002519030-A/64.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2029)

AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.

TITLE Human signal peptide-containing protein

JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;

INCYTE PHARMACEUTICALS INC

COMMENT OS Homo sapiens (human)

PN JP 2002519030-A/64

PD 02-JUL-2002

PF 25-JUN-1999 JP 2000557363

PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR

01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI

LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,

PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,

PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN

PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,

PC A61P25/00,

PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC

C12N1/19,

PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC

C12N15/00,

PC A61K37/02,C12N5/00

CC Incyte Clone No: 3044710

FH Key Location/Qualifiers

FT source 1..2029

FT /organism='Homo sapiens (human)'

FEATURES source Location/Qualifiers

1..2029 /organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7.24e-83 Length: 2029
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x BD222718 (1-2029)

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20

Db 231 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGC 290

QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 291 AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTCACAGAA 350

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 351 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA 410

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 411 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTC 470

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 471 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCCTGATTGG 530

QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 531 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACT 590

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 591 AACTCGTGCATTC CAGAAATTTATCACCACCAAGATCCCATATTC AACACTCAAAC TGCA 650

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 651 ACACAAACAACAGAAATTTATTGT CAGTGACAGTACTCGGTGGCATCCCTTACTCT 710

QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180

Db 711 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 770

Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200

Db 771 AAAAAATTGATTGTGTACAGAGTTTATGGAAACTAGCACCATGTCTACAGAAACT 830

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218

Db 831 GAACCATTTGTTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA 884

RESULT 6

AR204700

LOCUS AR204700 2029 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 13 from patent US 6368794.

ACCESSION AR204700

VERSION AR204700.1 GI:21502094

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2029)

AUTHORS Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.

TITLE Detection of altered expression of genes regulating cell proliferation

JOURNAL Patent: US 6368794-A 13 09-APR-2002;

FEATURES Location/Qualifiers

source 1..2029

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.24e-83 Length: 2029

Score: 1125.00 Matches: 218

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AR204700 (1-2029)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20

Db 231 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCTATGC 290

Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGlu 40

Db 291 AGAATTATGGGATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTTCACAGAA 350

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 351 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 410

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 411 GCCTTGAAAGCTAGCTTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTC 470

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 471 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTGTCCTGATTGG 530

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 531 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACT 590

Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 591 AACTGTGCATTCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCA 650

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 651 ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCCTTACTCT 710

Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180

Db 711 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 770

Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200

Db 771 AAAAAATTGATTGTGTACAGAGTTTATGGAAACTAGCACCATGTCTACAGAAACT 830

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218

Db 831 GAACCATTTGTTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA 884

RESULT 7

CQ720788

LOCUS CQ720788 2312 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 6722 from Patent WO02068579.

ACCESSION CQ720788

VERSION CQ720788.1 GI:42281645

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 6722 06-SEP-2002;

FEATURES Location/Qualifiers

source 1..2312

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 8.48e-83 Length: 2312

Score: 1125.00 Matches: 218

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x CQ720788 (1-2312)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20

Db 140 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCTATGC 199

Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 200 AGAATTATGGGATCACCCCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTTCACAGAA 259

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 260 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 319

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 320 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC 379

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 380 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTGG 439

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 440 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 499

Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 500 AACTCGTGCATTCCAGAAATTATCACCACCACCAAGATCCCATATTCAACACTCAAACACTGCA 559

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
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Db 560 ACACAAACAACAGAAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCCCTACTCT 619

Qy 161 ThrIleProAlaProThrThrProProAlaProAlaSerThrSerIleProArgArg 180
|||||

Db 620 ACAATACCTGCCCTACTACT 679

Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
|||||

Db 680 AAAAAATTGATTGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATTGCTCTACAGAAACT 739

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
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Db 740 GAACCAATTTGTTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGA 793

RESULT 8

BD172392

LOCUS

DEFINITION

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

BD172392

VERSION

BD172392.1 GI:28413692

KEYWORDS

JP 2002223786-A/165.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL

Patent: JP 2002223786-A 165 13-AUG-2002;

COMMENT

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002223786-A/165

PD 13-AUG-2002

PF 18-DEC-2001 JP 2001385135

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR

31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC

C12N5/10,

PC

C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC

(C12P21/02,C12R1:645),C12N15/00,C12N5/00

CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same

FH Key Location/Qualifiers

FT source 1..2372

FT /organism='Homo sapiens (human)'. FEATURES source 1..2372

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 8.75e-83 Length: 2372

Score: 1125.00 Matches: 218

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x BD172392 (1-2372)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
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Db 208 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGC 267

Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
|||||

Db 268 AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACAGCAGCTGAATTTACAGAA 327

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
|||||

Db 328 GCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACA 387

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
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Db 388 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGGTGC 447

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
|||||

Db 448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGTGTCTCGATTGG 507

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
|||||

Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTGGACT 567

Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
|||||

Db 568 AACTCGTGCATTCCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACACTGCA 627

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
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Db 628 ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTACTCT 687

Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
|||||

Db 688 ACAATACCTGCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747

Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
|||||

Db 748 AAAAAATTGATTGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT 807

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
|||||

Db 808 GAACCAATTTGTTGAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGA 861

RESULT 9

BD172711

LOCUS

DEFINITION

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION

BD172711

LOCUS

DEFINITION

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION

BD172711

VERSION BD172711.1 GI:28414015
KEYWORDS JP 2002238586-A/165.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 165 27-AUG-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002238586-A/165
PD 27-AUG-2002
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC
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encoding the same
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FT /organism='Homo sapiens (human)'.
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Pred. No.: 8.75e-83 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
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ACCESSION BD173030
VERSION BD173030.1 GI:28414336
KEYWORDS JP 2002238587-A/165.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238587-A 165 27-AUG-2002;
GENENTECH INC
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PN JP 2002238587-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385248
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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
JIAN ZHENG,		
PI JEAN YUAN		
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC		
C12N15/02,		
PC		
C12P21/02, C12P21/08// (C12P21/02, C12R1:91), (C12P21/02, C12R1:19), PC		
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VERSION	BD173349.1	GI:28414660	
KEYWORDS	JP 2002238588-A/165.		
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ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 2372) Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238588-A 165 27-AUG-2002;		
COMMENT	GENENTECH INC		
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	WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI		
	JIAN ZHENG,		
	PI	JEAN YUAN	
PC	C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21,	PC	

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encoding the same
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DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
BD175383 2372 bp DNA linear PAT 18-MAR-2003

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VERSION	BD175383.1 GI:29121079								
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AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.								
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JOURNAL	Patent: JP 2002253280-A 165 10-SEP-2002; GENENTECH INC								
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	PN JP 2002253280-A/165								
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI									
JIAN ZHENG,									
PI	JEAN YUAN								
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QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	268	AGAATTATGGGATCACCTTGTCAGCAAAAAGCGAACCCAGCAGCTGAATTCACAGAA	327
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	328	GCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTTGCCCGCAAGGACCAAGTTGAAACA	387
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	388	GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTC	447
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
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QY	101	lysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
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QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	568	AACTCGTGCATTCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA	627
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QY	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
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QY	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	748	AAAAAATTGATTGTGTCAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT	807
QY	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	808	GAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGGA	861
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LOCUS	AR410761	2372 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 200 from patent US 6635468.		
ACCESSION	AR410761		
VERSION	AR410761.1 GI:40162261		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2372)		
AUTHORS	Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: US 6635468-A 200 21-OCT-2003;		
FEATURES	Location/Qualifiers		
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	/mol_type="genomic DNA"		
ORIGIN			

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	268	AGAATTATGGGGATCACCTTGTGAGCAAAAAGSGCAACCCAGCAGCTGAATTTACACAGAA	327
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	328	GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA	387
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
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QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
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QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	508	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACT	567
QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
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QY	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL Patent: US 6664376-A 200 16-DEC-2003;
FEATURES Location/Qualifiers
source 1. .2372
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores: 8.75e-83 Length: 2372
Pred. No.: 1125.00 Matches: 218
Score: 1125.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AR439125 (1-2372)

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Db 268 AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAA 327

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
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Db 328 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 387

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80
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Db 388 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTC 447

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
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Db 568 AACTCGTGCATTCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 627

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
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QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
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LOCUS AR473145 2372 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 200 from patent US 6686451.
ACCESSION AR473145
VERSION AR473145.1 GI:42708520
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Mather,J.P.,

TITLE Williams,P.M. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6686451-A 200 03-FEB-2004;
FEATURES Location/Qualifiers
source 1. .2372
/organism="unknown"
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ORIGIN

Alignment Scores: 8.75e-83 Length: 2372
Pred. No.: 1125.00 Matches: 218
Score: 1125.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-063-670-6_COPY_17_234 (1-218) x AR473145 (1-2372)

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QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
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QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
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Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTGGACT 567

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
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QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
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Db 628 ACACAAACAACAGAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT 687

QY 161 ThrIleProAlaProThrThrProProAlaProAlaSerThrSerIleProArgArg 180
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Search completed: October 9, 2005, 01:20:55
Job time : 3815.72 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 16:31:30 ; Search time 2812.6 Seconds
 (without alignments)
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Title: US-10-063-670-6_COPY_17_234
Perfect score: 1125
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 Fgapop 6.0 , Fgapext 7.0
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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 7: gb_est6: *
 8: gb_gss1: *
 9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
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BE756611	210798 MA
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92	353.5	31.4	1298	7	CF110966	CF110966 Shultzomi	165	198.5	17.6	750	6	CD466893	CD466893 LeukoN2_8
93	349.5	31.1	479	2	BE847124	BE847124 uw22b07.y	166	198.5	17.6	2851	3	AK045226	AK045226 Mus muscu
94	344	30.6	883	5	BU239567	BU239567 603322730	167	197.5	17.5	831	4	BI856036	BI856036 603383421
95	341	30.3	656	4	BM426481	BM426481 pgf2n.pk0	168	197.5	17.5	886	7	CF251786	CF251786 hdm004_c0
96	322	28.6	371	2	BE684197	BE684197 184504_MA	169	197	17.5	976	4	BM562794	BM562794 AGENCOURT
97	309	27.5	807	5	BU125818	BU125818 603150355	170	196.5	17.5	499	6	CD285349	CD285349 G39163.54
98	305	27.1	328	1	AA297240	AA297240 EST112782	171	196.5	17.5	658	6	CD469720	CD469720 LeukoS2_8
99	299.5	26.6	469	2	BF471572	BF471572 UI-M-BH3-	172	196.5	17.5	660	6	CD469535	CD469535 LeukoS2_4
100	293.5	26.1	747	5	BU324601	BU324601 603492075	173	196.5	17.5	669	6	CD470836	CD470836 LeukoS5_2
101	277.5	24.7	449	2	BF041814	BF041814 BP250014B	174	196.5	17.5	810	6	CB314546	CB314546 AGENCOURT
102	269.5	24.0	351	6	CB780898	CB780898 AMGNNUC:C	175	196.5	17.5	819	4	BI333992	BI333992 602997261
103	262.5	23.3	652	7	CF250037	CF250037 esa007.f1	176	196.5	17.5	851	4	BM7450268	BM7450268 602709071
104	256.5	22.8	813	5	BU388030	BU388030 603582582	177	196	17.4	588	4	BM742218	BM742218 K-EST0014
105	250.5	22.3	353	5	BY318491	BY318491 BY318491	178	196	17.4	636	7	CV026388	CV026388 4311_Full1
106	250.5	22.3	801	7	CK030244	CK030244 AGENCOURT	179	196	17.4	654	7	CN347082	CN347082 170005318
107	248	22.0	811	7	CF285506	CF285506 AGENCOURT	180	196	17.4	666	7	CN347074	CN347074 170004248
108	246.5	21.9	895	6	CA474635	CA474635 AGENCOURT	181	196	17.4	698	7	CN347073	CN347073 170005325
109	245	21.8	906	7	CF546586	CF546586 AGENCOURT	182	196	17.4	699	4	BM763301	BM763301 K-EST0044
110	243.5	21.6	354	5	BY107653	BY107653 BY107653	183	196	17.4	728	4	BI769128	BI769128 603053720
111	241	21.4	723	7	CF547545	CF547545 AGENCOURT	184	196	17.4	730	7	CN347080	CN347080 170004708
112	240	21.3	242	2	AW318386	AW318386 um96a08.y	185	196	17.4	735	7	CN347081	CN347081 170004249
113	232.5	20.7	576	2	BQ400750	BQ400750 NISC.mp11	186	196	17.4	764	4	BG759720	BG759720 602711117
114	226.5	20.1	385	7	W29485	W29485 mc02a12.rl	187	196	17.4	791	1	AL548444	AL548444 AL548444
115	226.5	20.1	579	1	AI391129	AI391129 mc02a12.y	188	196	17.4	820	4	BG760275	BG760275 602716678
116	226	20.1	868	7	CF379047	CF379047 AGENCOURT	189	196	17.4	827	4	BI833320	BI833320 603087916
117	224	19.9	759	7	CF285642	CF285642 AGENCOURT	190	196	17.4	858	5	BQ223902	BQ223902 AGENCOURT
118	224	19.9	833	6	CD361163	CD361163 AGENCOURT	191	196	17.4	864	1	AL548999	AL548999 AL548999
119	220.5	19.6	431	4	BG657011	BG657011 dab27a03.	192	196	17.4	879	5	BQ962000	BQ962000 AGENCOURT
120	218	19.4	600	6	CB512734	CB512734 ssalrgb54	193	196	17.4	885	7	CF257093	CF257093 pha006_f1
121	217	19.3	827	7	CK471875	CK471875 AGENCOURT	194	196	17.4	889	7	CF251893	CF251893 hdm005_f1
122	216	19.2	774	5	BP169122	BP169122	195	196	17.4	890	5	BU158569	BU158569 AGENCOURT
123	216	19.2	905	5	BP166057	BP166057	196	196	17.4	903	6	CA455121	CA455121 AGENCOURT
124	215.5	19.2	766	5	BP167565	BP167565	197	196	17.4	906	5	BU149945	BU149945 AGENCOURT
125	215	19.1	599	6	CB515759	CB515759 ssalrgb51	198	196	17.4	916	5	BU166171	BU166171 AGENCOURT
126	215	19.1	825	5	BP157524	BP157524	199	196	17.4	923	5	BQ946450	BQ946450 AGENCOURT
127	214.5	19.1	423	2	AW419846	AW419846 fj84c10.y	200	196	17.4	940	4	BG747697	BG747697 602705169
128	213.5	19.0	800	9	AY411059	AY411059 Mus muscu	201	196	17.4	985	5	BU168480	BU168480 AGENCOURT
129	213	18.9	974	7	CK404422	CK404422 AUF_lfhdk	202	196	17.4	985	5	BX356719	BX356719 BX356719
130	212	18.8	913	7	CK410366	CK410366 AUF_lphdk	203	196	17.4	1004	5	BX439725	BX439725 BX439725
131	211.5	18.8	599	6	CB582683	CB582683 AMGNNUC:N	204	196	17.4	1010	1	AL552534	AL552534 AL552534
132	211.5	18.8	763	7	CO570158	CO570158 AGENCOURT	205	196	17.4	1085	5	BM913991	BM913991 AGENCOURT
133	211.5	18.8	810	7	CK476032	CK476032 AGENCOURT	206	196	17.4	1876	3	CR596847	CR596847 full-leng
134	209.5	18.6	563	5	BQ566621	BQ566621 gi64e12.y	207	196	17.4	1955	3	CR621045	CR621045 full-leng
135	209	18.6	721	7	CF763972	CF763972 CES004694	208	195.5	17.4	832	4	BG114530	BG114530 602284857
136	208	18.5	793	7	CN823883	CN823883 Oa splbn	209	195.5	17.4	984	5	BQ677018	BQ677018 AGENCOURT
137	205.5	18.3	824	7	CK791054	CK791054 AGENCOURT	210	195.5	17.4	1054	5	BM918483	BM918483 AGENCOURT
138	203.5	18.1	598	6	CA367101	CA367101 642837_NC	211	195	17.3	476	2	AW501445	AW501445 UI-HF-BP0
139	203	18.0	706	7	CN823877	CN823877 Oa splbn	212	195	17.3	579	5	BP268197	BP268197 BP268197
140	202.5	18.0	619	5	BQ393883	BQ393883 NISC_ng06	213	195	17.3	738	5	BU195946	BU195946 AGENCOURT
141	202.5	18.0	838	7	CF727499	CF727499 UI-M-HB0-	214	195	17.3	801	2	BE570280	BE570280 601332944
142	202	18.0	828	4	BG170766	BG170766 602323885	215	195	17.3	928	5	BQ683148	BQ683148 AGENCOURT
143	201	17.9	821	6	CA846294	CA846294 haa12a06.	216	195	17.3	1067	1	AL544334	AL544334 AL544334
144	201	17.9	867	5	BU184888	BU184888 AGENCOURT	217	194	17.2	574	4	BM742230	BM742230 K-EST0015
145	201	17.9	1085	4	BM550721	BM550721 AGENCOURT	218	194	17.2	583	5	BP280870	BP280870 BP280870
146	200.5	17.8	864	5	BQ690615	BQ690615 AGENCOURT	219	194	17.2	625	4	BG822513	BG822513 602725591
147	200	17.8	1024	5	BM904914	BM904914 AGENCOURT	220	194	17.2	660	4	BM745022	BM745022 K-EST0018
148	199.5	17.7	750	6	CD467776	CD467776 LeukoS1_6	221	194	17.2	662	5	BQ109366	BQ109366 imageqc_6
149	199	17.7	578	4	BI008726	BI008726 QV3-RT007	222	194	17.2	667	6	CB125104	CB125104 K-EST0173
150	199	17.7	627	5	BP280494	BP280494 BP280494	223	194	17.2	668	4	BG421565	BG421565 602452141
151	199	17.7	834	5	BU150725	BU150725 AGENCOURT	224	194	17.2	668	4	BM763472	BM763472 K-EST0044
152	199	17.7	1906	3	AK087472	AK087472 Mus muscu	225	194	17.2	670	6	CB141293	CB141293 K-EST0194
153	198.5	17.6	592	7	CN660471	CN660471 A0705G09-	226	194	17.2	676	4	BG250321	BG250321 602362454
154	198.5	17.6	615	7	CF907877	CF907877 A0516A04-	227	194	17.2	678	6	CB136318	CB136318 K-EST0188
155	198.5	17.6	623	7	CN661635	CN661635 A0721H04-	228	194	17.2	757	4	BI821097	BI821097 603035569

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229	194	17.2	796	5	BU527984	AGENCOURT	302	190	16.9	581	5	BP225898	BP225898
230	194	17.2	805	4	BG822701	602725835	303	190	16.9	581	5	BP237035	BP237035
231	194	17.2	883	5	BQ877431	AGENCOURT	304	190	16.9	581	5	BP252243	BP252243
232	194	17.2	913	4	BG327238	602426190	305	190	16.9	581	5	BP252906	BP252906
233	193.5	17.2	677	6	BY744790	BY744790	306	190	16.9	581	5	BP278646	BP278646
234	193.5	17.2	1036	5	BM908486	AGENCOURT	307	190	16.9	581	5	BP280300	BP280300
235	193	17.2	630	6	CD470529	LeukoS4_5	308	190	16.9	581	5	BP280869	BP280869
236	193	17.2	635	6	CD468828	LeukoS3_7	309	190	16.9	581	5	BP285640	BP285640
237	193	17.2	647	6	CD469564	LeukoS2_4	310	190	16.9	581	5	BP295553	BP295553
238	193	17.2	649	6	CD469238	LeukoS2_2	311	190	16.9	581	5	BP297294	BP297294
239	193	17.2	668	4	BI855939	603383313	312	190	16.9	581	5	BP323904	BP323904
240	192.5	17.1	572	6	CB016588	pgn1c.pk0	313	190	16.9	581	5	BP354214	BP354214
241	192.5	17.1	1184	5	BM906074	AGENCOURT	314	190	16.9	581	5	BP355784	BP355784
242	192	17.1	582	5	BP236685	BP236685	315	190	16.9	582	5	BP215631	BP215631
243	192	17.1	582	5	BP278321	BP278321	316	190	16.9	582	5	BP222379	BP222379
244	192	17.1	582	5	BP353372	BP353372	317	190	16.9	582	5	BP222548	BP222548
245	192	17.1	743	6	CB318661	AGENCOURT	318	190	16.9	582	5	BP223038	BP223038
246	192	17.1	959	5	BQ935522	AGENCOURT	319	190	16.9	582	5	BP225812	BP225812
247	192	17.1	976	5	BQ957776	AGENCOURT	320	190	16.9	582	5	BP230984	BP230984
248	191.5	17.0	500	6	CD734509	4048585_1	321	190	16.9	582	5	BP231716	BP231716
249	191.5	17.0	582	7	CF256984	pha005_c0	322	190	16.9	582	5	BP278171	BP278171
250	191.5	17.0	608	7	CF257313	pha009_f1	323	190	16.9	582	5	BP278171	BP278171
251	191.5	17.0	660	6	CD468968	LeukoS3_8	324	190	16.9	582	5	BP278231	BP278231
252	191.5	17.0	739	1	AJ450624	AJ450624	325	190	16.9	582	5	BP278305	BP278305
253	191.5	17.0	775	7	CN218866	RJA040G05	326	190	16.9	582	5	BP278475	BP278475
254	191.5	17.0	855	7	CF257095	pha006_g0	327	190	16.9	582	5	BP278491	BP278491
255	191.5	17.0	859	7	CF257757	pha015_a1	328	190	16.9	582	5	BP279295	BP279295
256	191.5	17.0	881	7	CF251803	hdm004_e0	329	190	16.9	582	5	BP279324	BP279324
257	191	17.0	393	7	CF144025	UI-HF-BP0	330	190	16.9	582	5	BP279363	BP279363
258	191	17.0	515	4	BM753415	K-EST0030	331	190	16.9	582	5	BP280048	BP280048
259	191	17.0	536	5	BP162646	BP162646	332	190	16.9	582	5	BP280228	BP280228
260	191	17.0	565	5	BP267691	BP267691	333	190	16.9	582	5	BP280613	BP280613
261	191	17.0	582	5	BP278066	BP278066	334	190	16.9	582	5	BP280921	BP280921
262	191	17.0	582	5	BP356315	BP356315	335	190	16.9	582	5	BP280955	BP280955
263	191	17.0	587	5	BP354072	BP354072	336	190	16.9	582	5	BP280957	BP280957
264	191	17.0	598	5	BP279982	BP279982	337	190	16.9	582	5	BP298145	BP298145
265	191	17.0	602	5	BP279073	BP279073	338	190	16.9	582	5	BP303210	BP303210
266	191	17.0	625	2	AW732339	bb03b02.y	339	190	16.9	582	5	BP335831	BP335831
267	191	17.0	697	4	BG912337	BG912337	340	190	16.9	582	5	BP336193	BP336193
268	190.5	16.9	503	6	CA573126	K0546C07-	341	190	16.9	582	5	BP352339	BP352339
269	190.5	16.9	504	5	BQ562475	H4076B11-	342	190	16.9	582	5	BP353072	BP353072
270	190.5	16.9	509	2	AW761944	ur51f10.y	343	190	16.9	582	5	BP353576	BP353576
271	190.5	16.9	519	6	CA570202	K0503C08-	344	190	16.9	582	5	BP355366	BP355366
272	190.5	16.9	521	6	CA570891	K0513B10-	345	190	16.9	582	5	BP363182	BP363182
273	190.5	16.9	522	6	CA873377	K0924G02-	346	190	16.9	582	5	BP363335	BP363335
274	190.5	16.9	546	6	CA883079	B0101A04-	347	190	16.9	582	5	BP365020	BP365020
275	190.5	16.9	581	6	CA896005	B0196A07-	348	190	16.9	582	5	BP365667	BP365667
276	190.5	16.9	820	4	BM051234	603634189	349	190	16.9	582	5	BP365708	BP365708
277	190.5	16.9	951	4	BG119674	602347092	350	190	16.9	582	5	BP365745	BP365745
278	190.5	16.9	973	4	BI820251	603036802	351	190	16.9	583	5	BP234498	BP234498
279	190	16.9	512	4	BM744870	K-EST0018	352	190	16.9	583	5	BP234878	BP234878
280	190	16.9	545	6	CB135807	K-EST0188	353	190	16.9	583	5	BP236879	BP236879
281	190	16.9	550	5	BP377364	BP377364	354	190	16.9	583	5	BP278008	BP278008
282	190	16.9	553	4	BM846600	K-EST0125	355	190	16.9	583	5	BP278196	BP278196
283	190	16.9	556	6	CB141325	K-EST0194	356	190	16.9	583	5	BP278366	BP278366
284	190	16.9	556	6	CB141372	K-EST0194	357	190	16.9	583	5	BP278548	BP278548
285	190	16.9	558	7	CN482614	hw22e06.y	358	190	16.9	583	5	BP278697	BP278697
286	190	16.9	561	4	BM743702	K-EST0016	359	190	16.9	583	5	BP278792	BP278792
287	190	16.9	563	4	BM840881	K-EST0118	360	190	16.9	583	5	BP278933	BP278933
288	190	16.9	569	4	BM848299	K-EST0128	361	190	16.9	583	5	BP279202	BP279202
289	190	16.9	569	4	BM853235	K-EST0134	362	190	16.9	583	5	BP279356	BP279356
290	190	16.9	573	1	AU280746	AU280746	363	190	16.9	583	5	BP279519	BP279519
291	190	16.9	576	5	BP279188	BP279188	364	190	16.9	583	5	BP279772	BP279772
292	190	16.9	578	4	BM742678	K-EST0015	365	190	16.9	583	5	BP280081	BP280081
293	190	16.9	579	5	BP363851	BP363851	366	190	16.9	583	5	BP280334	BP280334
294	190	16.9	580	5	BP236550	BP236550	367	190	16.9	583	5	BP280604	BP280604
295	190	16.9	580	5	BP272835	BP272835	368	190	16.9	583	5	BP280708	BP280708
296	190	16.9	581	4	BI824066	603038788	369	190	16.9	583	5	BP280810	BP280810
297	190	16.9	581	5	BP206044	BP206044	370	190	16.9	583	5	BP280838	BP280838
298	190	16.9	581	5	BP221857	BP221857	371	190	16.9	583	5	BP281053	BP281053
299	190	16.9	581	5	BP221889	BP221889	372	190	16.9	583	5	BP281058	BP281058
300	190	16.9	581	5	BP222451	BP222451	373	190	16.9	583	5	BP281074	BP281074
301	190	16.9	581	5	BP222755	BP222755	374	190	16.9	583	5	BP341512	BP341512

375 190 16.9 583 5 BP352289 BP352289 448 186 16.5 521 6 CD469959 LeukoS4_2
376 190 16.9 583 5 BP353855 BP353855 449 186 16.5 526 6 CD464259 LeukoN4_2
377 190 16.9 583 5 BP354184 BP354184 450 186 16.5 533 6 CD471150 LeukoS5_4
378 190 16.9 584 5 BP280286 BP280286 451 186 16.5 548 6 CD469967 LeukoS4_2
379 190 16.9 585 5 BP253708 BP253708 452 186 16.5 549 6 CD469106 LeukoS2_1
380 190 16.9 585 6 CB129134 CB129134 K-EST0178 453 186 16.5 549 6 CD471912 LeukoS6_2
381 190 16.9 587 5 BP278759 BP278759 454 186 16.5 554 6 CD469251 LeukoS2_2
382 190 16.9 587 5 BP278794 BP278794 455 186 16.5 571 6 CD470950 LeukoS5_3
383 190 16.9 587 5 BP279977 BP279977 456 186 16.5 576 6 CD471137 LeukoS5_4
384 190 16.9 587 5 BP280171 BP280171 457 186 16.5 579 6 CD465192 LeukoN1_2
385 190 16.9 587 5 BP365344 BP365344 458 186 16.5 582 5 BP365073 BP365073
386 190 16.9 588 5 BP236489 BP236489 459 186 16.5 584 6 CD468526 LeukoS3_3
387 190 16.9 588 5 BP277748 BP277748 460 186 16.5 596 6 CD471747 LeukoS6_4
388 190 16.9 588 5 BP278268 BP278268 461 186 16.5 599 6 CD471683 LeukoS6_4
389 190 16.9 588 5 BP279065 BP279065 462 186 16.5 602 6 CD470977 LeukoS5_3
390 190 16.9 588 5 BP365173 BP365173 463 186 16.5 602 6 CD535917 LeukoN5_5
391 190 16.9 589 5 BP233222 BP233222 464 186 16.5 607 5 BP280139 BP280139
392 190 16.9 592 6 CB130851 CB130851 K-EST0180 465 186 16.5 612 6 CD469627 LeukoS2_7
393 190 16.9 592 4 BM848361 BM848361 K-EST0128 466 186 16.5 821 6 CD559300 AGENCOURT
394 190 16.9 592 5 BP277740 BP277740 467 185.5 405 6 BY766304 BY766304
395 190 16.9 593 4 BM742647 BM742647 K-EST0015 468 185.5 502 6 CA567008 K0408F05-
396 190 16.9 594 5 BP279022 BP279022 469 185.5 761 1 AA637653 vu10e10.r
397 190 16.9 597 5 BP280234 BP280234 470 185 16.4 488 6 CD536274 LeukoN6_4
398 190 16.9 598 5 BP279140 BP279140 471 185 16.4 515 6 CD464497 LeukoN4_4
399 190 16.9 598 5 BP280362 BP280362 472 185 16.4 516 6 CD470165 LeukoS4_1
400 190 16.9 598 5 BP281033 BP281033 473 185 16.4 548 4 BI960855 MONO1_1_G
401 190 16.9 598 5 BP351569 BP351569 474 185 16.4 574 5 BP297283 BP297283
402 190 16.9 598 6 CB124471 CB124471 K-EST0173 475 185 16.4 592 5 BP279039 BP279039
403 190 16.9 598 6 CB132093 CB132093 K-EST0182 476 185 16.4 598 5 BP366031 BP366031
404 190 16.9 598 6 CB149427 CB149427 K-EST0205 477 185 16.4 605 6 CD471149 LeukoS5_4
405 190 16.9 600 4 BM742193 BM742193 K-EST0014 478 185 16.4 941 6 BI602405 603251183
406 190 16.9 601 6 CD469117 LeukoS2_1 479 184.5 590 1 AI151808 ui46C06.y
407 190 16.9 603 5 BP278981 BP278981 480 184 16.4 329 7 W40206 zc83a06.r1
408 190 16.9 608 4 BM846665 BM846665 K-EST0125 481 184 16.4 544 4 BM762984 K-EST0044
409 190 16.9 613 4 BM846787 BP278547 482 184 16.4 582 5 BP254097 BP254097
410 190 16.9 617 5 BP278547 BP278547 483 184 16.4 583 5 BP280763 BP280763
411 190 16.9 625 5 BP280558 BP280558 484 183.5 735 7 CK364727 AGENCOURT
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583	168	14.9	930	5	BQ878706	BQ878706 AGENCOURT
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608	164	14.6	737	7	CF121799	CF121799 UI-HF-BP0
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613	162.5	14.4	476	6	CD465241	CD465241 LeukoN1_2
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619	160	14.2	887	4	BG528427	BG528427 602579863
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636	156	13.9	583	5	BP278490	BP278490 BP278490
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640	155	13.8	583	5	BP363547	BP363547 BP363547
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642	155	13.8	915	5	BQ432026	BQ432026 AGENCOURT
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644	153.5	13.6	432	4	BM764097	BM764097 K-EST0045
645	153.5	13.6	438	4	BM785480	BM785480 K-EST0063
646	153.5	13.6	444	4	BM826025	BM826025 K-EST0097
647	153.5	13.6	483	4	BM739115	BM739115 K-EST0008
648	153.5	13.6	641	6	BY726835	BY726835 BY726835
649	153.5	13.6	879	5	BQ962151	BQ962151 AGENCOURT
650	152.5	13.6	573	6	CD535920	CD535920 LeukoN5_5
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671	147	13.1	702	7	CN347076	170004248	
672	147	13.1	998	2	BE616364	601279172	
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674	146.5	13.0	1073	2	BE904427	601496388	
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691	145	12.9	760	7	CV079185	AGENCOURT	
692	145	12.9	806	7	CO556630	AGENCOURT	
693	145	12.9	866	7	CO390036	AGENCOURT	
694	145	12.9	868	5	BQ230041	AGENCOURT	
695	144.5	12.8	500	1	AL5444354	AL5444354	
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710	144	12.8	688	6	CD469382	LeukoS2_3	
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713	144	12.8	895	6	CB205022	AGENCOURT	
714	143.5	12.8	417	4	BM743706	K-EST0016	
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717	143	12.7	743	4	BI961594	MONO1_1_G	
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745	139	12.4	674	7	CK685212	2F101-P00	
746	138.5	12.3	451	2	BB858834	BB858834	
747	137.5	12.2	432	6	CB128106	K-EST0177	
748	136.5	12.1	595	9	FR0036223	Fugu rubr	
749	136	12.1	589	1	AI830544	wj5la03.x	
750	136	12.1	694	4	BI771330	603059323	
751	136	12.1	808	6	CD512219	AGENCOURT	
752	135.5	12.0	718	5	BM951526	UI-M-EG0-	
753	135.5	12.0	2661	9	AY402614	Mus muscu	
754	134.5	12.0	378	7	W68991	T2873 MVAT4	
755	134.5	12.0	442	7	CK608407	IFNb_B08	
756	134.5	12.0	466	5	BY153109	BY153109	
757	134.5	12.0	694	6	CA376384	654727 NC	
758	134	11.9	582	5	BP363410	BP363410	
759	134	11.9	3025	3	BC049247	Mus muscu	
760	133.5	11.9	729	7	CN056501	Salamande	
761	133	11.8	245	1	AA360733	EST70005	
762	133	11.8	291	1	AA347120	EST53364	
763	133	11.8	669	5	BU631966	UI-H-FE1-	
764	132	11.7	327	7	W40210	zc83b06.r1	
765	132	11.7	770	5	BU749989	CH3#030_C	
766	131.5	11.7	860	4	BG541514	602570961	
767	131.5	11.7	874	2	BF582542	602094513	
768	131	11.6	986	5	BX390379	BX390379	
769	130.5	11.6	358	6	BY770042	BY770042	
770	130.5	11.6	584	5	BP217677	BP217677	
771	130.5	11.6	906	1	AA717936	vt09f11.r	
772	130	11.6	329	7	W93163	zd93d04.r1	
773	130	11.6	362	5	BY019901	BY019901	
774	130	11.6	582	5	BP301774	BP301774	
775	130	11.6	640	2	BE371133	601218624	
776	129.5	11.5	784	4	BG866546	602785510	
777	129	11.5	706	2	AW954379	EST366449	
778	128.5	11.4	931	7	CN321916	AGENCOURT	
779	128.5	11.4	1110	7	CK028468	AGENCOURT	
780	127.5	11.3	581	5	BP250869	BP250869	
781	127.5	11.3	1832	3	CR613805	full-leng	
782	127.5	11.3	1844	3	AY037161	Homo sapi	
783	127.5	11.3	2485	3	BC023209	Homo sapi	
784	127.5	11.3	2736	9	AY402612	Homo sapi	
785	127.5	11.3	2759	3	BC029313	Homo sapi	
786	127.5	11.3	3105	3	BC053689	Homo sapi	
787	127.5	11.3	3270	3	BC035457	Homo sapi	
788	127.5	11.3	3295	3	BC029348	Homo sapi	
789	127	11.3	422	1	AV670072	AV670072	
790	127	11.3	642	7	CV078311	AGENCOURT	
791	127	11.3	732	7	CK805674	AGENCOURT	
792	127	11.3	938	7	CK799651	AGENCOURT	
793	127	11.3	964	4	BI222267	602939755	
794	126.5	11.2	750	7	CK699945	2F101-P00	
795	126	11.2	1079	9	CNS05DEJ	Tetraodon	
796	126	11.2	3085	3	AK034522	Mus muscu	
797	125.5	11.2	446	2	BB840038	BB840038	
798	125.5	11.2	572	7	CN532870	UI-M-HO0-	
799	125.5	11.2	648	5	BP765140	BP765140	
800	125.5	11.2	765	7	CN508989	AGENCOURT	
801	125.5	11.2	878	6	CD359001	AGENCOURT	
802	125.5	11.2	2189	3	AK003582	Mus muscu	
803	125.5	11.2	2194	3	AK048107	Mus muscu	
804	125.5	11.2	2876	3	AK032750	Mus muscu	
805	125	11.1	683	4	BJ523552	BJ523552	
806	124.5	11.1	504	7	N24337	yx24f11.r1	
807	124	11.0	572	6	CB268774	1007680 H	
808	124	11.0	690	2	BF342700	602013653	
809	124	11.0	915	5	BX748376	BX748376	
810	123.5	11.0	885	6	CA496501	AGENCOURT	
811	123	10.9	524	5	BQ259314	fz97g05.y	
812	123	10.9	562	4	BM254875	516445 MA	

813	123	10.9	568	2	BE200989	BE200989 fk84e04.y	886	116	10.3	380	5	BY011815	BY011815
814	123	10.9	591	5	BQ093786	BQ093786 fz51h01.y	887	116	10.3	2809	3	BC021652	BC021652 Mus muscu
815	123	10.9	758	7	CF998236	CF998236 AGENCOURT	888	115.5	10.3	382	6	BY772496	BY772496
816	123	10.9	780	7	CF348306	CF348306 AGENCOURT	889	115.5	10.3	588	5	BM949590	BM949590 UI-M-EGOp
817	123	10.9	800	7	CK028357	CK028357 AGENCOURT	890	115.5	10.3	736	7	CF457207	CF457207 AGENCOURT
818	123	10.9	814	7	CK030082	CK030082 AGENCOURT	c 891	115.5	10.3	1023	1	AL526824	AL526824
819	123	10.9	822	7	CN510127	CN510127 AGENCOURT	892	115	10.2	362	6	BY766890	BY766890
820	123	10.9	840	7	CN506106	CN506106 AGENCOURT	893	115	10.2	364	5	BY171892	BY171892
821	123	10.9	868	7	CK018837	CK018837 AGENCOURT	894	115	10.2	375	2	BF175470	BF175470 MYE5034.M
822	123	10.9	872	4	BG541447	BG541447 602570880	895	115	10.2	707	4	BG770063	BG770063 602745189
823	122.5	10.9	416	5	BY208234	BY208234	896	114.5	10.2	714	4	BG760615	BG760615 602717366
824	122.5	10.9	567	2	BE016734	BE016734 fk68b07.y	897	114.5	10.2	389	5	BY165009	BY165009
825	122.5	10.9	724	4	BI755270	BI755270 603022711	898	114.5	10.2	722	2	BF529219	BF529219 602041665
826	122	10.8	497	4	BI326214	BI326214 fr29d09.y	899	114.5	10.2	738	2	BF346219	BF346219 602017695
827	122	10.8	513	2	AW343039	AW343039 fi72f05.y	900	114.5	10.2	819	5	BX717115	BX717115
828	122	10.8	583	5	BP2330565	BP2330565	901	114	10.1	638	2	BB590171	BB590171 BB590171
829	122	10.8	721	4	BG764304	BG764304 602736181	902	114	10.1	792	7	CF456942	CF456942 AGENCOURT
830	122	10.8	894	5	BX431647	BX431647	903	114	10.1	2143	3	AK040503	Mus muscu
831	122	10.8	946	5	BQ720761	BQ720761 AGENCOURT	904	113.5	10.1	385	6	BY770884	BY770884
832	121.5	10.8	384	5	BY172775	BY172775	905	113.5	10.1	431	5	BY226451	BY226451
833	121.5	10.8	436	7	CF371048	CF371048 TgESTzyj6	906	113.5	10.1	444	5	BY155496	BY155496
834	121.5	10.8	790	1	AV704163	AV704163	907	113.5	10.1	461	2	BB858159	BB858159
835	121	10.8	377	5	BY075544	BY075544	908	113.5	10.1	584	5	BP250707	BP250707
836	121	10.8	492	1	AV671084	AV671084	909	113	10.0	444	7	T96904	Ye52909.r1
837	121	10.8	526	5	BQ565916	BQ565916 gi47g06.y	910	113	10.0	713	7	CN312058	CN312058 170005318
838	121	10.8	557	4	BM254894	BM254894 516470.MA	911	113	10.0	723	5	BU410657	BU410657 603158435.
839	121	10.8	683	5	BW300493	BW300493	912	113	10.0	7102	9	AY418551	AY418551 Homo sapi
c 840	121	10.8	688	6	CA308497	CA308497 UI-H-FT1-	c 913	112.5	10.0	611	2	AW593307	AW593307 hg12h10.x
841	121	10.8	703	5	BW301620	BW301620	914	112.5	10.0	748	7	CK138733	CK138733 AGENCOURT
842	120.5	10.7	1071	5	BX447415	BX447415	915	112.5	10.0	883	7	CN019296	CN019296 AGENCOURT
843	120	10.7	223	5	BQ132939	BQ132939 fz35g10.y	916	112	10.0	372	4	BM743705	BM743705 K-EST0016
844	120	10.7	353	5	BY016053	BY016053	917	112	10.0	629	7	CN412529	CN412529 170005325
c 845	120	10.7	534	1	AV605303	AV605303	c 918	112	10.0	648	6	CB442867	CB442867 693703.MA
846	120	10.7	875	2	BF531009	BF531009	919	112	10.0	669	9	DR49F8T	AL976731 Danio rer
847	119.5	10.6	395	6	CB140481	CB140481 K-EST0193	920	112	10.0	721	4	BI219897	BI219897 602936347
848	119.5	10.6	398	6	CD465668	CD465668 LeukoN1.6	921	112	10.0	961	6	BY717654	BY717654
849	119.5	10.6	582	5	BP289784	BP289784	922	111.5	9.9	552	5	BQ472599	BQ472599 HB09A18T
850	119.5	10.6	848	7	CK236600	CK236600 AGENCOURT	c 923	111.5	9.9	652	5	BQ211047	BQ211047 UI-R-DY1.-
851	119	10.6	235	6	CA946461	CA946461 ni06c11.x	c 924	111.5	9.9	680	5	BQ191492	BQ191492 UI-R-DY0-
852	119	10.6	324	7	CN661075	CN661075 A0714A10-	c 925	111.5	9.9	776	7	CO387930	CO387930 AGENCOURT
853	119	10.6	367	5	BY330481	BY330481	926	111.5	9.9	783	5	BU479797	BU479797 603841693
854	119	10.6	371	6	BY767768	BY767768	927	111.5	9.9	911	2	BF339458	BF339458 602039113
855	119	10.6	377	5	BY352647	BY352647	928	111.5	9.9	977	4	BI857845	BI857845 603388405
856	119	10.6	381	5	BY164785	BY164785	929	111	9.9	360	6	CD471311	CD471311 LeukoS5.1
857	119	10.6	654	6	CB056916	CB056916 NISC_jj22	930	111	9.9	433	1	AL589309	AL589309 DXFPz45IH
858	119	10.6	841	2	BF528870	BF528870 602043330	931	111	9.9	570	2	BE233224	BE233224 139315.MA
859	119	10.6	931	5	BQ876201	BQ876201 AGENCOURT	c 932	111	9.9	585	4	BM812126	BM812126 fx14f12.y
860	118.5	10.5	491	6	CB153314	CB153314 K-EST0210	933	111	9.9	3642	3	BSM801377	AL133021 Homo sapi
861	118.5	10.5	515	6	CB153421	CB153421 K-EST0210	934	110.5	9.8	408	5	BY314612	BY314612
862	118.5	10.5	582	5	BP310145	BP310145	935	110.5	9.8	741	4	BG966850	BG966850 602834350
863	118	10.5	290	1	AA374988	AA374988 EST87204	936	110	9.8	357	5	BY019919	BY019919
864	118	10.5	373	5	BY134672	BY134672	937	110	9.8	630	6	CB044799	CB044799 NISC_gc06
865	118	10.5	520	4	BM798170	BM798170 K-EST0081	c 938	110	9.8	684	6	CA414871	CA414871 UI-H-EZ0-
866	118	10.5	562	5	BQ130854	BQ130854 ij88f05.y	939	110	9.8	781	9	AY418556	AY418556 Mus muscu
867	118	10.5	788	4	BG912617	BG912617 602808055	940	109.5	9.7	697	2	BF528688	BF528688 602043443
868	118	10.5	2273	3	AK034871	AK034871 Mus muscu	941	109.5	9.7	891	5	BU484122	BU484122 603471770
869	118	10.5	2448	3	AK014525	AK014525 Mus muscu	942	109	9.7	358	5	BY320846	BY320846
870	118	10.5	6914	9	AY418553	AY418553 Mus muscu	943	109	9.7	362	5	BY173073	BY173073
871	117.5	10.4	382	7	CN484304	CN484304 hw45d01.y	944	109	9.7	491	6	CA353467	CA353467 624978.NC
872	117.5	10.4	592	5	BP235883	BP235883	945	109	9.7	589	4	BM769767	BM769767 K-EST0053
873	117.5	10.4	932	5	BU438823	BU438823 603209228	c 946	109	9.7	759	5	BQ574012	BQ574012 UI-H-EZ0-
874	117	10.4	361	9	CG502350	CG502350 OST47179	947	109	9.7	783	5	BU479065	BU479065 603843018
875	117	10.4	457	1	AA305495	AA305495 EST176742	948	109	9.7	825	6	CA317002	CA317002 UI-M-FW0-
876	117	10.4	624	5	BX390371	BX390371	949	108.5	9.6	282	5	BU973380	BU973380 HB24L19r
877	117	10.4	639	4	BJ010521	BJ010521	950	108.5	9.6	308	1	AA296020	AA296020 EST10183
c 878	117	10.4	669	2	AW188198	AW188198 xj93f03.x	c 951	108.5	9.6	1116	1	AL571513	AL571513
c 879	117	10.4	1204	9	CL104582	CL104582 ISB1-43D1	952	108	9.6	233	2	AW839650	AW839650 RC6-LT007
c 880	117	10.4	1320	9	CL104648	CL104648 ISB1-43F1	953	108	9.6	508	4	BI671638	BI671638 fe50h08.y
881	116.5	10.4	445	2	BB840170	BB840170	954	108	9.6	563	1	AL874048	AL874048
882	116.5	10.4	558	4	BG896846	BG896846 HOA50-1-H	955	108	9.6	654	4	BM697249	BM697249 UI-E-DX0-
883	116.5	10.4	696	2	BF529489	BF529489 602043246	c 956	108	9.6	659	7	CO872953	CO872953 BovGen_01
884	116	10.3	366	5	BY324757	BY324757	957	108	9.6	701	6	CD354133	CD354133 UI-M-GM0-
885	116	10.3	366	6	BY767081	BY767081	958	108	9.6	756	7	CO738793	CO738793 SLE04c21

959	108	9.6	775	9	AY418554	AY418554 Homo sapi	1032	103	9.2	357	5	BY131735	BY131735
c 960	108	9.6	778	6	CA411964	CA411964 UI-H-EZ0-	1033	103	9.2	357	5	BY310928	BY310928
961	108	9.6	794	7	CK458738	CK458738 923144 MA	1034	103	9.2	738	7	CO423312	GGEZHT100
962	108	9.6	839	7	CV490818	CV490818 AGENCOURT	1035	103	9.2	932	2	BF346240	602018425
c 963	108	9.6	846	7	CK457667	CK457667 921992 MA	1036	102.5	9.1	495	6	CA343718	673899 NC
964	108	9.6	1029	1	AL539422	AL539422 AL539422	1037	102.5	9.1	578	5	BX666919	BX666919
965	108	9.6	1042	2	BF527690	BF527690 602040687	1038	102.5	9.1	606	6	CA728823	CA728823 wdilc.pk0
966	108	9.6	1161	4	BM467077	BM467077 AGENCOURT	1039	102.5	9.1	639	4	BM489811	BM489811 pgm2n.pk0
967	108	9.6	1278	3	CR597704	CR597704 full-leng	1040	102.5	9.1	640	4	BM637828	BM637828 170006875
968	108	9.6	1383	3	AK017865	AK017865 Mus muscu	1041	102.5	9.1	672	4	BM577341	BM577341 170006871
969	108	9.6	1433	3	AK016123	AK016123 Mus muscu	1042	102.5	9.1	694	4	BM620184	BM620184 170006874
970	108	9.6	1630	3	CR605965	CR605965 full-leng	1043	102.5	9.1	749	8	BZ637147	BZ637147 OGCCJ87TC
c 971	107.5	9.6	686	7	CF179894	CF179894 814933 MA	c1044	102.5	9.1	930	9	CNS06HMX	AL3399235 T3 end of
972	107	9.5	383	6	CD471716	CD471716 LeukoS6_4	1045	102	9.1	356	5	BU969369	BU969369 HB11F08r
973	107	9.5	561	2	BF527166	BF527166 602039844	c1046	102	9.1	424	1	AJ689562	AJ689562 AJ689562
974	107	9.5	598	5	BU400752	BU400752 603485038	1047	102	9.1	646	9	AG075707	AG075707 Pan trogl
975	107	9.5	680	5	BU249879	BU249879 603403239	c1048	102	9.1	646	9	AG075708	AG075708 Pan trogl
976	107	9.5	700	4	BG910156	BG910156 602805533	1049	102	9.1	707	6	CA274759	CA274759 SCSBSD102
977	107	9.5	716	7	CF536406	CF536406 UI-M-GI0-	1050	102	9.1	821	5	BM944051	BM944051 UI-M-EH0p
978	107	9.5	745	7	CF723087	CF723087 UI-M-GV0-	1051	102	9.1	882	5	BU249765	BU249765 603403663
979	107	9.5	763	5	BU410360	BU410360 603158087	1052	101.5	9.0	955	2	BE039709	BE039709 OC02G02 O
980	107	9.5	785	4	BG911337	BG911337 602807633	1053	101.5	9.0	996	2	BF345477	BF345477 602019224
981	107	9.5	798	6	CD802962	CD802962 UI-M-GV0-	1054	101.5	9.0	2736	9	AY402613	AY402613 Pan trogl
982	107	9.5	941	5	BU409087	BU409087 603158870	1055	101	9.0	308	6	CD740276	CD740276 4029308 1
983	107	9.5	979	5	BU410188	BU410188 602955232	1056	101	9.0	345	1	AI873583	AI873583 wk29h08.x
984	107	9.5	1158	5	BU409151	BU409151 603158151	1057	101	9.0	414	2	AW655801	AW655801 107075 MA
c 985	106.5	9.5	457	7	CN153458	CN153458 940572 MA	c1058	101	9.0	466	1	AA454641	AA454641 zx99d05.s
c 986	106.5	9.5	555	6	CD180838	CD180838 MS1-0027T	1059	101	9.0	531	6	CA915507	CA915507 PCSC16313
987	106.5	9.5	755	7	CN155571	CN155571 942876 MA	1060	101	9.0	660	6	CA883427	CA883427 B0103B06-
988	106.5	9.5	824	5	BU369144	BU369144 603596992	1061	101	9.0	684	2	BB614952	BB614952 BB614952
989	106.5	9.5	850	9	CR198040	CR198040 Forward s	1062	101	9.0	751	6	CD351061	CD351061 UI-M-GI0-
990	106.5	9.5	888	5	BU468347	BU468347 603372362	1063	101	9.0	797	4	BG819983	BG819983 602782506
991	106	9.4	362	5	BY173138	BY173138 BY173138	1064	101	9.0	872	5	BX336450	BX336450 BX336450
992	106	9.4	378	2	AW486980	AW486980 78517 MAR	1065	101	9.0	896	5	BU160160	BU160160 AGENCOURT
993	106	9.4	873	5	BU427310	BU427310 603232069	1066	100.5	8.9	304	1	AA285261	AA285261 PMY0643 K
994	105.5	9.4	371	6	CA599565	CA599565 waw1c.pk0	1067	100.5	8.9	535	1	AL909801	AL909801 AL909801
995	105.5	9.4	681	2	BF347167	BF347167 602020964	1068	100.5	8.9	581	4	BM087557	BM087557 500346 MA
996	105.5	9.4	791	6	CB998003	CB998003 AGENCOURT	1069	100.5	8.9	586	7	CK494474	CK494474 rswbb0_00
997	105.5	9.4	857	9	BX996872	BX996872 Reverse s	1070	100.5	8.9	765	2	BF345919	BF345919 602017920
998	105.5	9.4	948	9	BX989560	BX989560 Forward s	1071	100.5	8.9	865	6	CD459095	CD459095 Fg08_04g0
999	105	9.3	372	4	BM757210	BM757210 K-EST0035	1072	100.5	8.9	902	5	BU409490	BU409490 603158722
1000	105	9.3	499	5	BU534446	BU534446 AGENCOURT	1073	100.5	8.9	9330	3	AK090118	AK090118 Mus muscu
c1001	105	9.3	756	6	CB327411	CB327411 UI-R-FS0-	1074	100	8.9	359	2	AW417692	AW417692 54636 MAR
c1002	104.5	9.3	444	2	BF389806	BF389806 UI-R-BS2-	1075	100	8.9	376	4	BM742648	BM742648 K-EST0015
1003	104.5	9.3	649	6	CD312012	CD312012 StrPu691.	1076	100	8.9	379	6	CB139630	CB139630 K-EST0192
1004	104.5	9.3	690	6	CD294616	CD294616 StrPu691.	1077	100	8.9	564	6	CA905778	CA905778 PCS04511
1005	104.5	9.3	999	5	BX446538	BX446538 BX446538	c1078	100	8.9	618	1	AI973128	AI973128 wr47h08.x
1006	104.5	9.3	1253	5	BQ884322	BQ884322 AGENCOURT	1079	100	8.9	631	5	BQ246369	BQ246369 Tae15012F
1007	104	9.2	503	5	BU480294	BU480294 603844970	c1080	100	8.9	719	6	CA412730	CA412730 UI-H-EZ0-
1008	104	9.2	663	7	CN368025	CN368025 170005999	1081	100	8.9	848	5	BU410207	BU410207 603159488
1009	104	9.2	664	1	AJ637165	AJ637165 AJ637165	1082	100	8.9	935	2	BF580970	BF580970 602100673
1010	104	9.2	668	1	AJ637187	AJ637187 AJ637187	1083	99.5	8.8	563	6	CA998062	CA998062 S234X H10
1011	104	9.2	707	7	CK836545	CK836545 4061500 B	c1084	99.5	8.8	652	1	AI950438	AI950438 wq35dI0.x
c1012	104	9.2	952	3	CNS08HPM	BX012374 Single re	1085	99.5	8.8	722	6	CD349219	CD349219 UI-M-FY0-
1013	104	9.2	962	2	BF300451	BF300451 602032375	c1086	99.5	8.8	727	4	BJ778009	BJ778009 BJ778009
1014	104	9.2	1070	5	BX359755	BX359755 BX359755	c1087	99.5	8.8	731	4	BJ811105	BJ811105 BJ811105
1015	104	9.2	2248	3	AK081264	AK081264 Mus muscu	1088	99.5	8.8	845	7	CO571803	CO571803 AGENCOURT
1016	104	9.2	7102	9	AY418552	AY418552 Pan trogl	c1089	99.5	8.8	872	3	CNS08HU8	BX012540 Single re
1017	103.5	9.2	657	7	CK494148	CK494148 rswba0_00	1090	99.5	8.8	941	3	CNS08HU7	BX012539 Single re
1018	103.5	9.2	672	5	BQ263492	BQ263492 faa23e07.	1091	99.5	8.8	1040	5	BQ714183	BQ714183 AGENCOURT
1019	103.5	9.2	680	7	CK499523	CK499523 rswbb0_00	1092	99.5	8.8	1116	2	BF527687	BF527687 602040683
1020	103.5	9.2	708	2	BE193339	BE193339 HVSMEH008	1093	99	8.8	449	6	CB743206	CB743206 AMGNNUC:N
1021	103.5	9.2	710	1	AU002237	AU002237 AU002237	c1094	99	8.8	507	2	BE655314	BE655314 UI-M-BH0-
1022	103.5	9.2	723	1	AU002317	AU002317 AU002317	1095	99	8.8	532	1	AU265139	AU265139 AU265139
1023	103.5	9.2	767	6	CD777760	CD777760 TDsubs_RZ	1096	99	8.8	553	4	BG367700	BG367700 HVSMEi001
1024	103.5	9.2	781	1	AL669025	AL669025 AL669025	c1097	99	8.8	652	6	CD369984	CD369984 UI-H-FT1-
1025	103.5	9.2	888	2	BF581527	BF581527 602101046	1098	99	8.8	686	6	CD535240	CD535240 LeukoN5_1
c1026	103.5	9.2	942	1	AL538775	AL538775 AL538775	c1099	99	8.8	711	6	CD193256	CD193256 MS1-0078G
1027	103.5	9.2	963	2	BE196206	BE196206 HVSMEh009	1100	99	8.8	836	7	CO738752	CO738752 SLE04c21
1028	103	9.2	353	5	BY135479	BY135479 BY135479	c1101	99	8.8	885	3	CNS08EMW	BX008388 Single re
1029	103	9.2	353	5	BY337424	BY337424 BY337424	1102	99	8.8	922	5	BQ949185	BQ949185 AGENCOURT
1030	103	9.2	354	5	BY132505	BY132505 BY132505	1103	99	8.8	940	7	CF454398	CF454398 AGENCOURT
1031	103	9.2	355	5	BY312652	BY312652 BY312652	1104	99	8.8	1002	3	CNS08YUL	BX034585 Single re

1105	99	8.8	1018	4	BM552398	BM552398	AGENCOURT	1178	96	8.5	516	6	CA915481	CA915481	PCS04166
1106	99	8.8	1025	3	BC024540	BC024540	Mus muscu	1179	96	8.5	518	6	CA915482	CA915482	PCS05618
1107	98.5	8.8	419	1	AA448801	AA448801	zx10G02.r	1180	96	8.5	532	4	BJ374459	BJ374459	BJ374459
1108	98.5	8.8	441	7	CN282071	CN282071	170005329	1181	96	8.5	538	6	CA915489	CA915489	PCSC09473
1109	98.5	8.8	548	7	CO876287	CO876287	BovGen_04	1182	96	8.5	543	6	CA898165	CA898165	PCEP04609
1110	98.5	8.8	582	2	BF695021	BF695021	602083052	1183	96	8.5	584	6	CA915502	CA915502	PCSC15104
1111	98.5	8.8	592	6	CB584777	CB584777	AMGNNUC:U	1184	96	8.5	612	6	CB054443	CB054443	NISC_gm04
1112	98.5	8.8	597	6	CD084905	CD084905	MCI-0013T	1185	96	8.5	648	4	BG765571	BG765571	602738208
1113	98.5	8.8	598	6	CB582909	CB582909	AMGNNUC:U	1186	96	8.5	653	6	CA915499	CA915499	PCSC14281
1114	98.5	8.8	624	2	BF586321	BF586321	FM1_27_D1	1187	96	8.5	655	6	CA915504	CA915504	PCSC15991
1115	98.5	8.8	638	4	BG052018	BG052018	RHI22_7_H	1188	96	8.5	658	6	CA915471	CA915471	PCS00339X
1116	98.5	8.8	654	1	AU205000	AU205000	AU205000	1189	96	8.5	676	6	CA915497	CA915497	PCSC14054
1117	98.5	8.8	713	2	BE979942	BE979942	UI-M-BG2-	1190	96	8.5	696	6	CA915498	CA915498	PCSC14091
1118	98.5	8.8	872	7	CO920977	CO920977	AGENCOURT	1191	96	8.5	807	9	CG206127	CG206127	PUIBB90TD
1119	98.5	8.8	877	6	CD253524	CD253524	AGENCOURT	1192	96	8.5	900	5	BQ686613	BQ686613	AGENCOURT
1120	98.5	8.8	922	3	CNS09DMV	CNS09DMV	Single re	1193	96	8.5	1799	2	BF683675	BF683675	602139925
1121	98.5	8.8	954	3	CNS08UPL	CNS08UPL	Single re	1194	95.5	8.5	280	5	BU971558	BU971558	HB17P20r
1122	98.5	8.8	977	3	CNS09KPQ	CNS09KPQ	Single re	1195	95.5	8.5	297	5	BU984229	BU984229	HF03F16r
1123	98	8.7	487	2	BF461115	BF461115	UI-M-CG0p	1196	95.5	8.5	529	6	CB155742	CB155742	K-EST0214
1124	98	8.7	581	2	BE956860	BE956860	UI-M-BG2-	1197	95.5	8.5	537	2	BF193254	BF193254	244772_MA
1125	98	8.7	719	4	BG283856	BG283856	602407585	1198	95.5	8.5	538	6	CD183315	CD183315	MS1-0038U
1126	98	8.7	794	6	CB326761	CB326761	UI-R-DZ0-	1199	95.5	8.5	554	1	AI425582	AI425582	mdl9b07.y
1127	98	8.7	801	6	CD794302	CD794302	EST665663	1200	95.5	8.5	566	5	BW334508	BW334508	BM334508
1128	98	8.7	823	7	CK147509	CK147509	AGENCOURT	1201	95.5	8.5	583	5	BP207390	BP207390	BP207390
1129	98	8.7	835	5	BW467001	BW467001	AGENCOURT	1202	95.5	8.5	601	4	BJ058236	BJ058236	BJ058236
1130	98	8.7	837	1	AU119529	AU119529	AU119529	1203	95.5	8.5	615	6	CD084873	CD084873	MCI-0013T
1131	98	8.7	886	5	BX458405	BX458405	BX458405	1204	95.5	8.5	651	4	BM267850	BM267850	MEST373-A
1132	98	8.7	889	7	CR582578	CR582578	CR582578	1205	95.5	8.5	663	7	CF333111	CF333111	JMT--01-O
1133	98	8.7	898	4	BI819191	BI819191	603034603	1206	95.5	8.5	707	8	BZ725029	BZ725029	OGECS9TM
1134	98	8.7	921	3	CR622952	CR622952	full-length	1207	95.5	8.5	745	9	CG440326	CG440326	OGVGS61TH
1135	98	8.7	1134	5	BX396679	BX396679	BX396679	1208	95.5	8.5	780	4	BG368072	BG368072	HVSMEI001
1136	97.5	8.7	510	5	BW076358	BW076358	BW076358	1209	95.5	8.5	798	8	BZ725025	BZ725025	OGECS9TC
1137	97.5	8.7	513	5	BW211988	BW211988	BW211988	1210	95.5	8.5	824	9	CG440337	CG440337	OGVGS61TV
1138	97.5	8.7	558	5	BQ264294	BQ264294	faa49f06.	1211	95.5	8.5	830	7	CR292477	CR292477	CR292477
1139	97.5	8.7	581	2	AW123236	AW123236	UI-M-BH2.	1212	95.5	8.5	839	4	BG914162	BG914162	602810407
1140	97.5	8.7	588	1	AI850361	AI850361	UI-M-BG1-	1213	95.5	8.5	888	5	BU480079	BU480079	603845914
1141	97.5	8.7	592	5	BQ309048	BQ309048	MR0-BT450	1214	95.5	8.5	891	3	CNS08UPM	CNS08UPM	Single re
1142	97.5	8.7	698	1	AA941503	AA941503	LD25669.5	1215	95.5	8.5	926	7	CK017503	CK017503	AGENCOURT
1143	97.5	8.7	713	5	BU408855	BU408855	603158450	1216	95.5	8.5	962	3	CNS08GHR	CNS08GHR	Single re
1144	97.5	8.7	742	5	BU427200	BU427200	603234473	1217	95.5	8.5	963	3	CNS08E4D	CNS08E4D	Single re
1145	97.5	8.7	751	7	CO892908	CO892908	BovGen_21	1218	95	8.4	238	4	BG939000	BG939000	cn29h03.y
1146	97.5	8.7	835	1	AJ816579	AJ816579	AJ816579	1219	95	8.4	418	5	BQ280320	BQ280320	UMN12C11
1147	97.5	8.7	836	1	AJ816601	AJ816601	AJ816601	1220	95	8.4	447	8	BH094533	BH094533	RPCI-24-3
1148	97.5	8.7	893	2	BF303297	BF303297	602030211	1221	95	8.4	513	6	CA915477	CA915477	PCS03575
1149	97.5	8.7	977	3	CNS08E4C	CNS08E4C	Single re	1222	95	8.4	515	9	CE173795	CE173795	tigr-gss-
1150	97.5	8.7	995	2	BE602834	BE602834	HVSMEH010	1223	95	8.4	541	6	CA915506	CA915506	PCSC16248
1151	97.5	8.7	1441	3	BC023911	BC023911	Mus muscu	1224	95	8.4	552	6	CA899714	CA899714	PCEP01747
1152	97	8.6	419	7	CF136553	CF136553	UI-HF-BN0	1225	95	8.4	557	4	BM258620	BM258620	523466_MA
1153	97	8.6	538	4	BJ047143	BJ047143	BJ047143	1226	95	8.4	598	4	BI170501	BI170501	RE11976.5
1154	97	8.6	665	4	BJ234010	BJ234010	BJ234010	1227	95	8.4	598	6	CA915510	CA915510	PCSC17379
1155	97	8.6	719	9	CL912807	CL912807	OA_ABA001	1228	95	8.4	606	2	BE430948	BE430948	SUN008.G1
1156	97	8.6	876	4	BG769059	BG769059	602743307	1229	95	8.4	610	7	CF843588	CF843588	psHB025xM
1157	97	8.6	1130	1	AL574194	AL574194	AL574194	1230	95	8.4	627	7	CF862698	CF862698	psZS004xI
1158	97	8.6	1518	3	CNS0ACU8	CNS0ACU8	Arabidops	1231	95	8.4	652	2	BE194104	BE194104	HVSMEH008
1159	96.5	8.6	461	6	CA915486	CA915486	PCSC06693	1232	95	8.4	675	6	CA905790	CA905790	PCSC20838
1160	96.5	8.6	517	6	CD201750	CD201750	MS1-0129T	1233	95	8.4	711	6	CB324201	CB324201	UI-R-DY0-
1161	96.5	8.6	522	5	BW307716	BW307716	BW307716	1234	95	8.4	717	5	BQ247092	BQ247092	TaE15001E
1162	96.5	8.6	525	2	BE603039	BE603039	HVSMEH010	1235	95	8.4	730	5	BX911585	BX911585	BX911585
1163	96.5	8.6	534	9	CE558576	CE558576	tigr-gss-	1236	95	8.4	758	5	BX872630	BX872630	BX872630
1164	96.5	8.6	569	9	BQ180668	BQ180668	UI-M-EX0-	1237	95	8.4	839	8	BZ450097	BZ450097	BONLB21TF
1165	96.5	8.6	593	5	CL924200	CL924200	OA_ABA002	1238	95	8.4	937	5	BX397909	BX397909	BX397909
1166	96.5	8.6	597	6	CA727188	CA727188	wdelf.pk0	1239	95	8.4	1114	4	BI692466	BI692466	603342981
1167	96.5	8.6	598	6	CA727063	CA727063	wdelf.pk0	1240	95	8.4	1599	3	CR643518	CR643518	Tetraodon
1168	96.5	8.6	603	2	AW180870	AW180870	MgAl041f	1241	94.5	8.4	268	7	R72730	R72730	yj95e06.r1
1169	96.5	8.6	633	6	CA325011	CA325011	UI-M-FY0-	1242	94.5	8.4	389	5	BU974675	BU974675	HB28L19r
1170	96.5	8.6	659	6	CA226780	CA226780	SCRFLF300	1243	94.5	8.4	450	1	AI168624	AI168624	ox65h05.s
1171	96.5	8.6	659	6	CA734124	CA734124	wde2f.pk0	1244	94.5	8.4	479	6	CD171033	CD171033	MS1-0007U
1172	96.5	8.6	665	7	CO395103	CO395103	AGENCOURT	1245	94.5	8.4	503	6	CD084981	CD084981	MC1-0013U
1173	96.5	8.6	743	7	CF488034	CF488034	POL1_47_H	1246	94.5	8.4	520	6	CD188553	CD188553	MS1-0063U
1174	96.5	8.6	750	6	CA285922	CA285922	SCEZSD108	1247	94.5	8.4	520	6	CD189474	CD189474	MS1-0063U
1175	96.5	8.6	860	4	BI951090	BI951090	HVSMEI002	1248	94.5	8.4	531	6	CD183627	CD183627	MS1-0038U
1176	96.5	8.6	939	4	BG365940	BG365940	HVSMEI000	1249	94.5	8.4	532	6	CD084942	CD084942	MC1-0013U
1177	96	8.5	515	6	CA915483	CA915483	PCSC05960	1250	94.5	8.4	542	6	CD088533	CD088533	MC1-0051T

c1251	94.5	8.4	548	6	CD071768	CD071768	MA2-0033T
c1252	94.5	8.4	555	6	CD180833	MS1-0027T	
1253	94.5	8.4	558	4	BG637332	AD15266.5	
1254	94.5	8.4	571	4	BG634902	AT31301.5	
1255	94.5	8.4	574	8	BZ711348	OGEAK29TC	
1256	94.5	8.4	597	4	BI947849	HVSMEI000	
1257	94.5	8.4	597	6	CD084848	MC1-0013T	
1258	94.5	8.4	597	6	CD084875	MC1-0013T	
1259	94.5	8.4	597	6	CD084878	MC1-0013T	
c1260	94.5	8.4	597	6	CD084908	MC1-0013T	
1261	94.5	8.4	598	4	BI578851	RE72782.5	
c1262	94.5	8.4	606	6	CD067866	MA1-0051P	
1263	94.5	8.4	609	4	BI635691	SD17118.5	
1264	94.5	8.4	610	1	AI258299	LP01451.5	
1265	94.5	8.4	611	1	AA736027	GM10804.5	
c1266	94.5	8.4	614	6	CD084886	MC1-0013T	
c1267	94.5	8.4	614	6	CD183516	MS1-0038U	
c1268	94.5	8.4	615	6	CD084887	MC1-0013T	
1269	94.5	8.4	615	6	CD084892	MC1-0013T	
1270	94.5	8.4	615	7	CK662434	LP22658.5	
1271	94.5	8.4	619	4	BI629526	RH58408.5	
1272	94.5	8.4	621	4	BI637617	SD19668.5	
1273	94.5	8.4	625	1	AI403890	GH23431.5	
1274	94.5	8.4	626	4	BI612186	RH40605.5	
1275	94.5	8.4	629	1	AI259764	LP03253.5	
1276	94.5	8.4	632	4	BI230753	RE14785.5	
1277	94.5	8.4	633	4	BI585810	RH25484.5	
1278	94.5	8.4	634	1	AI387752	GH18404.5	
c1279	94.5	8.4	635	4	BM350545	MEST267-F	
1280	94.5	8.4	636	1	AI532736	SD04336.5	
1281	94.5	8.4	637	7	CR285301	CR285301	
1282	94.5	8.4	641	1	AI294933	LP08424.5	
1283	94.5	8.4	641	4	BI640558	SD23469.5	
1284	94.5	8.4	646	4	BI632782	SD26650.5	
1285	94.5	8.4	659	4	BI484574	RE67695.5	
1286	94.5	8.4	661	4	BG636508	SD14239.5	
1287	94.5	8.4	662	7	CK662002	LP21896.5	
1288	94.5	8.4	670	7	CK659917	LP18051.5	
c1289	94.5	8.4	672	6	CD132840	MGL-0024U	
1290	94.5	8.4	672	6	CD673033	fg19f07.Y	
1291	94.5	8.4	676	4	BG640688	SD11828.5	
1292	94.5	8.4	682	1	AA695503	GM02930.5	
1293	94.5	8.4	682	4	BI640035	SD22786.5	
c1294	94.5	8.4	682	4	BM336252	MEST191-E	
1295	94.5	8.4	687	4	BM625803	170006874	
1296	94.5	8.4	688	4	BG641327	SD12647.5	
1297	94.5	8.4	696	4	BI639642	SD22278.5	
1298	94.5	8.4	701	4	BI641486	SD24835.5	
1299	94.5	8.4	712	2	BE454779	HVSMEH009	
1300	94.5	8.4	717	7	CK658252	LP15051.5	
1301	94.5	8.4	719	6	CD493958	CDA08-A11	
1302	94.5	8.4	719	7	CK662192	LP22224.5	
c1303	94.5	8.4	738	4	BM351144	MEST273-H	
c1304	94.5	8.4	787	1	AV653736	AV653736	
1305	94.5	8.4	1014	3	CNS08HPL	BX012373 Single re	
1306	94	8.4	357	6	BY776755	BY776755	
c1307	94	8.4	422	4	BF962319	CM2-NN024	
c1308	94	8.4	429	1	AV612005	AV612005	
c1309	94	8.4	431	1	AV613377	AV613377	
1310	94	8.4	440	4	BI682719	463878 MA	
1311	94	8.4	478	6	CD472195	Leukos6_1	
c1312	94	8.4	523	4	BJ377114	BJ377114	
1313	94	8.4	558	7	CN811449	Fg14_02d0	
1314	94	8.4	559	2	BF720471	mab54g02.	
1315	94	8.4	576	4	BI640324	SD23150.5	
1316	94	8.4	579	6	CA915519	PCSC18921	
c1317	94	8.4	580	7	CK771636	BY705907	
c1318	94	8.4	648	6	BY705907	BY705907	
1319	94	8.4	662	6	CA915478	PCS03761	
1320	94	8.4	686	5	BQ472335	HB09O18T	
1321	94	8.4	725	6	CA362129	636116 NC	
1322	94	8.4	791	4	BG913452	602811347	
1323	94	8.4	806	3	AY108509	Zea may	

c1324	94	8.4	810	8	BZ560225	BZ560225	pac2-164
1325	94	8.4	929	2	BE195896	HVSMEh009	
1326	94	8.4	979	7	CN812392	Fgl13_01b2	
1327	94	8.4	1017	5	BX382734	BX382734	
1328	94	8.4	1137	6	CD505293	CDA72-H08	
1329	94	8.4	1174	8	CC251710	CH261-75N	
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1341	93.5	8.3	453	5	BU967209	HB03J15r	
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	93	8.3	390	6	CB148204	CB148204 K-EST0204	

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C1398	93	8.3	484	7	CR451426	CR451426	CR451426
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1401	93	8.3	583	5	BU061948	BU061948	Fgr_1_C09
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1404	93	8.3	611	5	BU063938	BU063938	Fgr_3_M10
1405	93	8.3	616	5	BQ240366	BQ240366	TaE05018E
C1406	93	8.3	619	7	CV062592	CV062592	BNEL80g3
1407	93	8.3	628	5	BU060427	BU060427	Fgr-C_1_C
1408	93	8.3	629	5	BU063391	BU063391	Fgr_3_A22
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1410	93	8.3	652	5	BU061832	BU061832	Fgr_10_P1
1411	93	8.3	662	5	BU065057	BU065057	Fgr_6_I08
C1412	93	8.3	669	3	CNS08YUM	CNS08YUM	Single re
1413	93	8.3	673	5	BU066047	BU066047	Fgr_9_D09
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1417	93	8.3	699	4	BM617026	BM617026	170006871
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1419	93	8.3	831	9	CL959549	CL959549	OsIFCC003
1420	93	8.3	856	4	BI732810	BI732810	603353915
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1422	93	8.3	967	2	BF303662	BF303662	601886309
1423	93	8.3	1108	5	EX446348	EX446348	BX446348
1424	93	8.3	1120	7	CK208889	CK208889	FGAS02061
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1428	92.5	8.2	420	1	AJ481820	AJ481820	AJ481820
1429	92.5	8.2	420	1	AJ481825	AJ481825	AJ481825
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1433	92.5	8.2	480	1	AJ481823	AJ481823	AJ481823
1434	92.5	8.2	480	1	AJ481824	AJ481824	AJ481824
1435	92.5	8.2	498	2	AW207527	AW207527	UI-H-B11-
1436	92.5	8.2	540	1	AJ481822	AJ481822	AJ481822
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1439	92.5	8.2	629	5	BU109792	BU109792	603002182
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C1442	92.5	8.2	659	8	BH335046	BH335046	CH230-99F
1443	92.5	8.2	660	4	BM621556	BM621556	170006874
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1445	92.5	8.2	741	2	BE194453	BE194453	HVSMEH008
C1446	92.5	8.2	818	5	BU292688	BU292688	603607107
1447	92.5	8.2	855	9	CC904230	CC904230	t012122ba
C1448	92.5	8.2	946	3	CNS08NIX	EX019909	Single re
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1450	92.5	8.2	1011	9	CNS06HQQ	AL399326	T3 end of
1451	92.5	8.2	1018	4	BG913279	BG913279	602811967
1452	92.5	8.2	1068	9	CNS06GGQ	AL397680	T3 end of
1453	92.5	8.2	3219	3	AK034300	AK034300	Mus muscu
1454	92	8.2	320	5	BQ472530	BQ472530	HB09E15T
C1455	92	8.2	394	4	BJ374584	BJ374584	BJ374584
1456	92	8.2	401	5	BX251968	BX251968	BX251968
C1457	92	8.2	414	4	BJ374319	BJ374319	BJ374319
1458	92	8.2	452	1	AU034607	AU034607	AU034607
1459	92	8.2	457	4	BI230016	BI230016	RE27933.5
1460	92	8.2	458	4	BG900403	BG900403	HOA5-1-H5
1461	92	8.2	460	1	AU052892	AU052892	AU052892
1462	92	8.2	462	4	BI606019	BI606019	RH72092.5
1463	92	8.2	486	4	BI578639	BI578639	RE72533.5
1464	92	8.2	489	4	BI363185	BI363185	RE47940.5
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1470	92	8.2	585	4	BM135198
1471	92	8.2	587	1	AU060244
1472	92	8.2	601	1	AU038566
1473	92	8.2	622	1	AU039441
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1475	92	8.2	637	5	BW331082
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1481	92	8.2	658	4	BJ344640
1482	92	8.2	672	5	BU289149
1483	92	8.2	716	5	BW191082
1484	92	8.2	791	7	CV482121
1485	92	8.2	799	6	CB290356
1486	92	8.2	803	5	BQ804754
1487	92	8.2	842	4	BJ727525
1488	92	8.2	874	6	CB655800
1489	92	8.2	962	5	BU523208
1490	92	8.2	968	8	BZ782674
1491	92	8.2	996	9	CG128856
1492	92	8.2	1015	5	BX379260
1493	91.5	8.1	341	2	BE171025
1494	91.5	8.1	369	6	CD087457
1495	91.5	8.1	414	1	AI991634
1496	91.5	8.1	465	6	CD060848
1497	91.5	8.1	471	4	BI950216
1498	91.5	8.1	477	4	BG366481
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ALIGNMENTS

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RESULT 1
AL546217
LOCUS
DEFINITION
AL546217 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI025YP16 5-PRIME, mRNA sequence.
AL546217
ACCESSION
AL546217.3 GI:45746685
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31268051.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r

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FEATURES
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 2.41e-105 Length: 769
Pred. No.: 1125.00 Matches: 218
Score: 1125.00
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AL546217 (1-769)

QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys	20
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QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
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QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	233	GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAAGTTGGCCGGCAAGGACCAAGTTGAAACA	292
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	293	GCCTTGAAAGCTAGCTTTGAAACTTGACGATATGGCTGGGTGGAGATGGATTTCGTGGTC	352
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	353	ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCCTGATTTGG	412
QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
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QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	473	AACTCGTGCAATCCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAAC TGCA	532
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	533	ACACAAACAACAGAATTATTGTGTCAGTGACGTACCTACTCGGTGGCATCCCCCTTACTCT	592
QY	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	593	ACAATACCTGCCCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	652
QY	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	653	AAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT	712
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RESULT 2
BX459046
LOCUS BX459046 Homo sapiens PLACENTA 845 bp mRNA linear EST 05-MAY-2004
DEFINITION BX459046 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YN20
5-PRIME, mRNA sequence.

ACCESSION BX459046
VERSION BX459046.2 GI:47051789
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 845)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE

JOURNAL

COMMENT

Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31021086.
Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of invitrogen.

This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DE011DG10QP1&c=5952.r.

FEATURES

source

Location/Qualifiers

1..845

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/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2.75e-105 Length: 845
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x BX459046 (1-845)

QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys	20
Db	112	ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGC	171
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	172	AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAACCGACGCTGAATTTACAGAA	231
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Db	232	GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACA	291
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QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	472	AACTCGTGCAATTCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAAC TGCA	531
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	532	ACACAAACAACAGAAATTATTGTGCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT	591
QY	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180

Db	592																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Db	267	GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA	326
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	327	GCCTTGAAAGCTAGCTTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGC	386
Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	387	ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGG	446
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThr	120
Db	447	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACT	506
Qy	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	507	AACTCGTGCAATCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACGTGCA	566
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	567	ACACAAACAACAGAAATTTATTGTCAAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT	626
Qy	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	627	ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	686
Qy	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	687	AAAAAATTGATTGTGTGCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT	746
Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	747	GAACCATTTGTTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGCA	800
RESULT 4			
AL553858			
LOCUS	AL553858 946 bp mRNA linear EST 30-MAR-2004		
DEFINITION	AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI077YJ17 5-PRIME, mRNA sequence.		
ACCESSION	AL553858		
VERSION	AL553858.3 GI:45858623		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 946)		
TITLE	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:31275672. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotiI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r		
FEATURES	For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI077CE09QP1&c=5952.r.		
source	Location/Qualifiers 1. .946 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DI077YJ17" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotiI-oligo(dT)		

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 3.23e-105 Length: 946
Pred. No.: 1125.00 Matches: 218
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 1

US-10-063-670-6_COPY_17_234 (1-218) x AL553858 (1-946)

QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys	20
Db	142	ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGACTTTCCTCCAGGTGTCATGC	201
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	202	AGAATTATGGGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAA	261
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	262	GCTAAGGAGGCTGTAGGCTGCTGGACTTAAGTTTGGCCGGAAGCAAGTTGAAACA	321
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	322	GCCTTGAAAGCTAGCTTTGAAACTTGACGTATGGCTGGTGGTGGAGATGGATTCGTGGTC	381
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	382	ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGG	441
QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	442	AAGGTTCCAGTGCCGACAGTTTGCAGCCATTGTTACAACCTCATCTGATACTTGGACT	501
QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	502	AACCTCGTGCATCCAGAAATTATCACCACCAAGAATCCCATATTCAACACTCAAACTGCA	561
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	562	ACACAAACACAGAAATTTATTGTCAGTACAGTACCTACTCGGTGGCATCCCCCTTACTCT	621
QY	161	ThrIleProAlaProThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	622	ACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	681
QY	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	682	AAAAAATTGATTGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACT	741
QY	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	742	GAACCATTTGTTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGG	795

RESULT 5
AL552299
LOCUS AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION AL552299.3 GI:45857087
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 965)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31274114.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI069DG01QP1&c=5952.r.

FEATURES

source
Location/Qualifiers
1..965
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:	3.33e-105	Length:	965
Pred. No.:	1125.00	Matches:	218
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	1		
US-10-063-670-6_COPY_17_234 (1-218) x AL552299 (1-965)			
QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys	20
Db	142	ACGAGGCTCCTGGTCCAAGGCTCTTGGCTGCAGAAAGCTTTCATCCAGGTGTCATGC	201
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	202	AGAATTATGGGGATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAA	261
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	262	GCTAAGGAGGCTGTAGGCTGCTGGACTTAAGTTTGGCCGGAAGCAAGTTGAAACA	321
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	322	GCCTTGAAAGCTAGCTTTGAAACTTGACAGCTATGGCTGGTGGAGATGGATTCGTGGTC	381
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	382	ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGG	441
QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	442	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCATTGTTACAACCTCATCTGATACTTGGACT	501
QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	502	AACTCGTGCATTCAGAAATTATCACCACCAAGAATCCCATATTCAACACTCAAACTGCA	561
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	562	ACACAAACACAGAAATTTATTGTCAGTACAGTACCTACTCGGTGGCATCCCCCTTACTCT	621
QY	161	ThrIleProAlaProThrThrProProAlaProAlaSerThrSerIleProArgArg	180

Db 622 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 681

QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
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Db 682 AAAAAATTGATTGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACT 741

QY 201 GluPropheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
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Db 742 GAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGA 795

RESULT 6

AL544430

LOCUS

DEFINITION AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI018YG12 5-PRIME, mRNA sequence.

ACCESSION AL544430

VERSION AL544430.3 GI:45744933

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:31266274.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI018BD06QP1&c=5952.r.

FEATURES

source

1. .1017
/organism="Homo sapiens"
/db_xref="taxon:9606"
/mol_type="mRNA"
/clone="CSODI018YG12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 3.59e-105 Length: 1017

Score: 1125.00 Matches: 218

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AL544430 (1-1017)

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20
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Db 219 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGCATGC 278

QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
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Db 279 AGAATTATGGGGATCACCTGTGTAGCAAAAAGCGAACACGACAGCTGAATTTACAGAA 338

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
|||||

Db 339 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGCAAGTTGAAACA 398

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
|||||

Db 399 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTC 458

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
|||||

Db 459 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGTTGGTGTCTCTGATTGG 518

QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
|||||

Db 519 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTGGACT 578

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
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Db 579 AACTCGTGCAATTCAGAAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACACTGCA 638

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
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Db 639 ACACAAACAACAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTACTCT 698

QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
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Db 699 ACAATACCTGCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 758

QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
|||||

Db 759 AAAAAATTGATTGTGTCAAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT 818

QY 201 GluPropheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
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Db 819 GAACCATTTGTTGAAAAATAAAGCAGCAATTCAGAATGAAGCTGCTGGGTTTGA 872

RESULT 7

BX402505

LOCUS

DEFINITION BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI045YA10 5-PRIME, mRNA sequence.

ACCESSION BX402505

VERSION BX402505.2 GI:46921551

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 13, 2003 this sequence version replaced gi:30630733.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AI012ZA06QP1&c=5952.r.

FEATURES

source

1. .1036
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI045YA10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 3.58e-105 Length: 1036
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x BX402505 (1-1036)

Table with 2 columns: Accession/Qualifiers and Source. Rows include QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20, Db 202 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGC 261, QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40, Db 262 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGGAACCGACGCTGAATTTACAGAA 321, QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60, Db 322 GCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA 381, QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80, Db 382 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTC 441, QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100, Db 442 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGCTCTGATTTGG 501, QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120, Db 502 AAGGTTCCAGTGAGCGACAGTTTTCAGCCCTATTGTTACAACCTCATCTGATACTTGGACT 561, QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140, Db 562 AACTCGTGCATTCAGAAATATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 621, QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160, Db 622 ACACAAACAACAGAAATTTATTGTCAGTACAGTACCTACTCGGTGGCATCCCTTACTCT 681, QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180, Db 682 ACAATACCTGCCCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 741, QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200, Db 742 AAAAAATTGATTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACT 801, QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218, Db 802 GAACCATTTGTTGAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA 855

RESULT 8
AL551020
LOCUS AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI066YL13 5-PRIME, mRNA sequence.
ACCESSION AL551020
VERSION AL551020.3 GI:45751381
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1043)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization

JOURNAL COMMENT

Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272837.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster S952.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI066CF07QP1&c=5952.r.

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 3.72e-105 Length: 1043
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AL551020 (1-1043)

Table with 2 columns: Accession/Qualifiers and Source. Rows include QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20, Db 79 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCATGC 138, QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40, Db 139 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGGAACCGACGCTGAATTTACAGAA 198, QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60, Db 199 GCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGCAAGTTGAAACA 258, QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80, Db 259 GCCTTGAAAGCTAGCTTTGAAACITTCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTC 318, QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100, Db 319 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGG 378, QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120, Db 379 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACT 438, QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140, Db 439 AACTCGTGCATTCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 498, QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160, Db 499 ACACAAACAACAGAAATTTATTGTCAGTACAGTACCTACTCGGTGGCATCCCTTACTCT 558, QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180, Db 559 ACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACCTTCTATTCCACGGAGA 618

ORIGIN

sites of the pCMVSPORT 6 vector. Library was normalized."

Alignment Scores: 3.96e-105 Length: 1090

Pred. No.: 1125.00 Matches: 218

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 100.00% Gaps: 0

DB: 1

US-10-063-670-6_COPY_17_234 (1-218) x AL546669 (1-1090)

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20

Db 112 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGC 171

QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 172 AGAATTATGGGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCACAGAA 231

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 232 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 291

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 292 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTC 351

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 352 ATCTCTAGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCCTGATTTGG 411

QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 412 AAGGTTCCAGTGAGCGACAGTTTGCAGCCCTATTGTACAACCTCATCTGATACTTGGACT 471

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 472 AACTCGTGCAATTCAGAAATTATCACCCAAAGATCCCATATTTCAAACACTCAAAC TGCA 531

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 532 ACACAAACAACAGAAATTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT 591

QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180

Db 592 ACAATACCTGCCCCCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTTCCACGGAGA 651

QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200

Db 652 AAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAAACTAGCACCATGTCTACAGAAACT 711

QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218

Db 712 GAACCATTTGTTGAAAAATAAGCAGCATTCACAGATGAAGCTGCTGGGTTTGA 765

RESULT 11

AL550279

LOCUS

DEFINITION AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI039YJ06 5-PRIME, mRNA sequence.

ACCESSION AL550279

VERSION AL550279.3 GI:45750655

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1091)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT

On Feb 15, 2001 this sequence version replaced gi:31272096.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DI039DE03QP1&c=5952.r.

FEATURES

source

1..1091

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/mol_type="mRNA"

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 3.97e-105 Length: 1091

Pred. No.: 1125.00 Matches: 218

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 100.00% Gaps: 0

DB: 1

US-10-063-670-6_COPY_17_234 (1-218) x AL550279 (1-1091)

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20

Db 107 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGC 166

QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 167 AGAATTATGGGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAA 226

QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

Db 227 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 286

QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80

Db 287 GCCTTGAAAGCTAGCTTTGAAACTTGCACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTC 346

QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100

Db 347 ATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGG 406

QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120

Db 407 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACTTGGACT 466

QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 467 AACTCGTGCAATTCAGAAATTATCACCCAAAGATCCCATATTTCAACACTCAAACACTGCA 526

QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 527 ACACAAACAACAGAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT 586

QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180

Db 587 ACAATACCTGCCCCCTACTACTACTCTCCTCTGCTCCAGCTTCCAGCTTCCACTTCTATTCCACGGAGA 646

Best Local Similarity: 100.00%			Mismatches: 0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
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QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCys	20
Db	112	ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGC	171
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	172	AGAATTATGGGGATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAA	231
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	232	GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA	291
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	292	GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTC	351
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	352	ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGG	411
QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	412	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACT	471
QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	472	AACCTCGTGCAATCCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCA	531
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	532	ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT	591
QY	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	592	ACAATACCTGCCCTTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	651
QY	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	652	AAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT	711
QY	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	712	GAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGGA	765
RESULT 14			
CR604450			
LOCUS	1797 bp mRNA linear HTC 21-JUL-2004		
DEFINITION	full-length cDNA clone CS0DI065YD17 of Placenta Cot 25-normalized of Homo sapiens (human).		
ACCESSION	CR604450		
VERSION	CR604450.1 GI:50485257		
KEYWORDS	HTC; CNSLT_cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1797)		
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue		
REFERENCE	2 (bases 1 to 1797)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :		
BP 191 91006 EVRY cedex -FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES			
Location/Qualifiers			
source			
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Alignment Scores:			
Pred. No.:	8.09e-105	Length:	1797
Score:	1125.00	Matches:	218
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
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QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCys	20
Db	142	ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGC	201
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	202	AGAATTATGGGGATCACCCCTTGTGAGCAAAAAAGGCGAACCCAGCAGCTGAATTTACAGAA	261
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	262	GCTAAGGAGGCCCTGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA	321
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	322	GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTC	381
QY	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	382	ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGG	441
QY	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	442	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT	501
QY	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	502	AACTCGTGCATTCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA	561
QY	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	562	ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT	621
QY	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	622	ACAATACCTGCCCTTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA	681
QY	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	682	AAAAAATTGATTGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACT	741
QY	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	742	GAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGGA	795
RESULT 15			
CR612000			

LOCUS CR612000 1820 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI069YN02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612000
VERSION CR612000.1 GI:50492807
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1820)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue
REFERENCE 2 (bases 1 to 1820)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/clone="CS0DI069YN02"
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ORIGIN
Alignment Scores:
Pred. No.: 8.24e-105 Length: 1820
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-063-670-6_COPY_17_234 (1-218) x CR612000 (1-1820)
QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20
Db 146 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGCATGC 205
QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 206 AGAATTATGGGATCACCCCTGTGTAGCAAAAAGCGCAACCAGCAGCTGAATTTCACAGAA 265
QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 266 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTGGCCGCAAGGACCAAGTTGAAACA 325
QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db 326 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTC 385
QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db 386 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTGCTGATTTGG 445
QY 101 LysValProValSerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 446 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 505
QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 506 AACTCGTGCATTCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCA 565
QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 566 ACACAAACAACAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTTACTCT 625
QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db 626 ACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 685
QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 686 AAAAAATTGATTTGTGTCAAGAGTTTTTTATGGAAGCTAGCACCATGTCTACAGAAACT 745
QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 746 GAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA 799

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 22:45:22 ; Search time 582.544 Seconds
 (without alignments)
 2606.386 Million cell updates/sec

Perfect score: 1125
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Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-DB=Published_Applications_NA -OPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications_NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1125	100.0	2029	15	US-10-079-111-2	Sequence 2, Appli
2	1125	100.0	2029	22	US-10-820-474A-198	Sequence 198, App
3	1125	100.0	2324	18	US-10-276-774-999	Sequence 999, App
6	1125	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
95	1125	100.0	2372	15	US-10-223-085-31	Sequence 31, Appl
96	1125	100.0	2372	15	US-10-223-084-31	Sequence 31, Appl
97	1125	100.0	2372	15	US-10-223-088-31	Sequence 31, Appl
98	1125	100.0	2372	15	US-10-223-090-31	Sequence 31, Appl
100	1125	100.0	2372	15	US-10-223-087-31	Sequence 31, Appl
103	1125	100.0	2372	15	US-10-223-083-31	Sequence 31, Appl
104	1125	100.0	2372	15	US-10-223-089-31	Sequence 31, Appl
109	1125	100.0	2372	16	US-10-299-976-200	Sequence 200, App
137	1125	100.0	2372	16	US-10-063-742-5	Sequence 5, Appli
212	1125	100.0	2372	16	US-10-299-937-200	Sequence 200, App
215	1125	100.0	2372	16	US-10-223-081-31	Sequence 31, Appl
225	1125	100.0	2372	16	US-10-223-082-31	Sequence 31, Appl
231	1125	100.0	2372	17	US-10-298-993-200	Sequence 200, App
232	1125	100.0	2372	17	US-10-305-654-31	Sequence 31, Appl
233	1125	100.0	2372	17	US-10-448-923-200	Sequence 200, App
234	1125	100.0	2372	17	US-10-449-656-200	Sequence 200, App
235	1125	100.0	2372	17	US-10-448-713-200	Sequence 200, App
236	1125	100.0	2372	17	US-10-425-447-200	Sequence 200, App
237	1125	100.0	2372	18	US-10-081-056-31	Sequence 31, Appl
239	1125	100.0	2372	19	US-10-215-371-200	Sequence 200, App
240	1125	100.0	2372	19	US-10-771-187-200	Sequence 200, App
241	1125	100.0	2372	21	US-10-972-317-5	Sequence 5, Appli
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243	1125	100.0	2372	21	US-10-978-255-200	Sequence 200, App
244	1125	100.0	2372	22	US-10-797-366-200	Sequence 200, App
245	1125	100.0	2372	22	US-10-970-823-200	Sequence 200, App
246	1125	100.0	2436	22	US-10-756-149-3836	Sequence 3836, Ap
247	1125	100.0	2667	20	US-10-723-860-7823	Sequence 7823, Ap
248	1119	99.5	2313	15	US-10-291-634-1	Sequence 1, Appli
249	1119	99.5	2369	17	US-10-264-237-1260	Sequence 1260, Ap
250	1106	98.3	2313	20	US-10-723-860-3908	Sequence 3908, Ap
251	1106	98.3	2313	22	US-10-287-436A-215	Sequence 215, App
252	979.5	87.1	1127	17	US-10-138-588-1	Sequence 1, Appli
253	669	59.5	1896	10	US-09-866-050A-595	Sequence 595, App
254	669	59.5	1896	14	US-10-152-661-595	Sequence 595, App
255	645	57.3	411	10	US-09-918-995-8107	Sequence 8107, Ap
256	508.5	45.2	531	21	US-10-696-639-2768	Sequence 2768, Ap
257	281.5	25.0	457	9	US-09-864-761-15431	Sequence 15431, A
258	277	24.6	492	15	US-10-291-634-12	Sequence 12, Appl
259	221.5	19.7	559	15	US-10-079-111-3	Sequence 3, Appli
260	213.5	19.0	2747	9	US-09-917-800A-1588	Sequence 7, Appli
261	213.5	19.0	2747	22	US-10-024-607-7	Sequence 24, Appl
262	209.5	18.6	1177	22	US-10-024-607-24	Sequence 57, Appl
263	209.5	18.6	5452	19	US-10-741-601-57	Sequence 219, App
264	209.5	18.6	5452	21	US-10-741-600-219	Sequence 25, Appl
265	207	18.4	1089	22	US-10-024-607-25	Sequence 226, App
266	203	18.0	3091	21	US-10-741-600-226	Sequence 86, Appl
267	203	18.0	3091	22	US-10-783-271-86	Sequence 196, App
268	203	18.0	3091	22	US-10-287-436A-196	Sequence 807, App
269	203	18.0	3091	22	US-10-287-436A-807	Sequence 60, Appl
270	203	18.0	5468	19	US-10-741-601-60	Sequence 225, App
271	203	18.0	5468	21	US-10-741-600-225	Sequence 54, Appl
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273	203	18.0	5674	21	US-10-741-600-218	Sequence 55, Appl
274	203	18.0	5739	19	US-10-741-601-55	Sequence 221, App
275	203	18.0	5739	21	US-10-741-600-221	Sequence 18, Appl
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279	199.5	17.7	2316	21	US-10-652-981-15	Sequence 474, App
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281	198.5	17.6	1737	22	US-10-024-607-22	

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1126	125	11.1	1414	11	US-09-968-007A-208	Sequence 208, App	1199	108	9.6	1640	14	US-10-091-438-33	Sequence 33, App
1127	125	11.1	1414	17	US-10-133-937-18	Sequence 18, Appl	1200	108	9.6	1641	9	US-09-764-853-420	Sequence 420, App
1128	125	11.1	1414	17	US-10-295-027-293	Sequence 293, App	1201	108	9.6	1641	14	US-10-091-438-94	Sequence 94, Appl
1129	125	11.1	1414	17	US-10-159-563-18	Sequence 18, Appl	1202	108	9.6	1957	18	US-10-120-907A-2	Sequence 2, Appli
1130	125	11.1	1414	19	US-10-755-889-117	Sequence 117, App	1203	108	9.6	1957	18	US-10-120-907A-6	Sequence 6, Appli
1131	125	11.1	1414	21	US-10-278-698-79	Sequence 79, Appl	1204	108	9.6	1957	18	US-10-120-907A-8	Sequence 8, Appli
1132	125	11.1	1414	21	US-10-278-698-593	Sequence 593, App	1205	108	9.6	1957	18	US-10-120-907A-10	Sequence 10, Appl
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1147	118.5	10.5	12319	16	US-10-240-965-240	Sequence 240, App	1220	107	9.5	2011	22	US-10-667-723-3	Sequence 3, Appli
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1172	112.5	10.0	3260	17	US-10-107-782-210	Sequence 210, App	1245	104.5	9.3	172569	13	US-10-087-192-1366	Sequence 1366, Ap
1173	112.5	10.0	4576	9	US-09-842-930A-24	Sequence 24, Appl	1246	104	9.2	484	17	US-10-172-118-144	Sequence 144, App
1174	112.5	10.0	4576	21	US-10-990-844-24	Sequence 24, Appl	1247	104	9.2	484	18	US-10-342-887-144	Sequence 144, App
1175	112.5	10.0	4642	15	US-10-133-172-3	Sequence 3, Appli	1248	104	9.2	4767	11	US-09-973-278-731	Sequence 731, App
1176	112.5	10.0	4962	15	US-10-133-172-19	Sequence 19, Appl	1249	104	9.2	4768	11	US-09-973-278-730	Sequence 730, App
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102	89.5	8.0	1014	3	US-09-362-230-31	Sequence 31, Appl
103	89.5	8.0	1014	5	PCT-US94-07926-31	Sequence 31, Appl
104	89.5	8.0	1731	1	US-08-028-463-15	Sequence 15, Appl

105	89.5	8.0	1731	1	US-08-461-836-15	Sequence 15, Appl	178	85.5	7.6	2316	4	US-09-476-242-4	Sequence 4, Appli
106	89	7.9	1298	4	US-09-311-784A-25	Sequence 25, Appl	179	85.5	7.6	2316	4	US-09-476-242-8	Sequence 8, Appli
107	89	7.9	2409	3	US-09-230-225B-3	Sequence 3, Appli	180	85.5	7.6	2322	4	US-09-476-242-5	Sequence 5, Appli
108	89	7.9	2422	4	US-09-949-016-3654	Sequence 3654, Ap	181	85.5	7.6	2322	4	US-09-476-242-18	Sequence 18, Appl
109	89	7.9	2455	1	US-08-073-807A-1	Sequence 1, Appli	182	85.5	7.6	2322	4	US-09-476-242-20	Sequence 20, Appl
110	88.5	7.9	1356	4	US-09-252-991A-630	Sequence 630, App	183	85.5	7.6	2328	4	US-09-476-242-6	Sequence 6, Appli
111	88.5	7.9	2310	4	US-09-476-242-21	Sequence 21, Appl	184	85.5	7.6	2334	4	US-09-476-242-7	Sequence 7, Appli
112	88.5	7.9	2535	4	US-09-476-242-13	Sequence 13, Appl	185	85.5	7.6	2352	4	US-09-476-242-26	Sequence 26, Appl
113	88.5	7.9	2955	4	US-09-252-991A-684	Sequence 684, App	186	85.5	7.6	2358	4	US-09-475-515-50	Sequence 50, Appl
c 114	88.5	7.9	3150	4	US-09-252-991A-727	Sequence 727, App	187	85.5	7.6	2358	4	US-09-476-242-25	Sequence 25, Appl
115	88	7.8	2165	4	US-09-620-312D-809	Sequence 809, App	188	85.5	7.6	2466	4	US-09-475-515-49	Sequence 49, Appl
116	88	7.8	2447	4	US-09-960-643-1	Sequence 1, Appli	189	85.5	7.6	2517	4	US-09-476-242-16	Sequence 16, Appl
117	87.5	7.8	795	4	US-09-252-991A-3803	Sequence 3803, Ap	190	85.5	7.6	2517	4	US-09-476-242-17	Sequence 17, Appl
118	87.5	7.8	1623	4	US-09-252-991A-3844	Sequence 3844, Ap	191	85.5	7.6	2523	4	US-09-476-242-15	Sequence 15, Appl
c 119	87.5	7.8	4167	4	US-09-252-991A-3666	Sequence 3666, Ap	192	85.5	7.6	2529	4	US-09-476-242-14	Sequence 14, Appl
120	87.5	7.8	5275	1	US-08-485-588-1	Sequence 1, Appli	193	85.5	7.6	2541	4	US-09-476-242-9	Sequence 9, Appli
121	87.5	7.8	5275	1	US-08-484-565-1	Sequence 1, Appli	194	85.5	7.6	2541	4	US-09-476-242-10	Sequence 10, Appl
122	87.5	7.8	5275	2	US-08-480-751-1	Sequence 1, Appli	195	85.5	7.6	2541	4	US-09-476-242-11	Sequence 11, Appl
123	87.5	7.8	5275	2	US-08-943-986-1	Sequence 1, Appli	196	85.5	7.6	2547	4	US-09-475-515-48	Sequence 48, Appl
124	87.5	7.8	5275	3	US-08-353-784-1	Sequence 1, Appli	c 197	85.5	7.6	3136	4	US-09-949-016-2550	Sequence 2550, Ap
125	87.5	7.8	5275	3	US-08-484-719B-1	Sequence 1, Appli	c 198	85.5	7.6	3136	4	US-09-949-016-2659	Sequence 2659, Ap
126	87.5	7.8	5275	3	US-08-484-159-1	Sequence 1, Appli	199	85.5	7.6	4104	4	US-09-614-221A-44	Sequence 44, Appl
127	87	7.7	790	4	US-09-771-357-97	Sequence 97, Appl	200	85.5	7.6	4227	4	US-09-902-540-8919	Sequence 8919, Ap
128	87	7.7	790	4	US-10-059-579A-97	Sequence 97, Appl	201	85.5	7.6	4608	4	US-09-475-515-76	Sequence 76, Appl
129	87	7.7	867	4	US-09-216-393B-340	Sequence 340, App	202	85.5	7.6	4689	4	US-09-475-515-74	Sequence 74, Appl
130	87	7.7	867	4	US-09-216-393B-342	Sequence 342, App	c 203	85.5	7.6	5043	4	US-09-902-540-574	Sequence 574, App
131	87	7.7	1397	4	US-09-216-393B-343	Sequence 343, App	c 204	85.5	7.6	9367	4	US-09-902-540-951	Sequence 951, App
c 132	87	7.7	1397	4	US-09-216-393B-345	Sequence 345, App	c 205	85	7.6	804	4	US-09-902-540-5636	Sequence 5636, Ap
c 133	87	7.7	67911	4	US-09-949-016-16979	Sequence 16979, A	206	85	7.6	985	3	US-09-160-246-9	Sequence 9, Appli
c 134	87	7.7	109690	4	US-09-949-016-13525	Sequence 13525, A	207	85	7.6	985	3	US-09-160-246-13	Sequence 13, Appl
c 135	86.5	7.7	1707	4	US-09-902-540-2659	Sequence 2659, Ap	208	85	7.6	1060	4	US-09-050-739-13	Sequence 13, Appl
136	86.5	7.7	1929	4	US-09-252-991A-10474	Sequence 10474, A	209	85	7.6	1371	4	US-09-350-756-3	Sequence 3, Appli
137	86.5	7.7	2322	4	US-09-476-242-19	Sequence 19, Appl	c 210	85	7.6	1752	4	US-09-902-540-8626	Sequence 8626, Ap
138	86.5	7.7	2541	4	US-09-476-242-12	Sequence 12, Appl	c 211	85	7.6	7661	4	US-09-902-540-912	Sequence 912, App
139	86.5	7.7	4435	4	US-09-612-402B-1	Sequence 1, Appli	c 212	85	7.6	12685	4	US-09-479-467A-3	Sequence 3, Appli
140	86.5	7.7	19068	4	US-09-902-540-1123	Sequence 1123, Ap	c 213	85	7.6	49225	4	US-09-902-540-1269	Sequence 1269, Ap
c 141	86.5	7.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli	214	85	7.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
142	86	7.6	813	4	US-09-949-016-2247	Sequence 2247, Ap	215	85	7.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 143	86	7.6	1150	4	US-09-771-357-96	Sequence 96, Appl	c 216	85	7.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 144	86	7.6	1150	4	US-10-059-579A-96	Sequence 96, Appl	217	84.5	7.5	813	4	US-09-248-796A-372	Sequence 372, App
145	86	7.6	1474	4	US-09-270-767-12852	Sequence 12852, A	218	84.5	7.5	1016	4	US-09-220-132-17	Sequence 17, Appl
146	86	7.6	5774	4	US-09-949-016-13989	Sequence 13989, A	219	84.5	7.5	1017	4	US-09-949-016-4435	Sequence 4435, Ap
c 147	86	7.6	33529	3	US-09-144-085-3	Sequence 3, Appli	220	84.5	7.5	3168	3	US-09-165-239A-3	Sequence 3, Appli
c 148	86	7.6	142783	4	US-09-949-016-15127	Sequence 15127, A	221	84.5	7.5	3486	4	US-09-614-221A-292	Sequence 292, App
149	86	7.6	176006	4	US-09-949-016-16804	Sequence 16804, A	222	84.5	7.5	5697	3	US-08-814-052-11	Sequence 11, Appl
150	86	7.6	253375	4	US-09-949-016-12849	Sequence 12849, A	223	84.5	7.5	5697	3	US-08-812-829-11	Sequence 11, Appl
151	85.5	7.6	1320	3	US-09-221-654-1	Sequence 1, Appli	224	84.5	7.5	51723	4	US-09-949-016-12152	Sequence 12152, A
152	85.5	7.6	1320	3	US-08-989-358A-1	Sequence 1, Appli	225	84.5	7.5	51723	4	US-09-949-016-16991	Sequence 16991, A
153	85.5	7.6	1323	4	US-09-475-515-35	Sequence 35, Appl	226	84.5	7.5	276237	4	US-09-949-016-17504	Sequence 17504, A
154	85.5	7.6	1387	4	US-09-475-515-34	Sequence 34, Appl	c 227	84	7.5	564	4	US-09-583-110-2585	Sequence 2585, Ap
155	85.5	7.6	1453	4	US-09-475-515-33	Sequence 33, Appl	228	84	7.5	795	4	US-09-248-796A-7800	Sequence 7800, Ap
156	85.5	7.6	1593	3	US-08-993-359-23	Sequence 23, Appl	229	84	7.5	1125	2	US-08-997-080-153	Sequence 153, App
157	85.5	7.6	1593	4	US-09-482-558A-23	Sequence 23, Appl	230	84	7.5	1125	2	US-08-997-362-153	Sequence 153, App
158	85.5	7.6	1638	4	US-09-799-451-412	Sequence 412, App	231	84	7.5	1125	3	US-09-095-855-153	Sequence 153, App
159	85.5	7.6	1836	4	US-09-475-515-41	Sequence 41, Appl	232	84	7.5	1125	3	US-09-324-542-153	Sequence 153, App
160	85.5	7.6	1836	4	US-09-475-515-44	Sequence 44, Appl	233	84	7.5	1125	3	US-09-205-426-153	Sequence 153, App
161	85.5	7.6	1836	4	US-09-475-515-47	Sequence 47, Appl	234	84	7.5	1176	2	US-08-387-942C-17	Sequence 17, Appl
162	85.5	7.6	1896	3	US-09-620-412C-324	Sequence 324, App	235	84	7.5	5163	3	US-08-700-651-1	Sequence 1, Appli
163	85.5	7.6	1896	4	US-09-598-419-324	Sequence 324, App	236	84	7.5	5163	3	US-08-928-361B-4	Sequence 4, Appli
164	85.5	7.6	1944	4	US-09-475-515-37	Sequence 37, Appl	237	84	7.5	5163	4	US-09-588-995A-4	Sequence 4, Appli
165	85.5	7.6	1944	4	US-09-475-515-38	Sequence 38, Appl	238	84	7.5	5318	3	US-08-700-651-2	Sequence 2, Appli
166	85.5	7.6	1944	4	US-09-475-515-40	Sequence 40, Appl	239	84	7.5	5318	3	US-08-928-361B-3	Sequence 3, Appli
167	85.5	7.6	1944	4	US-09-475-515-43	Sequence 43, Appl	240	84	7.5	5318	4	US-09-588-995A-3	Sequence 3, Appli
168	85.5	7.6	1944	4	US-09-475-515-46	Sequence 46, Appl	241	84	7.5	5511	3	US-08-928-361B-2	Sequence 2, Appli
169	85.5	7.6	2025	4	US-09-475-515-36	Sequence 36, Appl	242	84	7.5	5511	4	US-09-588-995A-2	Sequence 2, Appli
170	85.5	7.6	2025	4	US-09-475-515-39	Sequence 39, Appl	243	84	7.5	5679	3	US-08-814-052-9	Sequence 9, Appli
171	85.5	7.6	2025	4	US-09-475-515-42	Sequence 42, Appl	244	84	7.5	5679	3	US-08-812-829-9	Sequence 9, Appli
172	85.5	7.6	2025	4	US-09-475-515-45	Sequence 45, Appl	245	84	7.5	7334	3	US-08-928-361B-1	Sequence 1, Appli
c 173	85.5	7.6	2028	4	US-09-107-532A-1973	Sequence 1973, Ap	246	84	7.5	7334	4	US-09-588-995A-1	Sequence 1, Appli
174	85.5	7.6	2298	4	US-09-476-242-22	Sequence 22, Appl	247	84	7.5	12588	2	US-08-387-942C-1	Sequence 1, Appli
175	85.5	7.6	2298	4	US-09-476-242-23	Sequence 23, Appl	248	84	7.5	9960	4	US-09-762-311-2	Sequence 2, Appli
176	85.5	7.6	2298	4	US-09-476-242-24	Sequence 24, Appl	249	83.5	7.4	1107	2	US-08-991-300-1	Sequence 1, Appli
177	85.5	7.6	2310	4	US-09-476-242-3	Sequence 3, Appli	250	83.5	7.4	1459	3	US-09-377-557-13	Sequence 13, Appl

251	83.5	7.4	2353	4	US-09-369-247-12	Sequence 12, Appl	Sequence 12, Appl	324	80	7.1	597	4	US-09-902-540-8148	Sequence 8148, Ap
252	83.5	7.4	2455	3	US-09-103-429A-1	Sequence 1, Appli	Sequence 1, Appli	c 325	80	7.1	744	4	US-09-252-991A-15538	Sequence 15538, A
253	83.5	7.4	2455	4	US-09-294-663-1	Sequence 1, Appli	Sequence 1, Appli	c 326	80	7.1	807	4	US-09-252-991A-15427	Sequence 15427, A
254	83.5	7.4	2821	3	US-09-103-429A-2	Sequence 2, Appli	Sequence 2, Appli	327	80	7.1	975	3	US-09-365-150-4	Sequence 4, Appli
255	83.5	7.4	2821	4	US-09-294-663-2	Sequence 2, Appli	Sequence 2, Appli	328	80	7.1	1275	4	US-09-252-991A-15254	Sequence 15254, A
256	83.5	7.4	65848	4	US-09-949-016-13285	Sequence 13285, A	Sequence 13285, A	329	80	7.1	1359	4	US-09-252-991A-15302	Sequence 15302, A
257	83	7.4	630	4	US-09-270-767-1924	Sequence 1924, Ap	Sequence 1924, Ap	c 330	80	7.1	2538	4	US-09-248-796A-3859	Sequence 3859, Ap
258	83	7.4	630	4	US-09-270-767-17206	Sequence 17206, A	Sequence 17206, A	331	80	7.1	6269	4	US-09-902-540-836	Sequence 836, App
259	83	7.4	966	4	US-09-252-991A-11896	Sequence 11896, A	Sequence 11896, A	332	80	7.1	6301	4	US-09-902-540-842	Sequence 842, App
260	83	7.4	2905	4	US-09-949-016-410	Sequence 410, App	Sequence 410, App	333	80	7.1	9960	3	US-08-822-586-46	Sequence 46, Appl
261	83	7.4	2906	4	US-09-949-016-5249	Sequence 5249, Ap	Sequence 5249, Ap	c 334	80	7.1	16265	4	US-09-902-540-1126	Sequence 1126, Ap
c 262	83	7.4	4063	4	US-09-902-540-595	Sequence 595, App	Sequence 595, App	c 335	80	7.1	40408	4	US-09-949-016-16331	Sequence 16331, A
263	83	7.4	4545	3	US-09-221-017B-1011	Sequence 1011, Ap	Sequence 1011, Ap	c 336	80	7.1	247781	4	US-09-949-016-14193	Sequence 14193, A
c 264	83	7.4	72704	4	US-09-902-540-1273	Sequence 1273, Ap	Sequence 1273, Ap	337	80	7.1	254405	4	US-09-949-016-14381	Sequence 14381, A
265	83	7.4	1230230	4	US-09-438-185A-1	Sequence 1, Appli	Sequence 1, Appli	c 338	80	7.1	536165	4	US-09-214-808-1	Sequence 1, Appli
c 266	82.5	7.3	1842	4	US-09-016-434-1236	Sequence 1236, Ap	Sequence 1236, Ap	c 339	79.5	7.1	601	4	US-09-949-016-22247	Sequence 22247, A
267	82.5	7.3	2298	4	US-09-252-991A-13540	Sequence 13540, A	Sequence 13540, A	c 340	79.5	7.1	601	4	US-09-949-016-51354	Sequence 51354, A
c 268	82.5	7.3	2412	4	US-09-252-991A-13908	Sequence 13908, A	Sequence 13908, A	341	79.5	7.1	612	4	US-09-270-767-3415	Sequence 3415, Ap
269	82.5	7.3	6022	4	US-08-956-171E-92	Sequence 92, Appl	Sequence 92, Appl	342	79.5	7.1	612	4	US-09-270-767-18697	Sequence 18697, A
270	82.5	7.3	6022	4	US-08-781-986A-92	Sequence 92, Appl	Sequence 92, Appl	343	79.5	7.1	768	4	US-09-248-796A-7148	Sequence 7148, Ap
271	82.5	7.3	23847	4	US-09-902-540-1177	Sequence 1177, Ap	Sequence 1177, Ap	344	79.5	7.1	909	4	US-09-252-991A-2103	Sequence 2103, Ap
c 272	82.5	7.3	194937	4	US-09-949-016-17032	Sequence 17032, A	Sequence 17032, A	345	79.5	7.1	959	4	US-09-902-540-102	Sequence 102, App
c 273	82.5	7.3	194937	4	US-09-949-016-17033	Sequence 17033, A	Sequence 17033, A	346	79.5	7.1	975	4	US-09-489-039A-1422	Sequence 1422, Ap
274	82	7.3	423	1	US-08-470-179-160	Sequence 160, App	Sequence 160, App	347	79.5	7.1	1002	4	US-09-252-991A-2014	Sequence 2014, Ap
275	82	7.3	466	2	US-08-892-880-13	Sequence 13, Appl	Sequence 13, Appl	348	79.5	7.1	1270	4	US-09-270-767-12871	Sequence 12871, A
c 276	82	7.3	855	4	US-09-252-991A-10673	Sequence 10673, A	Sequence 10673, A	349	79.5	7.1	1371	4	US-09-252-991A-9440	Sequence 9440, Ap
277	82	7.3	875	4	US-09-443-067-27	Sequence 27, Appl	Sequence 27, Appl	350	79.5	7.1	1963	2	US-08-809-763-5	Sequence 5, Appli
278	82	7.3	993	4	US-09-252-991A-10494	Sequence 10494, A	Sequence 10494, A	351	79.5	7.1	1965	3	US-08-956-253-5	Sequence 5, Appli
c 279	82	7.3	1383	4	US-09-489-039A-3928	Sequence 3928, Ap	Sequence 3928, Ap	352	79.5	7.1	3048	1	US-08-188-228-47	Sequence 47, Appl
280	82	7.3	1662	1	US-08-651-572-1	Sequence 1, Appli	Sequence 1, Appli	353	79.5	7.1	3048	1	US-08-332-643-41	Sequence 41, Appl
281	82	7.3	1662	3	US-09-066-544-1	Sequence 1, Appli	Sequence 1, Appli	354	79.5	7.1	3048	1	US-08-332-638-47	Sequence 47, Appl
282	82	7.3	1662	3	US-08-951-086-1	Sequence 1, Appli	Sequence 1, Appli	355	79.5	7.1	4359	4	US-08-943-144-3	Sequence 3, Appli
283	82	7.3	1662	3	US-09-430-669-1	Sequence 1, Appli	Sequence 1, Appli	356	79.5	7.1	5491	4	US-09-262-537-5	Sequence 5, Appli
c 284	82	7.3	4808	4	US-09-774-528-19	Sequence 19, Appl	Sequence 19, Appl	357	79.5	7.1	5597	4	US-09-262-537-1	Sequence 1, Appli
285	82	7.3	13926	3	US-08-961-527-5	Sequence 5, Appli	Sequence 5, Appli	358	79.5	7.1	5598	4	US-09-262-537-33	Sequence 33, Appl
286	82	7.3	40586	4	US-09-949-016-16965	Sequence 16965, A	Sequence 16965, A	359	79.5	7.1	5617	4	US-09-262-537-3	Sequence 3, Appli
c 287	81.5	7.2	879	5	PCT-US96-03916-16	Sequence 16, Appl	Sequence 16, Appl	360	79.5	7.1	6474	4	US-09-854-856-51	Sequence 51, Appl
288	81.5	7.2	2309	3	US-09-091-725-9	Sequence 9, Appli	Sequence 9, Appli	361	79.5	7.1	6558	4	US-09-854-856-35	Sequence 35, Appl
289	81.5	7.2	2406	2	US-08-687-702-2	Sequence 2, Appli	Sequence 2, Appli	362	79.5	7.1	6554	4	US-09-854-856-19	Sequence 19, Appl
290	81.5	7.2	12687	1	US-08-676-169-1	Sequence 1, Appli	Sequence 1, Appli	363	79.5	7.1	6738	4	US-09-854-856-3	Sequence 3, Appli
291	81.5	7.2	12687	3	US-08-981-459-1	Sequence 1, Appli	Sequence 1, Appli	364	79.5	7.1	6885	4	US-09-854-856-49	Sequence 49, Appl
292	81.5	7.2	12687	3	US-09-063-431A-1	Sequence 1, Appli	Sequence 1, Appli	365	79.5	7.1	6969	4	US-09-854-856-33	Sequence 33, Appl
293	81.5	7.2	13473	5	PCT-US96-03916-1	Sequence 1, Appli	Sequence 1, Appli	366	79.5	7.1	7065	4	US-09-854-856-17	Sequence 17, Appl
294	81.5	7.2	18912	5	PCT-US96-03916-59	Sequence 59, Appl	Sequence 59, Appl	367	79.5	7.1	7149	4	US-09-854-856-1	Sequence 1, Appli
295	81.5	7.2	20250	4	US-09-902-540-1213	Sequence 1213, Ap	Sequence 1213, Ap	368	79.5	7.1	20870	4	US-09-949-016-16017	Sequence 16017, A
c 296	81.5	7.2	421491	4	US-09-949-016-12805	Sequence 12805, A	Sequence 12805, A	369	79.5	7.1	121427	4	US-09-949-016-11950	Sequence 11950, A
c 297	81.5	7.2	421494	4	US-09-949-016-14060	Sequence 14060, A	Sequence 14060, A	370	79.5	7.1	121433	4	US-09-949-016-13230	Sequence 13230, A
298	81	7.2	621	1	US-08-028-463-7	Sequence 7, Appli	Sequence 7, Appli	c 371	79.5	7.1	157866	4	US-09-949-016-12982	Sequence 12982, A
299	81	7.2	621	1	US-08-461-836-7	Sequence 7, Appli	Sequence 7, Appli	c 372	79.5	7.1	157866	4	US-09-949-016-12983	Sequence 12983, A
300	81	7.2	1389	4	US-09-602-787A-77	Sequence 77, Appl	Sequence 77, Appl	c 373	79.5	7.1	157866	4	US-09-949-016-12984	Sequence 12984, A
301	81	7.2	1850	4	US-09-848-726-1	Sequence 1, Appli	Sequence 1, Appli	374	79.5	7.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
302	81	7.2	2465	5	PCT-US92-08090-1	Sequence 1, Appli	Sequence 1, Appli	375	79.5	7.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 303	81	7.2	2911	4	US-09-799-451-888	Sequence 888, App	Sequence 888, App	385	79	7.0	465	4	US-09-377-502-58	Sequence 58, Appl
304	81	7.2	3498	4	US-09-520-781-3	Sequence 3, Appli	Sequence 3, Appli	386	79	7.0	714	4	US-09-252-991A-8966	Sequence 8966, Ap
c 305	81	7.2	23673	3	US-09-773-816-1	Sequence 1, Appli	Sequence 1, Appli	387	79	7.0	767	4	US-09-270-767-2226	Sequence 2226, Ap
306	80.5	7.2	771	4	US-09-902-540-5814	Sequence 5814, Ap	Sequence 5814, Ap	388	79	7.0	767	4	US-09-270-767-17508	Sequence 17508, A
307	80.5	7.2	1099	4	US-09-949-016-1829	Sequence 1829, Ap	Sequence 1829, Ap	c 389	79	7.0	837	4	US-09-252-991A-9123	Sequence 9123, Ap
308	80.5	7.2	1227	3	US-09-074-912-3	Sequence 3, Appli	Sequence 3, Appli	c 390	79	7.0	975	4	US-09-498-520A-1	Sequence 1, Appli
309	80.5	7.2	1227	3	US-09-290-136-3	Sequence 3, Appli	Sequence 3, Appli	c 391	79	7.0	975	4	US-09-583-110-1252	Sequence 1252, Ap
c 310	80.5	7.2	2458	3	US-09-071-101-5	Sequence 5, Appli	Sequence 5, Appli	c 392	79	7.0	975	4	US-09-968-129-1	Sequence 1, Appli
c 311	80.5	7.2	2458	3	US-09-369-618-6	Sequence 6, Appli	Sequence 6, Appli	c 393	79	7.0	996	4	US-09-107-433-2480	Sequence 2480, Ap
c 312	80.5	7.2	2458	3	US-09-369-617-6	Sequence 6, Appli	Sequence 6, Appli	394	79	7.0	1470	3	US-09-292-225-40	Sequence 40, Appl
313	80.5	7.2	5220	4	US-09-677-046A-1	Sequence 1, Appli	Sequence 1, Appli	c 395	79	7.0	1470	3	US-09-292-225-42	Sequence 42, Appl
c 314	80.5	7.2	7948	4	US-09-949-016-14929	Sequence 14929, A	Sequence 14929, A	396	79	7.0	1527	3	US-09-292-225-37	Sequence 37, Appl
c 315	80.5	7.2	7960	4	US-09-949-016-14930	Sequence 14930, A	Sequence 14930, A	c 397	79	7.0	1527	3	US-09-292-225-39	Sequence 39, Appl
316	80.5	7.2	9542	3	US-08-968-685A-9	Sequence 9, Appli	Sequence 9, Appli	c 398	79	7.0	1621	3	US-09-292-225-34	Sequence 34, Appl
c 317	80.5	7.2	12180	4	US-09-949-016-12527	Sequence 12527, A	Sequence 12527, A	c 399	79	7.0	1621	3	US-09-292-225-36	Sequence 36, Appl
c 318	80.5	7.2	12180	4	US-09-949-016-14323	Sequence 14323, A	Sequence 14323, A	400	79	7.0	1686	4	US-09-252-991A-7673	Sequence 7673, Ap
319	80.5	7.2	16924	4	US-09-949-016-13720	Sequence 13720, A	Sequence 13720, A	401	79	7.0	1867	4	US-09-949-016-4889	Sequence 4889, Ap
320	80.5	7.2	43507	4	US-09-949-016-13297	Sequence 13297, A	Sequence 13297, A	402	79	7.0	1867	4	US-09-949-016-4890	Sequence 4890, Ap
321	80	7.1	156	1	US-08-225-477B-7	Sequence 7, Appli	Sequence 7, Appli	403	79	7.0	2032	3	US-09-241-581B-5	Sequence 5, Appli
322	80	7.1	156	5	PCT-US95-04353-7	Sequence 7, Appli	Sequence 7, Appli	404	79	7.0	2032	3	US-08-265-428-5	Sequence 5, Appli
323	80	7.1	288	4	US-09-252-991A-11933	Sequence 11933, A	Sequence 11933, A	405	79	7.0	2032	5	PCT-US95-07721-5	Sequence 5, Appli

406	79	7.0	2313	3	US-08-738-168B-14	Sequence 14, Appl	479	78	6.9	2804	1	US-08-446-794A-3	Sequence 3, Appli
c 407	79	7.0	2379	4	US-09-252-991A-9205	Sequence 9205, Ap	480	78	6.9	3793	4	US-09-902-540-587	Sequence 587, App
c 408	79	7.0	2553	4	US-09-949-016-488	Sequence 488, App	481	78	6.9	4152	3	US-08-826-134-5	Sequence 5, Appli
c 409	79	7.0	3767	4	US-09-823-038A-44	Sequence 44, Appl	482	78	6.9	4792	3	US-09-221-017B-107	Sequence 107, App
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c 412	79	7.0	3919	1	US-08-301-722A-1	Sequence 1, Appli	485	78	6.9	5294	3	US-08-826-134-1	Sequence 1, Appli
c 413	79	7.0	3926	4	US-09-949-016-1224	Sequence 1224, Ap	c 486	78	6.9	5541	1	US-08-920-812-20	Sequence 20, Appl
c 414	79	7.0	3946	4	US-09-949-016-146	Sequence 146, App	c 487	78	6.9	5541	1	US-08-920-827-20	Sequence 20, Appl
c 415	79	7.0	3960	4	US-09-902-540-8918	Sequence 8918, Ap	c 488	78	6.9	5541	1	US-08-921-177-20	Sequence 20, Appl
c 416	79	7.0	4014	4	US-09-949-016-4648	Sequence 4648, Ap	c 489	78	6.9	5541	1	US-08-362-577C-20	Sequence 20, Appl
c 417	79	7.0	4014	4	US-09-949-016-4649	Sequence 4649, Ap	c 490	78	6.9	5541	2	US-08-920-828-20	Sequence 20, Appl
c 418	79	7.0	4200	1	US-07-841-654B-1	Sequence 1, Appli	c 491	78	6.9	6008	4	US-09-949-016-5058	Sequence 5058, Ap
c 419	79	7.0	4200	1	US-07-946-234A-1	Sequence 1, Appli	c 492	78	6.9	6312	1	US-08-531-601-3	Sequence 3, Appli
c 420	79	7.0	4200	1	US-08-123-161A-1	Sequence 1, Appli	c 493	78	6.9	6312	2	US-08-859-032-3	Sequence 3, Appli
c 421	79	7.0	4200	1	US-08-483-278-1	Sequence 1, Appli	c 494	78	6.9	10085	4	US-09-902-540-964	Sequence 964, App
c 422	79	7.0	4200	5	PCT-US93-01560-1	Sequence 1, Appli	c 495	78	6.9	84875	4	US-09-949-016-17334	Sequence 17334, A
c 423	79	7.0	5183	1	US-08-459-568-3	Sequence 3, Appli	c 496	78	6.9	84875	4	US-09-949-016-17335	Sequence 17335, A
c 424	79	7.0	5183	2	US-08-399-411-3	Sequence 3, Appli	c 497	78	6.9	84875	4	US-09-949-016-17336	Sequence 17336, A
c 425	79	7.0	5868	3	US-08-516-859A-3	Sequence 3, Appli	c 498	78	6.9	84875	4	US-09-949-016-17337	Sequence 17337, A
c 426	79	7.0	5868	3	US-09-586-472-3	Sequence 3, Appli	c 499	78	6.9	85152	4	US-09-949-016-12665	Sequence 12665, A
c 427	79	7.0	5868	3	US-09-528-706-3	Sequence 3, Appli	c 500	78	6.9	85152	4	US-09-949-016-12666	Sequence 12666, A
c 428	79	7.0	6173	4	US-09-949-016-5511	Sequence 5511, Ap	c 501	78	6.9	85152	4	US-09-949-016-12667	Sequence 12667, A
c 429	79	7.0	6173	4	US-09-949-016-5512	Sequence 5512, Ap	c 502	78	6.9	85152	4	US-09-949-016-12668	Sequence 12668, A
c 430	79	7.0	9367	4	US-09-902-540-951	Sequence 951, App	c 503	78	6.9	152481	4	US-09-949-016-12521	Sequence 12521, A
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c 435	79	7.0	154746	4	US-09-827-688-8	Sequence 8, Appli	c 508	77.5	6.9	522	4	US-09-621-976-2854	Sequence 2854, Ap
c 436	78.5	7.0	532	4	US-09-270-767-1305	Sequence 1305, Ap	c 509	77.5	6.9	601	4	US-09-949-016-45651	Sequence 45651, A
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c 438	78.5	7.0	966	4	US-09-248-796A-9577	Sequence 9577, Ap	c 511	77.5	6.9	1239	4	US-09-252-991A-9383	Sequence 9383, Ap
c 439	78.5	7.0	1023	4	US-09-492-709A-102	Sequence 102, App	c 512	77.5	6.9	1425	4	US-09-578-063-2	Sequence 2, Appli
c 440	78.5	7.0	1291	2	US-08-887-365-35	Sequence 35, Appl	c 513	77.5	6.9	1482	4	US-09-252-991A-9689	Sequence 9689, Ap
c 441	78.5	7.0	1315	4	US-09-902-540-215	Sequence 215, App	c 514	77.5	6.9	1505	1	US-07-915-246-1	Sequence 1, Appli
c 442	78.5	7.0	1401	4	US-09-252-991A-10908	Sequence 10908, A	c 515	77.5	6.9	1614	4	US-09-252-991A-9607	Sequence 9607, Ap
c 443	78.5	7.0	1440	4	US-09-252-991A-11041	Sequence 11041, A	c 516	77.5	6.9	1623	4	US-09-252-991A-9650	Sequence 9650, Ap
c 444	78.5	7.0	1722	4	US-09-902-540-9668	Sequence 9668, Ap	c 517	77.5	6.9	1656	4	US-09-578-063-1	Sequence 1, Appli
c 445	78.5	7.0	1764	4	US-09-857-669-5	Sequence 5, Appli	c 518	77.5	6.9	1857	3	US-09-377-557-9	Sequence 9, Appli
c 446	78.5	7.0	1770	4	US-09-902-540-7164	Sequence 7164, Ap	c 519	77.5	6.9	1874	4	US-09-270-767-11069	Sequence 11069, A
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c 448	78.5	7.0	1870	3	US-09-071-709-6	Sequence 6, Appli	c 521	77.5	6.9	2325	2	US-08-393-540-3	Sequence 3, Appli
c 449	78.5	7.0	2055	4	US-09-248-796A-6094	Sequence 6094, Ap	c 522	77.5	6.9	2325	2	US-08-714-537-3	Sequence 3, Appli
c 450	78.5	7.0	2158	4	US-09-949-016-3018	Sequence 3018, Ap	c 523	77.5	6.9	3073	2	US-08-714-677-11	Sequence 11, Appl
c 451	78.5	7.0	2158	4	US-09-949-016-3026	Sequence 3026, Ap	c 524	77.5	6.9	3073	2	US-08-393-540-11	Sequence 11, Appl
c 452	78.5	7.0	2341	4	US-09-520-781-9	Sequence 9, Appli	c 525	77.5	6.9	3073	2	US-08-714-537-11	Sequence 11, Appl
c 453	78.5	7.0	2467	4	US-09-799-451-628	Sequence 628, App	c 526	77.5	6.9	8132	3	US-08-766-528-3	Sequence 3, Appli
c 454	78.5	7.0	2482	4	US-09-742-201-1	Sequence 1, Appli	c 527	77.5	6.9	8132	4	US-09-661-858-3	Sequence 3, Appli
c 455	78.5	7.0	2607	4	US-09-520-781-11	Sequence 11, Appl	c 528	77.5	6.9	9171	2	US-08-629-001A-2	Sequence 2, Appli
c 456	78.5	7.0	3352	4	US-10-101-464A-868	Sequence 868, App	c 529	77.5	6.9	9171	3	US-08-642-274D-2	Sequence 2, Appli
c 457	78.5	7.0	3424	3	US-09-336-643A-9	Sequence 9, Appli	c 530	77.5	6.9	9171	3	US-08-952-127-2	Sequence 2, Appli
c 458	78.5	7.0	3941	4	US-09-902-540-660	Sequence 660, App	c 531	77.5	6.9	9171	3	US-08-952-014C-2	Sequence 2, Appli
c 459	78.5	7.0	14555	4	US-09-902-540-1096	Sequence 1096, Ap	c 532	77.5	6.9	9196	4	US-08-984-090-1	Sequence 1, Appli
c 460	78.5	7.0	16011	4	US-09-600-319-3	Sequence 3, Appli	c 533	77.5	6.9	9385	2	US-08-874-266-1	Sequence 1, Appli
c 461	78.5	7.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli	c 534	77.5	6.9	9385	3	US-09-360-416-1	Sequence 1, Appli
c 462	78	6.9	510	4	US-09-252-991A-9469	Sequence 9469, Ap	c 535	77.5	6.9	9389	4	US-09-949-016-4409	Sequence 4409, Ap
c 463	78	6.9	786	4	US-09-248-796A-176	Sequence 176, App	c 536	77.5	6.9	9870	1	US-08-508-836A-9	Sequence 9, Appli
c 464	78	6.9	1245	4	US-09-489-039A-5399	Sequence 5399, Ap	c 537	77.5	6.9	11706	4	US-09-902-540-1038	Sequence 1038, Ap
c 465	78	6.9	1510	1	US-08-361-920-26	Sequence 26, Appl	c 538	77.5	6.9	13987	2	US-08-804-227C-13	Sequence 13, Appl
c 466	78	6.9	1510	1	US-08-479-939-26	Sequence 26, Appl	c 539	77.5	6.9	28804	2	US-08-592-874-1	Sequence 1, Appli
c 467	78	6.9	1510	1	US-08-483-432-26	Sequence 26, Appl	c 540	77.5	6.9	28804	3	US-09-096-942-2	Sequence 2, Appli
c 468	78	6.9	1596	1	US-08-531-601-2	Sequence 2, Appli	c 541	77.5	6.9	28804	3	US-09-096-867-2	Sequence 2, Appli
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c 470	78	6.9	1758	4	US-09-902-540-9019	Sequence 9019, Ap	c 543	77.5	6.9	43280	2	US-08-804-227C-1	Sequence 1, Appli
c 471	78	6.9	2007	3	US-09-052-089A-7	Sequence 7, Appli	c 544	77.5	6.9	110243	4	US-09-949-016-13698	Sequence 13698, A
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c 473	78	6.9	2016	4	US-09-949-016-5734	Sequence 5734, Ap	c 546	77.5	6.9	137956	4	US-09-949-016-17260	Sequence 17260, A
c 474	78	6.9	2065	2	US-08-968-751-1	Sequence 1, Appli	c 547	77.5	6.9	150394	4	US-09-949-016-13042	Sequence 13042, A
c 475	78	6.9	2071	4	US-09-949-016-1517	Sequence 1517, Ap	c 548	77	6.8	346	4	US-09-377-502-53	Sequence 53, Appl
c 476	78	6.9	2157	4	US-09-252-991A-15294	Sequence 15294, A	c 549	77	6.8	542	4	US-09-167-206-23	Sequence 23, Appl
c 477	78	6.9	2361	4	US-09-252-991A-15546	Sequence 15546, A	c 550	77	6.8	543	4	US-09-489-039A-5453	Sequence 5453, Ap
c 478	78	6.9	2454	4	US-09-614-221A-393	Sequence 393, App	c 551	77	6.8	939	4	US-09-252-991A-9154	Sequence 9154, Ap

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	559	77	6.8	1719	4	US-09-252-991A-12741	Sequence 12741, A
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C	564	77	6.8	2040	3	US-08-604-789B-12	Sequence 12, Appl
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C	566	77	6.8	2040	3	US-09-312-721A-12	Sequence 12, Appl
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C	568	77	6.8	2040	4	US-09-733-300-12	Sequence 12, Appl
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	570	77	6.8	2463	4	US-09-252-991A-8582	Sequence 8582, Ap
	571	77	6.8	2481	1	US-08-324-243-35	Sequence 35, Appl
	572	77	6.8	2481	1	US-08-532-390-35	Sequence 35, Appl
	573	77	6.8	2481	3	US-08-717-294-35	Sequence 35, Appl
	574	77	6.8	2481	5	PCT-US95-11511-35	Sequence 35, Appl
	575	77	6.8	2517	4	US-09-252-991A-9238	Sequence 9238, Ap
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	577	77	6.8	2571	4	US-09-936-572-4	Sequence 4, Appli
C	578	77	6.8	2607	4	US-09-252-991A-13249	Sequence 13249, A
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	580	77	6.8	2744	3	US-09-369-618-1	Sequence 1, Appli
	581	77	6.8	2744	3	US-09-369-617-1	Sequence 1, Appli
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	583	77	6.8	3464	4	US-09-949-016-1167	Sequence 1167, Ap
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	585	77	6.8	4108	3	US-08-981-729-8	Sequence 8, Appli
	586	77	6.8	4108	3	US-08-981-446B-1	Sequence 1, Appli
	587	77	6.8	4108	4	US-09-613-811-8	Sequence 1, Appli
	588	77	6.8	6359	4	US-09-475-252-1	Sequence 1, Appli
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c1342	72	6.4	1677	4	US-09-252-991A-9102	Sequence 9102, Ap	1415	72	6.4	2403	3	US-09-233-752A-7	Sequence 7, Appl
c1343	72	6.4	1723	1	US-07-841-646-28	Sequence 28, Appl	1416	72	6.4	2403	3	US-09-402-036-7	Sequence 7, Appl
c1344	72	6.4	1723	1	US-07-901-703-10	Sequence 10, Appl	1417	72	6.4	2403	3	US-09-904-226-7	Sequence 7, Appl
c1345	72	6.4	1723	1	US-08-147-023-28	Sequence 28, Appl	1418	72	6.4	2424	1	US-08-821-119-16	Sequence 16, Appl
c1346	72	6.4	1723	1	US-08-206-864-3	Sequence 3, Appl	1419	72	6.4	2460	4	US-09-902-540-4178	Sequence 4178, Ap
c1347	72	6.4	1723	1	US-08-278-729A-20	Sequence 20, Appl	1420	72	6.4	2610	3	US-09-545-814-1	Sequence 1, Appl
c1348	72	6.4	1723	1	US-08-480-528A-7	Sequence 7, Appl	c1421	72	6.4	2610	3	US-09-545-814-3	Sequence 3, Appl
c1349	72	6.4	1723	1	US-08-479-666-7	Sequence 7, Appl	1422	72	6.4	2619	3	US-08-337-797A-1	Sequence 1, Appl
c1350	72	6.4	1723	1	US-08-155-343A-20	Sequence 20, Appl	1423	72	6.4	2619	3	US-08-337-797A-3	Sequence 3, Appl
c1351	72	6.4	1723	1	US-08-406-672-20	Sequence 20, Appl	1424	72	6.4	2619	3	US-09-258-523-1	Sequence 1, Appl
c1352	72	6.4	1723	1	US-08-643-563A-20	Sequence 28, Appl	1425	72	6.4	2619	3	US-09-258-523-3	Sequence 3, Appl
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c1354	72	6.4	1723	1	US-08-643-763A-20	Sequence 20, Appl	1427	72	6.4	2668	3	US-09-031-606-11	Sequence 11, Appl
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cl1499	72	6.4	41927	4	US-09-902-540-1268	Sequence 1268, Ap
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ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:

RESULT 2

		; APPLICANT: Steve Daniel			
		; APPLICANT: James Gilmore			
		; APPLICANT: Susan G. Stuart			
		; APPLICANT: Laura Stuve			
		; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL			
		; FILE REFERENCE: PA-0003 US			
		; CURRENT APPLICATION NUMBER: US/09/232,160			
		; CURRENT FILING DATE: 1999-01-15			
		; NUMBER OF SEQ ID NOS: 23			
		; SOFTWARE: PERL Program			
		; SEQ ID NO 13			
		; LENGTH: 2029			
		; TYPE: DNA			
		; ORGANISM: Homo sapiens			
		; FEATURE: -			
		; OTHER INFORMATION: 3044710			
		US-09-232-160-13			
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		Score:	1125.00	Matches:	218
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		Best Local Similarity:	100.00%	Mismatches:	0
		Query Match:	100.00%	Indels:	0
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QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40		
Db	291	AGAATTATGGGATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAA	350		
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60		
Db	351	GCTAAGGAGGCTGTAGGCTGCTGGGACTTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA	410		
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80		
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US-09-949-016-1894
; Sequence 1894, Application US/09949016
; Patent No. 6812339

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1894
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1894

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
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; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
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; NUMBER OF SEQ ID NOS: 423

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; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 268 AGAATTATGGGATCACCTTGTGAGCAAAAAGCGCAACAGCAGCTGAATTCACAGAA 327
QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
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Db 688 ACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 747
QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 748 AAAAAATTGATTGTGTACAGAAAGTTTTTATGAAAAACTAGCACCATGTCTACAGAAACT 807
QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 808 GAACCAATTTGTTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA 861

RESULT 4

; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 9.55e-122 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 208 ACGAGGCTCCTGGTCCAAGGCTCTTTGGCGTGCAAGAGCTTTCCATCCAGGTGTCATGC 267
QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

Db 268 AGAATTATGGGATCACCCCTTGTTGAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAA 327
QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 328 GCTAAGGAGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACA 387
QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db 388 GCCTTGAAGCTAGCTTTGAAACTTGCACTATGGCTGGGTGGAGATGGATTCGTGGTC 447
QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db 448 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGG 507
QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACT 567
QY 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 568 AACTCGTGTATCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCA 627
QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 628 ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT 687
QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db 688 ACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 747
QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 748 AAAAAATTGATTGTGTACAGAAAGTTTATTGGAAACTAGCACCATGTCTACAGAAACT 807
QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 808 GAACCATTTGTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGGA 861

RESULT 5

; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.: 9.55e-122 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

QY 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 208 ACGAGGCTCCTGGTCCAAGGCTCTTGGCTGCAGAAGAGCTTCCATCCAGGTGTCATGC 267
QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 268 AGAATTATGGGATCACCCCTTGTGACAAAAAGCGAACCAGCAGCTGAATTCACAGAA 327
QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 328 GCTAAGGAGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACA 387
QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db 388 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC 447
QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db 448 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGG 507
QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACT 567


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RESULT 7
; Sequence 200, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
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; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:          9.55e-122          Length:          2372
Score:             1125.00           Matches:          218
Percent Similarity: 100.00%           Conservative:      0
Best Local Similarity: 100.00%         Mismatches:        0
Query Match:       100.00%           Indels:           0
DB:                4                  Gaps:            0

Qy      1  ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
      |||||
Db      208 ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCATCCAGGTGTGATGC 267

Qy      21  ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
      |||||
Db      268 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAACCGACAGCTGAATTTTCACAGAA 327

Qy      41  AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
      |||||
Db      328 GCTAAGGAGGCCTGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 387

Qy      61  AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
      |||||
Db      388 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTC 447

Qy      81  IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
      |||||
Db      448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGG 507

Qy      101 LysValProValSerArgGlnPheAlaAlaTyrCystYrAsnSerSerAspThrTrpThr 120
      |||||
Db      508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACT 567

Qy      121 AsnSerCysIleProGluIleIleThrThrLysAspProfilePheAsnThrGlnThrAla 140
      |||||
Db      568 AACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACACTGCA 627

Qy      141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
      |||||
Db      628 ACACAAACAACAGAAATTTATTGTGTCAGTGACAGTACCTACTCGTGGCATCCCTTTACTCT 687

Qy      161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
      |||||
Db      688 ACAATACCTGCCCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGGAGA 747

Qy      181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
      |||||
Db      748 AAAAAAATTGATTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACT 807

Qy      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
      |||||
Db      808 GAACCATTTGTTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGGA 861

RESULT 8
; Sequence 200, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```


; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 9.55e-122 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

Qy 1 ThrArgLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 208 ACGAGGCTCCTGGTCCAAAGGCTCTTTGGCGTCAGAAGAGCTTTCATCCAGGTGCATGC 267

Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 268 AGAATTATGGGATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTCACAGAA 327

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 328 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGCACAAGTTGAAACA 387

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db 388 GCCTTGAAAGTAGCTTTGAAACTTGACGTATGGCTGGGTTGGAGATGGATTCGTGGTC 447

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db 448 ATCTCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGG 507

Qy 101 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 508 AAGGTTCCAGTCAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 567

Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 568 AACTCGTGCATTCCAGAAAATTATCACCAAAAGATCCCATATTTCAACTCAAACACTGCA 627

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 628 ACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCT 687

Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db 688 ACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCACACTTCTATTCCACGGAGA 747

Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 748 AAAAAAATTGATTTGTGTCACAGAAAGTTTATTGAAACTAGCACCATGTCTACAGAAACT 807

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 808 GAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGA 861

RESULT 10

; Sequence 200, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.: 9.55e-122 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

QY 1 ThrArgLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db |||||
QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db |||||
QY 268 AGAATTATGGGGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCACAGAA 327
Db |||||
QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db |||||
QY 328 GCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGCCCGGCAAGGACCAAGTTGAAACA 387
QY 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db |||||
QY 388 GCCTTGAAAGCTAGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTGCGTGTC 447
QY 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db |||||
QY 448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCCTGATTGG 507
QY 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db |||||
QY 508 AAGGTTCCAGTGAGCCGACAGTTTGACGCTATTGTACAACTCATCTGATACTGGACT 567
QY 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db |||||
QY 568 AACTCGTGCAATCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 627
QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db |||||
QY 628 ACACAAACAAACAGAAATTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT 687
QY 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db |||||
QY 688 ACAATACCTGCCCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGA 747
QY 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db |||||
QY 748 AAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACT 807
QY 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db |||||
QY 808 GAACCATTTGTTGAAAAATAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGA 861
Db |||||

RESULT 11

; Sequence 200, Application US/09906618

; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:

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Pred. No.:          9.55e-122          Length:          2372
Score:             1125.00          Matches:           218
Percent Similarity: 100.00%          Conservative:      0
Best Local Similarity: 100.00%        Mismatches:       0
Query Match:       100.00%          Indels:           0
DB:                4                Gaps:           0

QY      1  ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
      |||
Db      208 ACAGGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCATGC 267

QY      21  ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
      |||
Db      268 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAA 327

QY      41  AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
      |||
Db      328 GCTAAGGAGGCCTGTAGGCTGTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACA 387

QY      61  AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
      |||
Db      388 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTC 447

QY      81  IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
      |||
Db      448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGG 507

QY      101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
      |||
Db      508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACT 567

QY      121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
      |||
Db      568 AACTCGTGCAATTCAGAAAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 627

QY      141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
      |||
Db      628 ACACAAACAACAGAAATTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCT 687

QY      161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
      |||
Db      688 ACAATACCTGCCCTTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 747

QY      181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
      |||
Db      748 AAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACT 807

QY      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
      |||
Db      808 GAACCATTTGTTGAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGA 861
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```
RESULT 12
US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
;   APPLICANT: NI, JIAN
;   APPLICANT: GENTZ, REINER L.
;   APPLICANT: DILLON, PATRICK J.
;   TITLE OF INVENTION: CD44-LIKE PROTEIN
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;   STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
;   CITY: WASHINGTON
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005-3934
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2313 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1056
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1056
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..153
US-08-892-880-1

Alignment Scores:
Pred. No.:          4.65e-121          Length:          2313
Score:             1119.00          Matches:           217
Percent Similarity: 99.54%          Conservative:      0
Best Local Similarity: 99.54%        Mismatches:       1
Query Match:       99.47%          Indels:           0
DB:                2                Gaps:           0

QY      1  ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
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Db      139 ACGAGGCTCCTGGTCCAAGGCTCTTTCGTGCAGAAGAGCTTTCATCCAGGTGTCATGC 198

QY      21  ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
      |||
Db      199 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAA 258

QY      41  AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
      |||
Db      259 GCTAAGGAGGCCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACA 318

QY      61  AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
      |||
Db      319 GCCTTGAAAGCTAGCTTTTGCAACTTGCAGCTATGGCTGGGTTGGCCATGGATTCGTGGTC 378

QY      81  IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
      |||
Db      379 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTTGG 438

QY      101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
      |||
Db      439 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTGGACT 498

QY      121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
      |||
Db      499 AACTCGTGCATTCAGAAAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCA 558

QY      141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
      |||
Db      559 ACACAAACAACAGAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCT 618
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RESULT 15
US-08-892-880-12
; Sequence 12, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-12

Search completed: October 9, 2005, 01:25:42
Job time : 189.526 secs

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Best Local Similarity:	68.69%	Mismatches:	11	
Query Match:	24.62%	Indels:	16	
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QY	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys	20	
Db	147	ACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAAGAGAGCTTCCATCCAGGTGTCATGC	206	
QY	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40	
Db	207	AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAA	266	
QY	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60	
Db	267	GCTAAGGAGGCCCTGTAGGTTGCTNGGACTAGTTGGCCGGCAAGGCCAGTTG---AAC	323	
QY	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGly-----	75	
Db	324	AGCTTGAAAGT-AGCTTTGAAAT-TGCAGTTGGCTTGGTTGGGATGGTTCGNGNCATTT	381	
QY	76	-----AspGlyPheValIleSerArgIleSerPro	86	
Db	382	AGGTTAGCCCAACCCANTTTGGAAANTGGTGGNNCNCNATTTGNAGTCCCTTAGCCCN	438	

Run on: October 8, 2005, 16:25:15 ; Search time 455.378 Seconds
(without alignments)
2833.919 Million cell updates/sec

Title: US-10-063-670-6_COPY_17_234
Perfect score: 1125
Sequence: 1 TRLLVQGLRAEELSIQVSC.....ETEPFVENKAAFKNEAAGFG 218
Scoring table: BLOSUM62
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	ADD04999	standard;	CDNA;	1680	BP.	
DE	Human secreted/transmembrane protein	CDNA,	#40.			
PN	US2003104469-A1.					
PD	05-JUN-2003.					
PA	(GETH) GENENTECH INC.					
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
RESULT 2						
ID	AAF93818	standard;	CDNA;	1755	BP.	
DE	Human cDNA encoding a membrane or secretory protein	clone	PSEC0135.			
PN	EP1067182-A2.					
PD	10-JAN-2001.					
PA	(HELI-) HELIX RES INST.					
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
RESULT 3						
ID	ADE71449	standard;	CDNA;	2027	BP.	
DE	Human cDNA encoding PDEBC #2.					
PN	US2003124543-A1.					
PD	03-JUL-2003.					
PA	(STUA/) STUART S G.					
PA	(STRE/) STREETER D G.					
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
RESULT 4						
ID	AAZ98172	standard;	CDNA;	2029	BP.	
DE	Human signal peptide containing protein	HSPP-64	CDNA	SEQ ID NO:198.		
PN	WO200000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
RESULT 5						
ID	ADE71445	standard;	CDNA;	2029	BP.	
DE	Human cDNA encoding PDEBC Incyte	3044710CB1.				
PN	US2003124543-A1.					
PD	03-JUL-2003.					
PA	(STUA/) STUART S G.					
PA	(STRE/) STREETER D G.					

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 6

ID ABA09223 standard; cDNA; 2324 BP.
DE Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 7

ID ADR41319 standard; cDNA; 2369 BP.
DE Human CD-like molecule HEMFC27 cDNA, SEQ ID NO:118.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 8

ID AAX52250 standard; DNA; 2372 BP.
DE Protein PRO263 cDNA clone DNA34431-1171.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 9

ID ADC78520 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 10

ID AAF72408 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 11

ID AAF92060 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 12

ID ABS74380 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 13

ID ABL88087 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA sequence SEQ ID NO:31.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 14

ID ABL95576 standard; cDNA; 2372 BP.
DE Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA60164 standard; cDNA; 2372 BP.
DE Human cDNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACD07564 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA91166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACD81543 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA60365 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22

ID ACA58812 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ACA91252 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACD20169 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ACH66246 standard; cDNA; 2372 BP.

DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ACD02300 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ACA89291 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 34
ID ACA68928 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 35
ID ACA54972 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 36
ID ACA98450 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 37
ID ACA63375 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 38
ID ACD19807 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 39
ID ADB29405 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 40
ID ADB17062 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.

PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 41
ID ACH03578 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 42
ID ADA18261 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 43
ID ACD66954 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 44
ID ADA19867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 45
ID ADB17250 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 46
ID ACD83115 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 47
ID ADA16236 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 48
ID ADA20039 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 49
ID ACD82092 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003060601-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 50
ID ADA42381 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 51
ID ACD23293 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 52
ID ADA00336 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 53
ID ADA16660 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 54
ID ADA13089 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 55
ID ADA41957 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 56
ID ADA17304 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 57
ID ADA42807 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 58
ID ACD23655 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064923-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 59
ID ADB85578 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 60
ID ADB77726 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 61
ID ADB74862 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 62
ID ADB68257 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 63
ID ADB68064 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 64
ID ADB90881 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ADC28508 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 66
ID ADC39708 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 67
ID ADC40222 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ADC19046 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ADC34346 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ADC29401 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ADC28932 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ADC40817 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ADC19474 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ADC06961 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ADC17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
RESULT 77
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 86
ID ADD36009 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ADE34833 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADG01010 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADG08563 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADF95184 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADH24037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ADH34063 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ADH29896 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ADH23867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95

ID ADG85271 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ADH24547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ADH37403 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ADH01992 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ADH37573 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ADG85611 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 101
ID ADH24207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 102
ID ADH38501 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 103
ID ADG83622 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 104
ID ADH29430 standard; cDNA; 2372 BP.

DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 105
ID ADH27546 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 106
ID ADH37743 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 107
ID ADH37920 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 108
ID ADH57340 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 109
ID ADH59316 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 110
ID ADH53482 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 111
ID ADH53652 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 112
ID ADH51988 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 113
ID ADH49843 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.

PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 114
ID ADI25353 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 115
ID ADH90146 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 116
ID ADI25523 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 117
ID ADH97697 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 118
ID ADI38095 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 119
ID ADI03545 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 120
ID ADI11902 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 121
ID ADH89976 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 122
ID ADH98377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181707-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ADI11052 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ADI11562 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 128
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADI05025 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADI03375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADI04770 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADH78224 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADI19568 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADH90316 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADI03035 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADH77884 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADH97867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADI01252 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADI01947 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

RESULT 159
ID ADK65375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADH98717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADH79958 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADJ26363 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADL931689 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADC52143 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE79278 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADE79702 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168

ID ADE41281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.


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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ADH06405 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ADG68826 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ADH27716 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ADH25057 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ADH33689 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ADG92296 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 183
ID ADH02332 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 184
ID ADH07939 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ADG69336 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ADH39157 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ADG92723 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ADG83897 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADG85441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADH06235 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADH30231 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADH24377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADG69506 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ADH07769 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ADG85781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ADH39327 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ADH33519 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ADH33859 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ADH01069 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 200
ID ADG69676 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 201
ID ADH02162 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ADG69166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 203
ID ADG85951 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
RESULT 204
ID ADH24887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 205
ID ADH39504 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADH02502 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ADG68996 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ADH07599 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ADG86121 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADH24717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADH25765 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADH38331 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 213
ID ADH20512 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADH57170 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADH43464 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADH07367 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADH52158 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADH59912 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADH49524 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADH06940 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADH90486 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADI11222 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADI18682 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADH98887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI02117 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADH90656 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI37665 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH97461 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADI65829 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.

DE Human secreted/transmembrane protein cDNA, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 248
ID ADR17996 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 249
ID ADT03672 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ADS74635 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane cDNA #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 251
ID ADQ25003 standard; DNA; 2667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID AAC59803 standard; DNA; 2967 BP.
DE Human secreted protein encoding DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 253
ID AAV22687 standard; DNA; 2313 BP.
DE DNA encoding a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.47% Indels: 0
RESULT 254
ID ABL90698 standard; cDNA; 2369 BP.
DE Human polynucleotide SEQ ID NO 1260.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.47% Indels: 0
RESULT 255
ID ADP65684 standard; DNA; 2313 BP.
DE Human extracellular link domain containing 1 (XLKD1) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 256
ID ADM67137 standard; DNA; 2313 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 273.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 257
ID ADN05865 standard; cDNA; 2313 BP.
DE Antipsoriatic cDNA sequence #1164.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 258
ID ADQ21088 standard; DNA; 2313 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 259
ID ACA10111 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.

Best Local Similarity: 88.53% Mismatches: 0
Query Match: 87.07% Indels: 25
RESULT 260
ID ADO08254 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Best Local Similarity: 88.53% Mismatches: 0
Query Match: 87.07% Indels: 25
RESULT 261
ID ABT09892 standard; cDNA; 596 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 26.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 97.88% Mismatches: 4
Query Match: 80.09% Indels: 3
RESULT 262
ID AAF94017 standard; DNA; 716 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 451.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 94.23% Mismatches: 6
Query Match: 64.09% Indels: 3
RESULT 263
ID ADM67136 standard; DNA; 1516 BP.
DE Murine adipocyte specific DNA SeqID 272.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 264
ID AAD10132 standard; cDNA; 1896 BP.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 265
ID ABL35066 standard; cDNA; 1896 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 595.

PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 266
ID ACH20895 standard; cDNA; 411 BP.
DE Human adult liver cDNA #507.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.33% Indels: 0
RESULT 267
ID AAX41156 standard; cDNA; 451 BP.
DE Human secreted protein 5' EST SEQ ID NO:100.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.33% Indels: 0
RESULT 268
ID AAI33382 standard; DNA; 457 BP.
DE Probe #2068 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 25.02% Indels: 7
RESULT 269
ID ABS01959 standard; DNA; 457 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1950.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 25.02% Indels: 7
RESULT 270
ID ADE71146 standard; cDNA; 559 BP.
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 54.17% Mismatches: 29
Query Match: 19.69% Indels: 7
RESULT 271
ID ABN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 32.08% Mismatches: 76
Query Match: 18.98% Indels: 7
RESULT 272
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 32.08% Mismatches: 76
Query Match: 18.98% Indels: 7
RESULT 273
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.

PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
Best Local Similarity: 32.08% Mismatches: 76
Query Match: 18.98% Indels: 7
RESULT 274
ID ABN86522 standard; cDNA; 1177 BP.
DE Nucleotide sequence of mouse CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 32.70% Mismatches: 75
Query Match: 18.62% Indels: 7
RESULT 275
ID ADQ38556 standard; DNA; 5452 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 219.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 29.29% Mismatches: 96
Query Match: 18.62% Indels: 17
RESULT 276
ID ABN86523 standard; cDNA; 1089 BP.
DE Nucleotide sequence of hamster CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 32.76% Mismatches: 82
Query Match: 18.40% Indels: 12
RESULT 277
ID AAQ06236 standard; DNA; 1537 BP.
DE B7 adhesion receptor cDNA clone.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Best Local Similarity: 27.34% Mismatches: 92
Query Match: 18.09% Indels: 67
RESULT 278
ID AAX41003 standard; cDNA; 363 BP.
DE Human secreted protein 5' EST SEQ ID NO: 215.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 88.68% Mismatches: 5
Query Match: 18.04% Indels: 1
RESULT 279
ID ADP65670 standard; DNA; 3091 BP.
DE Human mRNA for transmembrane glycoprotein (CD44 gene) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 280
ID ADP65097 standard; DNA; 3091 BP.
DE Human CD44 antigen (homing function and Indian blood group DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 281
ID ADQ38563 standard; DNA; 3091 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 226.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 282
ID ADR67138 standard; DNA; 3091 BP.
DE Human bladder cancer associated nucleotide sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.

PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 283
ID ADQ38562 standard; DNA; 5468 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 225.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 284
ID ADQ38555 standard; DNA; 5674 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 218.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 285
ID ADQ38558 standard; DNA; 5739 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 221.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 18.04% Indels: 60
RESULT 286
ID ACN39193 standard; cDNA; 3083 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325446, SEQ ID NO:3187.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 25.96% Mismatches: 84
Query Match: 17.96% Indels: 60
RESULT 287
ID AAS03192 standard; cDNA; 2307 BP.
DE Human epithelial antigen CD44 cDNA sequence.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 288
ID AAQ21186 standard; DNA; 2308 BP.
DE Clone CD44 coding for epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 289
ID AAT14725 standard; cDNA; 2308 BP.
DE Human epithelial CD44 cDNA.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 290
ID AAV63462 standard; cDNA; 2308 BP.
DE Human CD44 antigen cDNA.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 291

ID AAV81219 standard; cDNA; 2308 BP.
DE Human CD44 antigen cDNA.
PN US5849898-A.
PD 15-DEC-1998.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 292
ID AAA50598 standard; cDNA; 2308 BP.
DE Human epithelial CD44 cDNA.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 293
ID ADO49374 standard; cDNA; 2308 BP.
DE Human CD44 cDNA #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.73% Indels: 75
RESULT 294
ID ABN86520 standard; cDNA; 1737 BP.
DE Nucleotide sequence of human CD44R cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 295
ID ADK61304 standard; DNA; 1737 BP.
DE Ovarian cancer-related DNA #459 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 296
ID ABX77520 standard; cDNA; 4674 BP.
DE Differentially expressed breast cancer associated cDNA #15.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 297
ID ADJ56375 standard; cDNA; 4674 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 181.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 298
ID ADM86790 standard; cDNA; 4674 BP.
DE Human cDNA #51 differentially expressed in lung cancer.
PN US2003175704-A1.
PD 18-SEP-2003.

PA (LASE/) LASEK A K W.
PA (SHYJ/) SHYJAN A W.
PA (TURN/) TURNER C M.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 299
ID ADI61729 standard; cDNA; 4675 BP.
DE Human cDNA upregulated in Alzheimer's disease, INCYTE 234630.26.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 17.64% Indels: 75
RESULT 300
ID ADQ38553 standard; DNA; 5053 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 216.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.56% Indels: 49
RESULT 301
ID AAQ21185 standard; DNA; 1354 BP.
DE Clone CD44.5 coding for haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 302
ID AAT14724 standard; cDNA; 1354 BP.
DE Human haematopoietic CD44 cDNA clone CD44.5.
PN US5506126-A.
PD 09-APR-1996.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 303
ID AAV63461 standard; cDNA; 1354 BP.
DE Human CD44 antigen cDNA.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 304
ID AAV81218 standard; cDNA; 1354 BP.
DE Human CD44 antigen cDNA.
PN US5849898-A.
PD 15-DEC-1998.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 305
ID AAA50597 standard; cDNA; 1354 BP.
DE Human haematopoietic CD44.5 cDNA.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 306
ID AAS03191 standard; cDNA; 1354 BP.
DE Human haematopoietic antigen CD44 cDNA sequence.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 307
ID ADO49372 standard; cDNA; 1354 BP.
DE Human CD44 cDNA #1.
PN US2004072283-A1.

PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 308
ID AAA91129 standard; DNA; 1468 BP.
DE CD44HextraFASTm/cyto coding sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 309
ID AAA91130 standard; DNA; 1483 BP.
DE CD44Hextra/tmFAScyto coding sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 310
ID AAA52811 standard; cDNA; 1794 BP.
DE Human CD44 CDNA.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 311
ID ABV94385 standard; cDNA; 1794 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:376.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 312
ID ABK84043 standard; cDNA; 1794 BP.
DE Human CDNA differentially expressed in granulocytic cells #614.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 313
ID ADH18929 standard; cDNA; 1874 BP.
DE Human cell adhesion and extracellular matrix CADECM-25 cDNA - SEQ 56.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 92
Query Match: 17.51% Indels: 43
RESULT 314
ID ADQ38557 standard; DNA; 4335 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 220.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 315
ID ADQ38561 standard; DNA; 4633 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 224.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 316
ID ADQ38554 standard; DNA; 4723 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 217.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 317
ID ADQ38560 standard; DNA; 4874 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 223.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.51% Indels: 14
RESULT 318
ID ABZ70446 standard; cDNA; 1824 BP.
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 319
ID ADD90595 standard; cDNA; 2097 BP.
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:5.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 320
ID AAA91011 standard; DNA; 2100 BP.
DE Human CD44 splice variant (RA-CD44) coding sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 321
ID ADD90593 standard; cDNA; 2100 BP.
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:3.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 322
ID ACN42246 standard; cDNA; 2342 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1121.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 323
ID ABX76192 standard; DNA; 2387 BP.
DE lung cancer-associated polynucleotide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 324
ID ADL61117 standard; DNA; 2387 BP.
DE Human protein tyrosine kinase biomarker CD44 antigen DNA.

PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 325
ID ABX63495 standard; cDNA; 2905 BP.
DE Human cDNA #495 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 326
ID ADA10891 standard; cDNA; 3474 BP.
DE Human cDNA differentially expressed in colon cancer #7.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Best Local Similarity: 25.42% Mismatches: 93
Query Match: 17.47% Indels: 49
RESULT 327
ID ADD90591 standard; cDNA; 1083 BP.
DE Human CD44std glycoprotein encoding cDNA SEQ ID NO:1.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 328
ID ADI60527 standard; DNA; 1190 BP.
DE Secreted polypeptide encoding gene #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 329
ID AAD48131 standard; DNA; 1807 BP.
DE Human CD44 antigen encoding DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 330
ID ADJ56374 standard; cDNA; 1981 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 180.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 331
ID ABZ35325 standard; cDNA; 1992 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 436.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 332
ID ADE25668 standard; cDNA; 4365 BP.
DE Human cDNA differentially expressed in foam cells #72.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.86% Mismatches: 84

Query Match: 17.42% Indels: 14
RESULT 333
ID ADP10572 standard; DNA; 4633 BP.
DE Reference mRNA sequences for marker probe #249.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 334
ID ADL61887 standard; DNA; 5165 BP.
DE Human ovarian cancer DNA marker #20099.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.42% Indels: 14
RESULT 335
ID AAX51631 standard; cDNA; 373 BP.
DE Human secreted protein 5' EST SEQ ID NO:210.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 17.33% Indels: 0
RESULT 336
ID ABN86521 standard; cDNA; 1297 BP.
DE Nucleotide sequence of human CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.24% Indels: 14
RESULT 337
ID ADI31550 standard; cDNA; 1297 BP.
DE Human cDNA #876.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 17.24% Indels: 14
RESULT 338
ID ACC43051 standard; DNA; 339 BP.
DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.28% Mismatches: 53
Query Match: 17.02% Indels: 1
RESULT 339
ID ACC43049 standard; DNA; 336 BP.
DE Nucleotide sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 16.89% Indels: 2
RESULT 340
ID ACC43052 standard; DNA; 336 BP.
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 16.71% Indels: 2
RESULT 341
ID ACC43053 standard; DNA; 336 BP.

ID Nucleotide sequence of a CD44-hyaluronic acid binding domain.
DE WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 16.53% Indels: 2
RESULT 342
ID ACC43054 standard; DNA; 336 BP.
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 16.36% Indels: 2
RESULT 343
ID ACC43050 standard; DNA; 336 BP.
DE Nucleotide sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 34.23% Mismatches: 51
Query Match: 16.18% Indels: 2
RESULT 344
ID AAS81254 standard; cDNA; 2764 BP.
DE DNA encoding novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.89% Mismatches: 87
Query Match: 15.60% Indels: 49
RESULT 345
ID AAS81258 standard; cDNA; 2273 BP.
DE DNA encoding novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.21% Mismatches: 93
Query Match: 15.16% Indels: 51
RESULT 346
ID AAI46523 standard; DNA; 106 BP.
DE Probe #15209 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.11% Indels: 0
RESULT 347
ID ABS14478 standard; DNA; 106 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14469.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.11% Indels: 0
RESULT 348
ID ACH49200 standard; cDNA; 399 BP.
DE Human leukocyte cDNA #794.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 37.36% Mismatches: 41
Query Match: 14.80% Indels: 1
RESULT 349

ID ABZ34973 standard; cDNA; 549 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 85.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 14.04% Indels: 8
RESULT 350
ID ABZ91738 standard; DNA; 549 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 14.04% Indels: 8
RESULT 351
ID ADK61306 standard; DNA; 549 BP.
DE Ovarian cancer-related DNA #461 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 14.04% Indels: 8
RESULT 352
ID ABD27968 standard; DNA; 549 BP.
DE AA282906 DNA fragment.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 14.04% Indels: 8
RESULT 353
ID ADB62456 standard; cDNA; 2863 BP.
DE Human cDNA encoding clone FEBRA20038970.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.56% Mismatches: 85
Query Match: 13.33% Indels: 56
RESULT 354
ID ACH48521 standard; cDNA; 425 BP.
DE Human leukocyte cDNA #115.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 36.59% Mismatches: 36
Query Match: 13.20% Indels: 1
RESULT 355
ID ABX74436 standard; cDNA; 781 BP.
DE Human cDNA sequence #8 up-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 356
ID ADL13961 standard; DNA; 834 BP.
DE Osteoarthritis-associated polymorphic nucleotide #493.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 357
ID ABX63446 standard; cDNA; 1144 BP.
DE Human cDNA #446 differentially expressed in activated vascular tissue.
PN US2002137081-A1.

PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 358
ID ADE25720 standard; cDNA; 1144 BP.
DE Human cDNA differentially expressed in foam cells #124.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 359
ID ADL13963 standard; DNA; 1414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #495.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 360
ID ABX76382 standard; DNA; 1422 BP.
DE Lung cancer-associated polynucleotide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 361
ID ACC72678 standard; cDNA; 1422 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:17.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 362
ID ADN38973 standard; cDNA; 1422 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:291.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 363
ID ADN39702 standard; cDNA; 1430 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C74.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 364
ID ADQ21505 standard; DNA; 1440 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4325.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 365
ID ADQ25341 standard; DNA; 1461 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8161.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 366
ID ABX63445 standard; cDNA; 1728 BP.
DE Human cDNA #445 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.

PA (BAND/) BANDMAN O.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 367
ID ADK67833 standard; cDNA; 7840 BP.
DE Human BRCC300 gene coding sequence.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 12.93% Indels: 13
RESULT 368
ID ABV95472 standard; cDNA; 351 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 880.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 369
ID ADM80849 standard; cDNA; 813 BP.
DE Human CADECM-36 encoding cDNA SEQ ID NO:78.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 370
ID AAQ27190 standard; cDNA; 1414 BP.
DE Tumour necrosis factor-induced glycoprotein TSG-6 gene.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 371
ID AAV71778 standard; cDNA; 1414 BP.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein encoding cDNA.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 372
ID AAD06019 standard; cDNA; 1414 BP.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) cDNA.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 373
ID ABS54635 standard; cDNA; 1414 BP.
DE Human cDNA encoding tumour necrosis factor stimulated gene 6, TSG-6.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.89% Indels: 2
RESULT 374
ID ADS85080 standard; DNA; 1605 BP.
DE Mouse atopic dermatitis-related gene sequence SeqID82.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 12.80% Indels: 2
RESULT 375
ID ACH30555 standard; cDNA; 396 BP.
DE Human testis cDNA #941.
PN US2003073623-A1.
PD 17-APR-2003.

PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 31.58% Mismatches: 58
Query Match: 12.76% Indels: 13
RESULT 376
ID AAH23114 standard; DNA; 1411 BP.
DE Osteoarthritis tissue-derived nucleic acid sequence #44.
PN WO200153531-A2.
PD 26-JUL-2001.
PA (PHAA) PHARMACIA CORP.
Best Local Similarity: 31.62% Mismatches: 62
Query Match: 12.31% Indels: 13
RESULT 377
ID AAF29464 standard; cDNA; 3153 BP.
DE Murine brevidin cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 12.04% Indels: 30
RESULT 378
ID ACD66770 standard; cDNA; 3153 BP.
DE Secreted polypeptide-related cDNA #76.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 12.04% Indels: 30
RESULT 379
ID ADB90788 standard; cDNA; 3153 BP.
DE Mouse cDNA encoding brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 12.04% Indels: 30
RESULT 380
ID ADF71523 standard; cDNA; 3153 BP.
DE Murine brevidin protein cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 12.04% Indels: 30
RESULT 381
ID ADQ10339 standard; cDNA; 3153 BP.
DE Human polynucleotide #61.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 12.04% Indels: 30
RESULT 382
ID AAD48132 standard; DNA; 3366 BP.
DE Rat CD44i DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 28.02% Mismatches: 62
Query Match: 11.91% Indels: 47

RESULT 383
ID ABS70406 standard; cDNA; 1734 BP.
DE Human bone remodelling gene #63.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.00% Mismatches: 61
Query Match: 11.87% Indels: 14
RESULT 384
ID ACN42826 standard; cDNA; 7678 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 11.78% Indels: 59
RESULT 385
ID ACN42825 standard; cDNA; 7975 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 11.78% Indels: 59
RESULT 386
ID ABZ81727 standard; cDNA; 2652 BP.
DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 11.69% Indels: 39
RESULT 387
ID ADK67780 standard; DNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 11.69% Indels: 39
RESULT 388
ID ABA04648 standard; cDNA; 4706 BP.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 24.75% Mismatches: 91
Query Match: 11.69% Indels: 32
RESULT 389
ID ABX13821 standard; cDNA; 4706 BP.
DE cDNA encoding rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 24.75% Mismatches: 91
Query Match: 11.69% Indels: 32
RESULT 390
ID ADL13490 standard; DNA; 6951 BP.
DE Osteoarthritis-associated polymorphic nucleotide #22.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 391
ID ADL13489 standard; DNA; 7137 BP.
DE Osteoarthritis-associated polymorphic nucleotide #21.
PN WO2003054166-A2.

PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 55
Best Local Similarity: 27.43% Indels: 59
Query Match: 11.60%
RESULT 392
ID ADP65694 standard; DNA; 7137 BP.
DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 393
ID ADP65777 standard; DNA; 7137 BP.
DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 394
ID ACH15082 standard; cDNA; 488 BP.
DE Human adult brain cDNA #2294.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 395
ID ADP07636 standard; DNA; 859 BP.
DE Human secreted protein encoding DNA, seq id 119.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 396
ID AAI58121 standard; cDNA; 1365 BP.
DE Human polynucleotide SEQ ID NO 324.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 397
ID ADL91792 standard; cDNA; 1844 BP.
DE Human PRO271 encoding cDNA SEQ ID NO:13.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 398
ID ADQ23710 standard; DNA; 1925 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6530.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 399
ID AAX52252 standard; DNA; 1984 BP.
DE Protein PRO271 cDNA clone DNA39423-1182.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 400

ID ADC78532 standard; cDNA; 1984 BP.
DE Human PRO271 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 401
ID ADR18008 standard; cDNA; 1984 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 402
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 403
ID AAS45938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 404
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 405
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 406
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036146-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 407
ID ACA05713 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 408
ID ACA66547 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 409
ID ACD07574 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 410
ID ACF20122 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040063-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 411
ID ACF19508 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040064-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 412
ID ACD21796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 413
ID ACF12961 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036160-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 414
ID ACD25064 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 415
ID ACF00113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 416
ID ACA72170 standard; cDNA; 1985 BP.

DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 417
ID ACD04694 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 418
ID ACD18155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 419
ID ACD08162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 420
ID ABX71622 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 421
ID ACA88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 422
ID ACA70038 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 423
ID ACD12260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 424
ID ACC74175 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 425
ID ACD15803 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 426
ID ACD25371 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 427
ID ACD17848 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 428
ID ACC88135 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 429
ID ACD21489 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 430
ID ACD18556 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 431
ID ACH06954 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane polypeptide PRO271 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 432
ID ABX98166 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN US2003036156-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 433
ID ACD13917 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 434
ID ACD09697 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 435
ID ACC88442 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027266-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 436
ID ACD21182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054483-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 437
ID ABX75554 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 438
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 439
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 440
ID ACAS7696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 441
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 442
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 443
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036132-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 444
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 445
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 446
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032137-A1.
PD 13-FEB-2003.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 447
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027269-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 448
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027268-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 449
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027274-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 450
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 451
ID ACA72477 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 452
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 453
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 454
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 455
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 456
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 457
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 458
ID ACC86105 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027263-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 459
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027271-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 460
ID ACD12585 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 461
ID ACF19815 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040068-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 462
ID ABX76759 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 463
ID ABX96191 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 464
ID ACA73091 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 465
ID ACA05512 standard; cDNA; 1985 BP.
DE cDNA encoding human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 466
ID ACA68634 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 467
ID ACA74478 standard; cDNA; 1985 BP.
DE CDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 468
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 469
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 470
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 471
ID ACA68203 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 472
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 473
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 474
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 475
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 476
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 477

ID ACF12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 478
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 479
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 480
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 481
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 482
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 483
ID ACD10618 standard; cDNA; 1985 BP.
DE CDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 484
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 485
ID ACD02649 standard; cDNA; 1985 BP.
DE CDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 486
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 487
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003027262-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 488
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 489
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 490
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 491
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 492
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 493
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 494
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 495
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 496
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 497
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 498
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 499
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 500
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 501
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 502
ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 503
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 504
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 505
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 506
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 507
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 508
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 509
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 510
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 511
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 512
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 513
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 514
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 515
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 516
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 517
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 518
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 519
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 520
ID ACD4632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 521
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 522
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 523
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 524
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 525
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 526
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 527
ID ACF48763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 528
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 529
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 530
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040075-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 531
ID ACF41110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 532
ID ACF15724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044930-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 533
ID ACF16031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 534
ID ACD31858 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 535
ID ACF18666 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 536
ID ACF09113 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 537
ID ACF78234 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 538
ID ACF51833 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064440-A1.
PD 03-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 539
ID ACF26320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 540
ID ACF24113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 541
ID ACF63424 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 542
ID ACF50298 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 543
ID ACH07769 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 544
ID ACF13575 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 545
ID ACD41501 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003065159-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 546
ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 547
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 548
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 549
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 550
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 551
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 552
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 553
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 554
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 555
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 556
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 557
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 558
ID ACF76699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 559
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 560
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 561
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 562
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 563
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
RESULT 564
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.

RESULT 583
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 584
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 585
ID ACH12188 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 586
ID ACD40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 587
ID ACF18052 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 588
ID ACF08499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 589
ID ACF31300 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 590
ID ACF52140 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 591
ID ACD50009 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 592
ID ACF38712 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 593
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 594
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 595
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 596
ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 597
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 598
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 599
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 600
ID ACH12495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 601
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 602
ID ACD03773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040055-A1.
PD 27-FEB-2003. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 11.33%
RESULT 603
ID ACD10311 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036164-A1.
PD 20-FEB-2003. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 11.33%
RESULT 604
ID ACD11953 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040074-A1.
PD 27-FEB-2003. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 11.33%
RESULT 605
ID ACD83125 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003044793-A1.
PD 06-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 606
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 607
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 608
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 609
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 610
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PD 13-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 611
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PD 17-APR-2003. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 11.33%
RESULT 612
ID ACF33793 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PD 03-APR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 613
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PD 10-APR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 614
ID ACD90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PD 13-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 615
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PD 13-MAR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 616
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003067478-A1.
PD 10-APR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 617
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068773-A1.
PD 10-APR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 618
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PD 17-APR-2003. Mismatches: 39
PA (GETH) GENENTECH INC. Indels: 4
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 619
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PD 08-MAY-2003. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 11.33%
RESULT 620
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003096353-A1.
PD 22-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 621
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 622
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 623
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 624
ID ACF07885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 625
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 626
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 627
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 628
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 629
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 630
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 631
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 632
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 633
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 634
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 635
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 636
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 637
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 638
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD. 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 639
ID ACD30630 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 640
ID ACD311551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 641
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 642
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 643
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 644
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 645
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 646
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 647
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 648
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 649
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 650
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 651
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 652
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 653
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 654
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 655
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 656
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 657
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 658
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.

PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 659
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 660
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 661
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 662
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 663
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 664
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 665
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 666
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 667
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 668
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 669
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 670
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 671
ID ACD90080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 672
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 673
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 674
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 675
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 676
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 677
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 678
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 679
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 680
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 681
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 682
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 683
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 684
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 685
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 686
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064449-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 687
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064441-A1.
PD 03-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 688
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 689
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 690
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 691
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073174-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 692
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 693
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 694
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104541-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 695
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 696
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 697
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 698
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 699
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032133-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 700
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032136-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 701
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036129-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 702
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 703
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040057-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 704
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 705
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044932-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 706
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027270-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 707
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 708
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 709
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 710
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 711
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 712
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049738-A1.
PD 13-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 713
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 714
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 715
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 716
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 717
ID ACF51219 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 718
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 719
ID ACF25706 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 720
ID ACF39019 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 721
ID ACF28776 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 722
ID ACD90693 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 723
ID ACD86396 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 724
ID ACH05258 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049754-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 725
ID ACF65054 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 726
ID ADB20139 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 727
ID ACF43527 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 728
ID ACH08997 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 729
ID ACH09304 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 730
ID ADA78391 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 731
ID ACF09727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 732
ID ACF50912 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 733
ID ACF23806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 734
ID ACD88238 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 735
ID ACH09611 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 736
ID ACH10532 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 737
ID ACD11339 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 738
ID ACC96389 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044924-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 739
ID ACC98419 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044927-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 740
ID ADA16672 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 741
ID ACF41724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040072-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 742
ID ACF16645 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040073-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 743
ID ADA13101 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049622-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 744
ID ACD32165 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 745
ID ACD30323 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 746
ID ACD41194 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 747
ID ACF07578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 748
ID ACF30993 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 749
ID ACF77313 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 750
ID ACF10955 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073170-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 751
ID ACF32835 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 752
ID ACF26013 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 753
ID ACD83326 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 754
ID ACF23499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 755
ID ACF42913 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 756
ID ACF43220 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 757
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 758
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 759
ID ADA41969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 760
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 761
ID ACF10648 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 762
ID ACC93463 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036120-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 763
ID ACC96082 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 764
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 765
ID ADA17316 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 766
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 767
ID ACF21964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 768
ID ACF22578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 769
ID ACF08806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 770
ID ACF33142 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 771
ID ACF54596 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064443-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 772
ID ACF48456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 773
ID ACD47246 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 774
ID ACD49088 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 775
ID ACF37791 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 776
ID ACF30004 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 777
ID ACD87317 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 778
ID ACF61906 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104538-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 779
ID ACH10839 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 780
ID ADA42819 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Mismatches: 39

Query Match: 11.33%
Indels: 4
RESULT 781
ID ACD10004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 782
ID ACD16729 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 783
ID ACC99026 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040067-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 784
ID ACF00420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054456-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 785
ID ACD40887 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 786
ID ACF14496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 787
ID ACF22271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 788
ID ACF78848 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 789
ID ACF11569 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 790
ID ACF51526 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064442-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 791
ID ACF33449 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 792
ID ACD49702 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 793
ID ACF37484 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068683-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 794
ID ACF28469 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 795
ID ACD88545 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068681-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 796
ID ACF75164 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 797
ID ACF60985 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 798
ID ACF44141 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 799
ID ACH08383 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 800
ID ACC93770 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036122-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 801
ID ACD20875 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 802
ID ACF06657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040065-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 803
ID ACD20568 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 804
ID ACD22717 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 805
ID ACF41417 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044928-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 806
ID ACF06964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 807
ID ACD23665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 808
ID ACF77620 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 809
ID ACD46018 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064459-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 810
ID ACF46921 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 811
ID ACF54289 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 812
ID ACF45693 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 813
ID ACF45386 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 814
ID ACF38405 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 815
ID ACD89466 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 816
ID ACD85168 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 817
ID ACD85782 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 818
ID ACF75778 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 819
ID ACF60678 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 820
ID ACH05565 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 821
ID ADA82462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 822
ID ACF55824 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068680-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 823
ID ACF55210 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 824
ID ADB77738 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 825
ID ADB74874 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 826
ID ADB85770 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 827
ID ACF56131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4

RESULT 828
ID ACF56438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 829
ID ACF55517 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 830
ID ACF54903 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 831
ID ADC28520 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 832
ID ADC39720 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 833
ID ADC40234 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 834
ID ADC19058 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 835
ID ADC34358 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 836
ID ADC29413 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 837
ID ADD03593 standard; cDNA; 1985 BP.

ID ADC28944 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 838
ID ADC40829 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 839
ID ADC19486 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 840
ID ADC33934 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 841
ID ADC13004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 842
ID ADC12456 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 843
ID ADD05500 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 844
ID ADD05011 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 845
ID ADD04017 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 846
ID ADD03593 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein cDNA, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 847
ID ADE34845 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 848
ID ADG02495 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 849
ID ADG01202 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 850
ID ADF95377 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 851
ID ADG12192 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 852
ID ADH08852 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 853
ID ADH59328 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 854
ID ADI38107 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 855
ID ABX78541 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027272-A1.

PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 856
ID ACA59070 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 857
ID ACA75513 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 858
ID ACA70993 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 859
ID ACC87521 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 860
ID ACC86907 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 861
ID ACD04080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040070-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 862
ID ACA69411 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 863
ID ACA90256 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 864
ID ACA58467 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 865
ID ACC89363 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027264-A1.
PD 06-FEB-2003.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 866
ID ACA98154 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 867
ID ACA93796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 868
ID ACD15189 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 869
ID ACD08776 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 870
ID ACC96696 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040056-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 871
ID ACF15417 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044926-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 872
ID ACA72784 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 873
ID ACD02956 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 874
ID ACD01771 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 875
ID ACA91963 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 876
ID ADJ26375 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 877
ID ADL32633 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US200307396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 878
ID ADM30167 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 879
ID ADE79290 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 880
ID ADE79714 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 881
ID ADE73390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 882
ID ADE74164 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 883
ID ADE73925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 884
ID ADE74776 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 885
ID ADE99479 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.

PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 886
ID ADE98598 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 887
ID ADE99025 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 888
ID ADG40495 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 889
ID ADF73889 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 890
ID ADF95989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 891
ID ADF73465 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 892
ID ADG04260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 893
ID ADG00420 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 894
ID ADG82676 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 895
ID ADG92308 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 896
ID ADG92735 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 897
ID ADH25957 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 898
ID ADH32926 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 899
ID ADH20524 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 900
ID ADH07379 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 901
ID ADH59924 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 902
ID ADH06952 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein cDNA, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 903
ID ADI18694 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 904
ID ADI65414 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 905
ID ADI37677 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 906
ID ADH97473 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 907
ID ADI65841 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 908
ID ADH60584 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 909
ID ADJ99641 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 910
ID ADL08834 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 911
ID ADJ54665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 912
ID ADM25175 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 913
ID ADM29925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 914
ID ADJ64436 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 915
ID ADM31332 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 916
ID ADM36379 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 917
ID ADM40184 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 918
ID ADO06247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #40.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4

RESULT 919
ID ADN37792 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 920
ID ADR11099 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 921
ID ADT03684 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 922
ID ADS74647 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane cDNA #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 923
ID AAF29460 standard; cDNA; 2013 BP.
DE Human TANGO 332 cDNA open reading frame.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 924
ID ACD66767 standard; cDNA; 2013 BP.
DE Secreted polypeptide-related cDNA #51.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MYER/) MYERS P S.

PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 925
ID ADB90775 standard; cDNA; 2013 BP.
DE Human TANGO 332 open reading frame.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 926
ID ADF71510 standard; cDNA; 2013 BP.
DE Human TANGO 332 CDS.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 927
ID ADQ10328 standard; cDNA; 2013 BP.
DE Human polynucleotide #58.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 928
ID ABZ81728 standard; cDNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYYA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Best Local Similarity: 23.00% Mismatches: 91
Query Match: 11.33% Indels: 33
RESULT 929
ID ADK67781 standard; DNA; 2652 BP.
DE Rat glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Best Local Similarity: 23.00% Mismatches: 91
Query Match: 11.33% Indels: 33
RESULT 930
ID AAF29459 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 931
ID ACD66766 standard; cDNA; 2730 BP.
DE Secreted polypeptide-related cDNA #50.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.

PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 932
ID ADB90774 standard; cDNA; 2730 BP.
DE Human cDNA encoding TANGO 332.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 933
ID ADF71509 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 934
ID ADQ10327 standard; cDNA; 2730 BP.
DE Human polynucleotide #57.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 935
ID AAD48133 standard; DNA; 2878 BP.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 936
ID ADN38941 standard; cDNA; 2878 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 937
ID ADK67783 standard; DNA; 2878 BP.
DE Human glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 938
ID ADB59097 standard; DNA; 3077 BP.
DE Toxicity-related gene, SEQ ID 4123.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.00% Mismatches: 91
Query Match: 11.33% Indels: 33
RESULT 939
ID ADP72861 standard; DNA; 3077 BP.
DE Renal toxin progression gene marker #1450.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.00% Mismatches: 91
Query Match: 11.33% Indels: 33
RESULT 940
ID ACN37482 standard; cDNA; 3275 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 941
ID ADH18923 standard; cDNA; 3293 BP.
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 942
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMCAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 943
ID ADQ83194 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 944
ID ADQ85107 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 945
ID AAA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 946
ID ABK69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 947
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 948
ID ADA43748 standard; cDNA; 3476 BP.
DE Human CDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 949
ID ADA43516 standard; cDNA; 3476 BP.
DE Human CDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 950
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 951
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 952
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 953
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 954
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 955
ID ADB99675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 956
ID ADB86958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 957
ID ADB66113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 958
ID ADB99791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 959
ID ADB99446 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 960
ID ADB65997 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 961
ID ADC23395 standard; cDNA; 3476 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 962
ID ADC26088 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 963
ID ADE04915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 964
ID ADE11221 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 965
ID ADD95447 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 966
ID ADD88152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 967
ID ADE06377 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073195-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 968
ID ADE38152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 969
ID ADD88268 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 970
ID ADD90849 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 971
ID ADF99404 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 972
ID ADG06497 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 973
ID ADG05448 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 974
ID ADG82449 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 975
ID ADE51702 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 976
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 977
ID ADE37676 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 978
ID ADE37560 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 979
ID ADD95331 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 980
ID ADE38031 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 981
ID ADE76120 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 982
ID ADE39443 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 983
ID ADE04247 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 984
ID ADE39844 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 985
ID ADE19709 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 986
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match: 11.33% Indels: 53
RESULT 986
ID ADE77287 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 987
ID ADE65395 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 988
ID ADE76004 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 989
ID ADE37915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 990
ID ADE64525 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 991
ID ADE38860 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 992
ID ADE51934 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 993
ID ADD90965 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 994
ID ADE38744 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53

RESULT 995
ID ADE37444 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 996
ID ADE06261 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 997
ID ADD90120 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 998
ID ADE38628 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 999
ID ADE39559 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1000
ID ADD89164 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1001
ID ADD88931 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1002
ID ADE19825 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1003
ID ADE77403 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1004

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ID ADE65279 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1005
ID ADE39327 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1006
ID ADE38512 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1007
ID ADG11065 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1008
ID ADG10949 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1009
ID ADH31477 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1010
ID ADH38725 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1011
ID ADH29360 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1012
ID ADH23663 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1013
ID ADH26993 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1014
ID ADH38261 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1015
ID ADH26877 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1016
ID ADH38145 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1017
ID ADH38841 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1018
ID ADH23779 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1019
ID ADH40155 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1020
ID ADH40039 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1021
ID ADH31361 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65%
Query Match: 11.33%
Mismatches: 76
Indels: 53
RESULT 1022
ID ADH29239 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
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PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1023
ID ADH49454 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1024
ID ADH51918 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1025
ID ADH49773 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1026
ID ADH52374 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1027
ID ADH52490 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1028
ID ADH58487 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1029
ID ADH51802 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1030
ID ADH58363 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1031
ID ADI13560 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119131-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1032
ID ADK00816 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1033
ID ADL08557 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1034
ID ACN42086 standard; cDNA; 4353 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1035
ID ACN42083 standard; cDNA; 4545 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1036
ID ACN42082 standard; cDNA; 4659 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1037
ID ABK62593 standard; cDNA; 2465 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #500.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 27.14% Mismatches: 69
Query Match: 11.29% Indels: 11
RESULT 1038
ID ADQ45337 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 7000.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.20% Indels: 2
RESULT 1039
ID ADB63670 standard; cDNA; 2160 BP.
DE Human cDNA encoding clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 24.64% Mismatches: 92
Query Match: 11.16% Indels: 40
RESULT 1040
ID ACF04000 standard; cDNA; 7879 BP.
DE Human CLEVER-1 encoding cDNA SEQ ID NO:1.
PN WO2003057130-A2.

PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Best Local Similarity: 24.64% Mismatches: 92
Query Match: 11.16% Indels: 40
RESULT 1041
ID ADQ22919 standard; DNA; 8038 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5739.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 24.64% Mismatches: 92
Query Match: 11.16% Indels: 40
RESULT 1042
ID ADQ45257 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6920.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1043
ID ADQ45308 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6971.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1044
ID ADQ45241 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6904.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1045
ID ADQ45225 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6888.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1046
ID ADQ45323 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6986.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1047
ID ADQ45215 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6878.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1048
ID ADQ45264 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1049
ID ADQ45280 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6943.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1050
ID ADQ45298 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6961.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 11.11% Indels: 2
RESULT 1051
ID ADL13960 standard; DNA; 834 BP.
DE Osteoarthritis-associated polymorphic nucleotide #492.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1052
ID ABL68341 standard; DNA; 1414 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6678.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1053
ID ABK83989 standard; cDNA; 1414 BP.
DE Human cDNA differentially expressed in granulocytic cells #560.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1054
ID ABX76383 standard; DNA; 1414 BP.
DE Lung cancer-associated polynucleotide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1055
ID ACC72679 standard; cDNA; 1414 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:18.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1056
ID ADL13959 standard; DNA; 1414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #491.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1057
ID ADN38975 standard; cDNA; 1414 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:293.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1058
ID ADO24484 standard; cDNA; 1414 BP.
DE Human PRO87343 encoding cDNA SEQ ID NO:123.
PN WO2004043397-A2.

PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1059
ID ADO24438 standard; cDNA; 1414 BP.
DE Human PRO87335 encoding cDNA SEQ ID NO:77.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1060
ID ADR14116 standard; DNA; 1414 BP.
DE Human NF-kappaB pathway-associated gene SeqID117.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 11.11% Indels: 8
RESULT 1061
ID AAA57363 standard; DNA; 1522 BP.
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 11.07% Indels: 40
RESULT 1062
ID ABL90758 standard; cDNA; 3681 BP.
DE Human polynucleotide SEQ ID NO 1320.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 11.07% Indels: 40
RESULT 1063
ID AAA57362 standard; DNA; 6761 BP.
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 11.07% Indels: 40
RESULT 1064
ID ACN37944 standard; cDNA; 7871 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324323, SEQ ID NO:1163.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 11.07% Indels: 40
RESULT 1065
ID ACH45565 standard; cDNA; 474 BP.
DE Human foetal brain cDNA #6290.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 34.52% Mismatches: 41
Query Match: 11.02% Indels: 2
RESULT 1066
ID ADM80846 standard; cDNA; 795 BP.
DE Human CADECM-33 encoding cDNA SEQ ID NO:75.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 34.94% Mismatches: 37

Query Match: 10.80% Indels: 3
RESULT 1067
ID AAV41923 standard; cDNA; 1587 BP.
DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Best Local Similarity: 24.06% Mismatches: 81
Query Match: 10.76% Indels: 48
RESULT 1068
ID ADB47730 standard; cDNA; 2753 BP.
DE Novel human secreted protein cDNA #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 24.15% Mismatches: 93
Query Match: 10.71% Indels: 40
RESULT 1069
ID ADJ55285 standard; cDNA; 2753 BP.
DE Novel human secreted protein cDNA #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 24.15% Mismatches: 93
Query Match: 10.71% Indels: 40
RESULT 1070
ID AAT05627 standard; cDNA; 3259 BP.
DE Bovine brevicin core protein cDNA.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Best Local Similarity: 24.64% Mismatches: 81
Query Match: 10.71% Indels: 47
RESULT 1071
ID ABL62702 standard; DNA; 11185 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1039.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1072
ID ABN96814 standard; DNA; 11185 BP.
DE Gene #3312 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1073
ID ADN95527 standard; DNA; 11185 BP.
DE Human BEC/LEC-related gene sequence SeqID450.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1074
ID ADJ75063 standard; DNA; 11185 BP.

DE Marker gene SEQ ID NO:315.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1075
ID ADN04530 standard; cDNA; 11185 BP.
DE Antipsoriatic cDNA sequence #467.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1076
ID ADP23737 standard; cDNA; 11185 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:915.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1077
ID AAS94985 standard; DNA; 12319 BP.
DE Human DNA sequence #240 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 25.47% Mismatches: 69
Query Match: 10.53% Indels: 27
RESULT 1078
ID ADJ75926 standard; DNA; 7375 BP.
DE Marker gene SEQ ID NO:1178.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 28.93% Mismatches: 57
Query Match: 10.49% Indels: 11
RESULT 1079
ID ABT08487 standard; cDNA; 8444 BP.
DE Human novel protein NOV1a coding sequence SEQ ID NO: 1.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.00% Mismatches: 84
Query Match: 10.31% Indels: 21
RESULT 1080
ID ADO09835 standard; cDNA; 8444 BP.
DE Human NOV1a cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.

PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Best Local Similarity: 24.00% Mismatches: 84
Query Match: 10.31% Indels: 21
RESULT 1081
ID ACH29430 standard; cDNA; 410 BP.
DE Human adult spleen cDNA #449.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 32.39% Mismatches: 32
Query Match: 10.27% Indels: 1
RESULT 1082
ID ABX34625 standard; cDNA; 1761 BP.
DE Human mddt cDNA SEQ ID 186.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 23.79% Mismatches: 90
Query Match: 10.27% Indels: 47
RESULT 1083
ID ADQ83195 standard; cDNA; 1771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #9.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 23.79% Mismatches: 90
Query Match: 10.27% Indels: 47
RESULT 1084
ID AAQ57710 standard; DNA; 5191 BP.
DE Neurocan DNA.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 24.16% Mismatches: 74
Query Match: 10.27% Indels: 39
RESULT 1085
ID ADQ38685 standard; DNA; 7291 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 348.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 24.18% Mismatches: 82
Query Match: 10.27% Indels: 27
RESULT 1086
ID ADQ38687 standard; DNA; 7358 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 350.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 24.18% Mismatches: 82
Query Match: 10.27% Indels: 27
RESULT 1087
ID ADQ38681 standard; DNA; 12553 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 344.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 24.18% Mismatches: 82
Query Match: 10.27% Indels: 27
RESULT 1088
ID ADQ38682 standard; DNA; 12620 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 345.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 24.18% Mismatches: 82

Query Match: 10.27% Indels: 27
RESULT 1089
ID ADM87060 standard; cDNA; 1783 BP.
DE Human protein encoding cDNA SEQ ID NO:153.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Best Local Similarity: 22.49% Mismatches: 63
Query Match: 10.13% Indels: 82
RESULT 1090
ID AAA63526 standard; DNA; 285 BP.
DE DNA encoding the domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Best Local Similarity: 27.10% Mismatches: 36
Query Match: 10.09% Indels: 27
RESULT 1091
ID ABA02881 standard; cDNA; 2087 BP.
DE Human versican isoform V3 encoding cDNA SEQ ID NO 1.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1092
ID ADQ38683 standard; DNA; 4330 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 346.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1093
ID ACH04002 standard; cDNA; 7182 BP.
DE Human CDNA differentially expressed in lung cancer #207.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1094
ID AAQ12261 standard; cDNA; 8224 BP.
DE Versican gene.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1095
ID ABT11088 standard; cDNA; 8224 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 1222.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1096
ID ACC50121 standard; cDNA; 8224 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:89.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1097
ID ADQ38686 standard; DNA; 9592 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 349.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1098
ID ACN89856 standard; DNA; 9647 BP.
DE Breast cancer related marker, seq id 11006.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENIUM PHARM INC.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1099
ID ADQ38684 standard; DNA; 9659 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 347.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 29.75% Mismatches: 57
Query Match: 10.04% Indels: 11
RESULT 1100
ID ADP71272 standard; DNA; 573 BP.
DE Human LP2 B-B' domain gene region SeqID7.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEK) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 26.62% Mismatches: 58
Query Match: 10.00% Indels: 29
RESULT 1101
ID ABA06490 standard; cDNA; 972 BP.
DE Human CDNA SEQ ID NO: 156.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.66% Mismatches: 66
Query Match: 10.00% Indels: 25
RESULT 1102
ID ABV83827 standard; cDNA; 972 BP.
DE Human polynucleotide SEQ ID NO 156.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.66% Mismatches: 66
Query Match: 10.00% Indels: 25
RESULT 1103
ID ADO09967 standard; cDNA; 3256 BP.
DE Human NOVIC CDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.

Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1104
ID ABT08489 standard; cDNA; 3260 BP.
DE Human novel protein NOV1c coding sequence SEQ ID NO: 210.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1105
ID ADH71311 standard; DNA; 3260 BP.
DE Human gene of the invention NOV9a SEQ ID NO:207.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1106
ID ADH71355 standard; DNA; 4527 BP.
DE Human gene of the invention NOV9w SEQ ID NO:251.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1107
ID ABA04662 standard; cDNA; 4576 BP.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1108
ID ABX13822 standard; cDNA; 4642 BP.
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1109
ID ABX13823 standard; cDNA; 4962 BP.
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1110
ID ADH71357 standard; DNA; 5416 BP.
DE Human gene of the invention NOV9x SEQ ID NO:253.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1111
ID ADM90626 standard; DNA; 5688 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 19.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1112

ID ADM91044 standard; DNA; 5688 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 437.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1113
ID ADH71359 standard; DNA; 7670 BP.
DE Human gene of the invention NOV9y SEQ ID NO:255.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.15% Mismatches: 84
Query Match: 10.00% Indels: 20
RESULT 1114
ID ADP71270 standard; DNA; 600 BP.
DE Human aggregan B-B' domain gene region SeqID5.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 37.36% Mismatches: 35
Query Match: 9.87% Indels: 14
RESULT 1115
ID AAV34196 standard; DNA; 1720 BP.
DE Human secreted protein gene 43 clone HSXCK41.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.94% Mismatches: 80
Query Match: 9.87% Indels: 49
RESULT 1116
ID ACD08067 standard; cDNA; 1720 BP.
DE cDNA encoding novel human secreted protein #43.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Best Local Similarity: 23.94% Mismatches: 80
Query Match: 9.87% Indels: 49
RESULT 1117
ID AAF87120 standard; DNA; 3625 BP.
DE NOV9 coding sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.87% Mismatches: 93
Query Match: 9.87% Indels: 28
RESULT 1118
ID ADH71325 standard; DNA; 3625 BP.
DE Human gene of the invention NOV9h SEQ ID NO:221.
PN WO2003102155-A2.
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.87% Mismatches: 93
Query Match: 9.87% Indels: 28
RESULT 1119
ID ABT08488 standard; cDNA; 8495 BP.
DE Human novel protein NOV1b coding sequence SEQ ID NO: 3.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.87% Mismatches: 93
Query Match: 9.87% Indels: 28
RESULT 1120
ID ADH71331 standard; DNA; 8495 BP.
DE Human gene of the invention NOV9k SEQ ID NO:227.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.87% Mismatches: 93
Query Match: 9.87% Indels: 28
RESULT 1121
ID ADO09837 standard; cDNA; 8495 BP.
DE Human NOV1b cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Best Local Similarity: 24.87% Mismatches: 93
Query Match: 9.87% Indels: 28
RESULT 1122
ID AAA57365 standard; DNA; 1259 BP.
DE DNA encoding a human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 24.56% Mismatches: 85
Query Match: 9.73% Indels: 20
RESULT 1123
ID AAD08974 standard; cDNA; 1354 BP.
DE Alternative version of human TNF stimulated gene-6 (TSG-6) cDNA.
PN US6210905-B1.
PD 03-APR-2001.
PA (UVNY) UNIV NEW YORK STATE.
Best Local Similarity: 26.79% Mismatches: 78
Query Match: 9.73% Indels: 16
RESULT 1124
ID ABT42226 standard; DNA; 5191 BP.
DE Toxicity modelling related rat gene SEQ ID No 1928.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.

Best Local Similarity: 23.60% Mismatches: 75
Query Match: 9.73% Indels: 39
RESULT 1125
ID ADO31199 standard; DNA; 5191 BP.
DE Rat neurocan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Best Local Similarity: 23.60% Mismatches: 75
Query Match: 9.73% Indels: 39
RESULT 1126
ID ACC49518 standard; cDNA; 6310 BP.
DE Tumour-associated antigenic target protein TAT185 cDNA SEQ ID NO:26.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 21.43% Mismatches: 92
Query Match: 9.69% Indels: 54
RESULT 1127
ID ADN38943 standard; cDNA; 6310 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:261.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 21.43% Mismatches: 92
Query Match: 9.69% Indels: 54
RESULT 1128
ID ADO31195 standard; DNA; 6310 BP.
DE Human neurocan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Best Local Similarity: 21.43% Mismatches: 92
Query Match: 9.69% Indels: 54
RESULT 1129
ID ADP71268 standard; DNA; 585 BP.
DE Human LP1 B-B' domain gene region SeqID3.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 33.33% Mismatches: 44
Query Match: 9.60% Indels: 7
RESULT 1130
ID ADL13630 standard; DNA; 1065 BP.
DE Osteoarthritis-associated polymorphic nucleotide #162.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1131
ID ABT43880 standard; DNA; 1492 BP.
DE 151P3D4 v-1 DNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1132
ID ABT43881 standard; DNA; 1492 BP.
DE DNA derived from mRNA of human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1133
ID AAS28787 standard; cDNA; 1640 BP.
DE Human immunoglobulin encoding cDNA SEQ ID No 33.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74

Query Match: 9.60% Indels: 22
RESULT 1134
ID ABA06583 standard; cDNA; 1640 BP.
DE Human cDNA SEQ ID NO: 249.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1135
ID ABV83920 standard; cDNA; 1640 BP.
DE Human polynucleotide SEQ ID NO 249.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1136
ID ADB31512 standard; cDNA; 1640 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 33.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1137
ID AAS28848 standard; cDNA; 1641 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 94.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1138
ID ABA06754 standard; cDNA; 1641 BP.
DE Human cDNA SEQ ID NO: 420.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1139
ID ABV84091 standard; cDNA; 1641 BP.
DE Human polynucleotide SEQ ID NO 420.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1140
ID ADB31573 standard; cDNA; 1641 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 94.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83%
Query Match: 9.60% Mismatches: 74
Indels: 22
RESULT 1141
ID ADH71347 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9s SEQ ID NO:243.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21%
Query Match: 9.60% Mismatches: 44
Indels: 2
RESULT 1142
ID ADL13629 standard; DNA; 1759 BP.
DE Osteoarthritis-associated polymorphic nucleotide #161.
PN WO2003054166-A2.

PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1143
ID ABT43866 standard; DNA; 1957 BP.
DE DNA of transcript variant 151P3D4 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1144
ID ABT43869 standard; cDNA; 1957 BP.
DE 151P3D4 v-1 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1145
ID ABT43878 standard; cDNA; 1957 BP.
DE 151P3D4 v-10 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1146
ID ABT43877 standard; cDNA; 1957 BP.
DE 151P3D4 v-9 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1147
ID ABT43879 standard; cDNA; 1957 BP.
DE 151P3D4 v-11 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1148
ID ABT43874 standard; cDNA; 1957 BP.
DE 151P3D4 v-6 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1149
ID ABT43876 standard; cDNA; 1957 BP.
DE 151P3D4 v-8 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1150
ID ABT43871 standard; cDNA; 1957 BP.
DE 151P3D4 v-3 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57%
Query Match: 9.60% Mismatches: 52
Indels: 8
RESULT 1151
ID ABT43872 standard; cDNA; 1957 BP.
DE 151P3D4 v-4 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.

PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1152
ID ABT43873 standard; cDNA; 1957 BP.
DE 151P3D4 v-5 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1153
ID ABT43875 standard; cDNA; 1957 BP.
DE 151P3D4 v-7 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1154
ID ABT43870 standard; cDNA; 2166 BP.
DE 151P3D4 v-2 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1155
ID ABT43865 standard; DNA; 2166 BP.
DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1156
ID ABT43867 standard; DNA; 2166 BP.
DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1157
ID ADQ24054 standard; DNA; 2538 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6874.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 9.60% Indels: 8
RESULT 1158
ID ADH71333 standard; DNA; 1599 BP.
DE Human gene of the invention NOV91 SEQ ID NO:229.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1159
ID ADH71335 standard; DNA; 1611 BP.
DE Human gene of the invention NOV9m SEQ ID NO:231.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1160
ID ADH71313 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9b SEQ ID NO:209.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1161
ID ADH71353 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9v SEQ ID NO:249.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1162
ID ADH71341 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9p SEQ ID NO:237.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1163
ID ADH71345 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9r SEQ ID NO:241.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1164
ID ADH71339 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9o SEQ ID NO:235.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1165
ID ADH71349 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9t SEQ ID NO:245.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1166
ID ADH71343 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9q SEQ ID NO:239.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 9.51% Indels: 2
RESULT 1167
ID ABA83182 standard; DNA; 1851 BP.
DE HOST-4 ovarian tumour marker gene sequence, SEQ ID NO:144.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 33.71% Mismatches: 41
Query Match: 9.51% Indels: 4
RESULT 1168
ID AAF87113 standard; DNA; 2011 BP.
DE NOV2 coding sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.14% Mismatches: 84
Query Match: 9.51% Indels: 22
RESULT 1169
ID ADH71315 standard; DNA; 2011 BP.
DE Human gene of the invention NOV9c SEQ ID NO:211.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.14% Mismatches: 84

Query Match: 9.51% Indels: 22
RESULT 1170
ID ADO31201 standard; DNA; 5259 BP.
DE Mouse neurocan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Best Local Similarity: 26.21% Mismatches: 44
Query Match: 9.51% Indels: 16
RESULT 1171
ID ADQ45269 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1172
ID ADQ45261 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1173
ID ADQ45247 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6910.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1174
ID ADQ45220 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6883.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1175
ID ADQ45210 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6873.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1176
ID ADQ45303 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6966.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1177
ID ADQ45335 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6998.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1178
ID ADQ45230 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6893.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2

RESULT 1179
ID ADQ45293 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6956.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1180
ID ADQ45313 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6976.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 9.42% Indels: 2
RESULT 1181
ID ADP71266 standard; DNA; 600 BP.
DE Human versican B-B' domain gene region SeqID1.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 32.63% Mismatches: 43
Query Match: 9.42% Indels: 9
RESULT 1182
ID ADH71337 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9n SEQ ID NO:233.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 46
Query Match: 9.42% Indels: 2
RESULT 1183
ID AAA61263 standard; DNA; 1308 BP.
DE Human secreted protein gene 4 clone HFHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 28.87% Mismatches: 50
Query Match: 9.38% Indels: 35
RESULT 1184
ID ADQ38559 standard; DNA; 3858 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 222.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.28% Mismatches: 91
Query Match: 9.38% Indels: 31
RESULT 1185
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 34.21% Mismatches: 35
Query Match: 9.29% Indels: 1
RESULT 1186
ID ADR24283 standard; DNA; 484 BP.
DE Breast cancer prognosis marker #144.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Best Local Similarity: 20.71% Mismatches: 61
Query Match: 9.24% Indels: 28
RESULT 1187
ID ADH71351 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9u SEQ ID NO:247.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 46
Query Match: 9.24% Indels: 2

RESULT 1188
ID ADN41609 standard; DNA; 4767 BP.
DE Novel human secreted protein polynucleotide seqid 731.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 33.33% Mismatches: 46
Query Match: 9.24% Indels: 13
RESULT 1189
ID ADN41608 standard; DNA; 4768 BP.
DE Novel human secreted protein polynucleotide seqid 730.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 33.33% Mismatches: 46
Query Match: 9.24% Indels: 13
RESULT 1190
ID ABL27120 standard; DNA; 8433 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32833.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 31.01% Mismatches: 39
Query Match: 9.20% Indels: 42
RESULT 1191
ID ADF80106 standard; DNA; 402 BP.
DE Leukaemia-related DNA sequence #662.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Best Local Similarity: 32.26% Mismatches: 30
Query Match: 9.16% Indels: 0
RESULT 1192
ID AAT01476 standard; cDNA; 1519 BP.
DE Cat brain-enriched hyaluronan binding protein cDNA.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Best Local Similarity: 21.74% Mismatches: 87
Query Match: 9.16% Indels: 82
RESULT 1193
ID ACN42085 standard; cDNA; 4391 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:960.
PN WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.00% Mismatches: 51
Query Match: 9.16% Indels: 14
RESULT 1194
ID ACN42084 standard; cDNA; 4536 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.00% Mismatches: 51
Query Match: 9.16% Indels: 14
RESULT 1195
ID ACA55632 standard; cDNA; 1482 BP.
DE Human signalling pathway polynucleotide probe SEQ ID NO 230.
PN US6500938-B1.
PD 31-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 9.11% Indels: 41
RESULT 1196
ID ADI55428 standard; DNA; 1482 BP.
DE Human polynucleotide probe #230.
PN US2004010136-A1.
PD 15-JAN-2004.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 24.15% Mismatches: 92
Query Match: 9.11% Indels: 41
RESULT 1197
ID AAV34254 standard; DNA; 1962 BP.
DE Human secreted protein gene 43 clone HSXCK41.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 24.88% Mismatches: 81
Query Match: 9.11% Indels: 48
RESULT 1198
ID ACD08125 standard; cDNA; 1962 BP.
DE cDNA encoding novel human secreted protein #101.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Best Local Similarity: 24.88% Mismatches: 81
Query Match: 9.11% Indels: 48
RESULT 1199
ID ACH79577 standard; DNA; 538 BP.
DE Human genome derived single exon probe #12772.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.98% Indels: 8
RESULT 1200

ID AAT01475 standard; cDNA; 1084 BP.
DE Rat brain-enriched hyaluronan binding protein cDNA.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Best Local Similarity: 25.00% Mismatches: 52
Query Match: 8.98% Indels: 14
RESULT 1201
ID ADL13962 standard; DNA; 160198 BP.
DE Osteoarthritis-associated polymorphic nucleotide #494.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 34.55% Mismatches: 23
Query Match: 8.98% Indels: 2
RESULT 1202
ID AAS17594 standard; cDNA; 1209 BP.
DE DNA encoding novel secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 8.93% Indels: 3
RESULT 1203
ID ADF58259 standard; cDNA; 1209 BP.
DE Human polynucleotide sequence SEQ ID NO:626.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 8.93% Indels: 3
RESULT 1204
ID ABK11078 standard; cDNA; 1475 BP.
DE cDNA encoding LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 8.93% Indels: 3
RESULT 1205
ID ADF74225 standard; cDNA; 5409 BP.
DE Human novel brain/hippocampus cDNA #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 8.93% Indels: 3
RESULT 1206
ID AAS28917 standard; DNA; 5430 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID No 279.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.97% Mismatches: 59
Query Match: 8.93% Indels: 11
RESULT 1207
ID ADB31758 standard; DNA; 5430 BP.
DE Human novel protein DNA SEQ ID NO 279.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.97% Mismatches: 59
Query Match: 8.93% Indels: 11
RESULT 1208
ID AAD56128 standard; DNA; 7596 BP.
DE Mouse Notch carcinoma associated (CA) gene coding region.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47

RESULT 1209
ID ADA02491 standard; cDNA; 7596 BP.
DE Mouse Notch1 carcinoma associated coding sequence, SEQ ID NO:1009.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47
RESULT 1210
ID ADB72229 standard; cDNA; 7596 BP.
DE Mouse Notch1 cDNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47
RESULT 1211
ID AAD56127 standard; DNA; 8064 BP.
DE Mouse Notch carcinoma associated (CA) DNA.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47
RESULT 1212
ID ADA02490 standard; cDNA; 8064 BP.
DE Mouse Notch1 carcinoma associated cDNA, SEQ ID NO:1008.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47
RESULT 1213
ID ADB72228 standard; mRNA; 8064 BP.
DE Mouse Notch1 mRNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 8.93% Indels: 47
RESULT 1214
ID ADR99037 standard; DNA; 9487 BP.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, DNA SEQ ID 43.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Best Local Similarity: 20.09% Mismatches: 98
Query Match: 8.89% Indels: 48
RESULT 1215
ID AAA37671 standard; DNA; 1241 BP.
DE Human peptidase, HPEP-15 coding sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 23.33% Mismatches: 74
Query Match: 8.84% Indels: 45
RESULT 1216
ID ABZ59662 standard; cDNA; 2622 BP.
DE Human secreted protein SECP-17 encoding cDNA SEQ ID NO:48.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYV/) LU Y.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 8.84% Indels: 3
RESULT 1217
ID ABL27121 standard; DNA; 4287 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 28.39% Mismatches: 59
Query Match: 8.80% Indels: 42

RESULT 1218
ID AAF86431 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #1.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Best Local Similarity: 23.50% Mismatches: 51
Query Match: 8.80% Indels: 80
RESULT 1219
ID AAA27366 standard; DNA; 1206 BP.
DE Sinorhizobium meliloti ribC gene.
PN WO200029607-A1.
PD 25-MAY-2000.
PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 27.07% Mismatches: 45
Query Match: 8.76% Indels: 33
RESULT 1220
ID ADS48391 standard; cDNA; 3799 BP.
DE Bacterial polynucleotide #3134.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.61% Mismatches: 64
Query Match: 8.76% Indels: 73
RESULT 1221
ID AAA27364 standard; DNA; 4248 BP.
DE Sinorhizobium meliloti ribC/ribD gene complex.
PN WO200029607-A1.
PD 25-MAY-2000.
PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 27.07% Mismatches: 45
Query Match: 8.76% Indels: 33
RESULT 1222
ID ADW43175 standard; DNA; 35167 BP.
DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.
PN WO2004018627-A2.
PD 04-MAR-2004.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 23.79% Mismatches: 68
Query Match: 8.76% Indels: 63
RESULT 1223
ID ADS00140 standard; DNA; 35167 BP.
DE Wild-type human adenovirus serotype 24 DNA SEQ ID NO:1.
PN WO2004083418-A1.
PD 30-SEP-2004.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 23.79% Mismatches: 68
Query Match: 8.76% Indels: 63
RESULT 1224
ID ABT23534 standard; DNA; 1341 BP.
DE Cellobiohydrolase I activity polynucleotide SEQ ID No 43.
PN WO2003000941-A2.
PD 03-JAN-2003.
PA (NOVO) NOVOZYMES AS.
Best Local Similarity: 26.46% Mismatches: 56
Query Match: 8.71% Indels: 61
RESULT 1225
ID AAH90018 standard; cDNA; 2313 BP.
DE Human bone marrow cDNA, SEQ ID NO: 262.
PN WO200153453-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1226
ID ACD05902 standard; cDNA; 2313 BP.
DE Novel human contig #76.
PN WO2003023013-A2.

PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1227
ID ADE09790 standard; DNA; 2313 BP.
DE Novel DNA-related contig nucleotide sequence #512.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1228
ID ADE07629 standard; DNA; 2514 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #695.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1229
ID AAH14562 standard; cDNA; 3118 BP.
DE Human cDNA sequence SEQ ID NO:12139.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1230
ID AAH14010 standard; cDNA; 3499 BP.
DE Human cDNA sequence SEQ ID NO:11101.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1231
ID ADO00911 standard; cDNA; 4011 BP.
DE Human homologue of Fruit fly AD-related cDNA CG1103 #2.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1232
ID ADR07180 standard; cDNA; 5131 BP.
DE Full length human cDNA useful for treating neurological disease Seq 686.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 27.44% Mismatches: 78
Query Match: 8.71% Indels: 45
RESULT 1233
ID ABL07173 standard; cDNA; 6353 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.88% Mismatches: 71
Query Match: 8.71% Indels: 34
RESULT 1234
ID ABL07172 standard; cDNA; 8429 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.88% Mismatches: 71
Query Match: 8.71% Indels: 34
RESULT 1235
ID ACH93277 standard; DNA; 334 BP.
DE Human genome derived single exon probe #26472.
PN US2003194704-A1.
PD 16-OCT-2003.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 27.27% Mismatches: 40
Query Match: 8.62% Indels: 8
RESULT 1236
ID AAQ51157 standard; DNA; 1190 BP.
DE Herpes simplex virus glycoprotein I DNA.
PN EP568178-A1.
PD 03-NOV-1993.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Best Local Similarity: 28.97% Mismatches: 38
Query Match: 8.62% Indels: 20
RESULT 1237
ID ADS63288 standard; cDNA; 3684 BP.
DE Bacterial polynucleotide #15275.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.77% Mismatches: 57
Query Match: 8.58% Indels: 114
RESULT 1238
ID ABX77167 standard; DNA; 125653 BP.
DE DNA sequence of human BAC clone RP11-8211.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Best Local Similarity: 33.68% Mismatches: 31
Query Match: 8.58% Indels: 21
RESULT 1239
ID ADO42013 standard; DNA; 784 BP.
DE Human cell adhesion and extracellular matrix protein 1 gene SeqID42.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 28.07% Mismatches: 48
Query Match: 8.53% Indels: 14
RESULT 1240
ID AAX22095 standard; DNA; 1767 BP.
DE Cellobiohydrolase CBH B coding sequence.
PN WO9906574-A1.
PD 11-FEB-1999.
PA (KONN) GIST-BROCADES BV.
Best Local Similarity: 26.79% Mismatches: 39
Query Match: 8.53% Indels: 26
RESULT 1241
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Best Local Similarity: 26.39% Mismatches: 57
Query Match: 8.49% Indels: 32
RESULT 1242
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.

PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Best Local Similarity: 26.39% Mismatches: 57
Query Match: 8.49% Indels: 32
RESULT 1243
ID ABL18341 standard; DNA; 1372 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6496.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 34.48% Mismatches: 34
Query Match: 8.40% Indels: 17
RESULT 1244
ID ADH12800 standard; cDNA; 2207 BP.
DE Abalone (Haliotis discus hannai) cellulase-encoding cDNA, SEQ ID NO:1.
PN JP2003235552-A.
PD 26-AUG-2003.
PA (HOKK-) HOKKAIDO TLO KK.
Best Local Similarity: 24.09% Mismatches: 62
Query Match: 8.40% Indels: 78
RESULT 1245
ID ABL18340 standard; DNA; 4492 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6493.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 34.48% Mismatches: 34
Query Match: 8.40% Indels: 17
RESULT 1246
ID ABL25979 standard; DNA; 5388 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29410.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 33.01% Mismatches: 56
Query Match: 8.40% Indels: 5
RESULT 1247
ID ABL25978 standard; DNA; 7782 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 33.01% Mismatches: 56
Query Match: 8.40% Indels: 5
RESULT 1248
ID ABD13413 standard; DNA; 1179 BP.
DE Pseudomonas aeruginosa polynucleotide #12017.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.60% Mismatches: 63
Query Match: 8.36% Indels: 59
RESULT 1249
ID AAS80823 standard; cDNA; 7568 BP.
DE DNA encoding novel human diagnostic protein #16627.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1250
ID ADL12996 standard; cDNA; 8146 BP.
DE Human steroid-induced C3A liver cell cDNA #725.
PN US6673549-B1.
PD 06-JAN-2004.

PA (INCY-) INCYTE CORP.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1251
ID ADL61871 standard; DNA; 9169 BP.
DE Human ovarian cancer DNA marker #20083.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1252
ID ABV24414 standard; cDNA; 9220 BP.
DE Human prostate expression marker cDNA 24405.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1253
ID ABV25265 standard; cDNA; 9220 BP.
DE Human prostate expression marker cDNA 25256.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1254
ID ABK83800 standard; cDNA; 9416 BP.
DE Human cDNA differentially expressed in granulocytic cells #371.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1255
ID ACF34559 standard; DNA; 9416 BP.
DE Gene encoding angiogenesis protein BNO382.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1256
ID ADN05259 standard; cDNA; 9416 BP.
DE Antipsoriatic cDNA sequence #849.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1257
ID ADRI4613 standard; DNA; 9416 BP.
DE Human NF-kappaB pathway-associated gene SeqID614.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1258
ID ADI61664 standard; cDNA; 11917 BP.
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 475473.1.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1259
ID ADE53871 standard; cDNA; 11950 BP.
DE Human prostate cancer cDNA #218.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.

PA (PEAR/) PEARSON C I.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1260
ID ADF90735 standard; DNA; 11965 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 197.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1261
ID ADN04560 standard; cDNA; 12004 BP.
DE Antipsoriatic cDNA sequence #484.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 8.31% Indels: 55
RESULT 1262
ID ABQ81848 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Best Local Similarity: 23.68% Mismatches: 62
Query Match: 8.31% Indels: 57
RESULT 1263
ID AAT29035 standard; cDNA; 1321 BP.
DE Endoglucanase (60 kDa Family 5 cellulase) cDNA sequence.
PN WO9611262-A1.
PD 18-APR-1996.
PA (NOVO) NOVO-NORDISK AS.
Best Local Similarity: 30.00% Mismatches: 32
Query Match: 8.27% Indels: 22
RESULT 1264
ID AAK94215 standard; cDNA; 1995 BP.
DE Human full-length cDNA, SEQ ID NO: 2788.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 26.98% Mismatches: 79
Query Match: 8.27% Indels: 45
RESULT 1265
ID ADL30755 standard; cDNA; 1995 BP.
DE Full length human cDNA clone SeqID 2788.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 26.98% Mismatches: 79
Query Match: 8.27% Indels: 45
RESULT 1266
ID ADP04444 standard; cDNA; 4849 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 39.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Best Local Similarity: 23.83% Mismatches: 94
Query Match: 8.27% Indels: 75
RESULT 1267
ID ABL25205 standard; DNA; 5931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.65% Mismatches: 34
Query Match: 8.27% Indels: 13
RESULT 1268
ID ABL25204 standard; DNA; 7931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Best Local Similarity: 32.65% Mismatches: 34
Query Match: 8.27% Indels: 13
RESULT 1269
ID AAS73740 standard; cDNA; 1365 BP.
DE DNA encoding novel human diagnostic protein #9544.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.46% Mismatches: 53
Query Match: 8.22% Indels: 33
RESULT 1270
ID ABD15716 standard; DNA; 1665 BP.
DE Pseudomonas aeruginosa polynucleotide #14320.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.90% Mismatches: 70
Query Match: 8.22% Indels: 78
RESULT 1271
ID AAQ71391 standard; DNA; 2589 BP.
DE Yeast 2.6 kb agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1272
ID AAQ67360 standard; DNA; 2685 BP.
DE S. cerevisiae FLO1 gene.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1273
ID AAQ54029 standard; DNA; 2685 BP.
DE Flocculation protein coding sequence of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1274
ID AAQ71390 standard; DNA; 4614 BP.
DE Yeast 4.7 kb agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1275
ID AAA95422 standard; DNA; 4614 BP.
DE S. cerevisiae FLO1 coding sequence.
PN WO200058342-A1.
PD 05-OCT-2000.
PA (VALW) VALTION TEKILLINEN TUTKIMUSKESKUS.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1276
ID ADS46655 standard; cDNA; 4614 BP.
DE Bacterial polynucleotide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 27.57% Mismatches: 79

Query Match: 8.22% Indels: 27
RESULT 1277
ID ADR32196 standard; DNA; 5613 BP.
DE Yeast FLO1 open reading frame fragment, SEQ ID NO:1.
PN WO2004067565-A1.
PD 12-AUG-2004.
PA (OSBO-) OSBORNE DISTRIBUIDORA SA.
PA (UYDO/) UNIV DE OLAVIDE PABLO.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1278
ID ADP87474 standard; DNA; 5864 BP.
DE S cerevisiae glucan synthase pathway gene YAR050W (FLO1) SeqID16.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Best Local Similarity: 27.57% Mismatches: 79
Query Match: 8.22% Indels: 27
RESULT 1279
ID AAL56704 standard; DNA; 36604 BP.
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Best Local Similarity: 23.31% Mismatches: 89
Query Match: 8.22% Indels: 61
RESULT 1280
ID ADH69807 standard; DNA; 684973 BP.
DE Human Vbeta gene.
PN US2002150891-A1.
PD 17-OCT-2002.
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
Best Local Similarity: 27.74% Mismatches: 64
Query Match: 8.22% Indels: 21
RESULT 1281
ID ABL68560 standard; DNA; 267156 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6897.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 27.74% Mismatches: 64
Query Match: 8.22% Indels: 21
RESULT 1282
ID ADJ41911 standard; cDNA; 632 BP.
DE Plant cDNA #2911.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Best Local Similarity: 23.33% Mismatches: 77
Query Match: 8.13% Indels: 43
RESULT 1283
ID AAS28824 standard; cDNA; 697 BP.
DE Human immunoglobulin encoding cDNA SEQ ID No 70.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1284
ID ABA06691 standard; cDNA; 697 BP.
DE Human cDNA SEQ ID NO: 357.
PN WO200154474-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1285
ID ABV84028 standard; cDNA; 697 BP.
DE Human polynucleotide SEQ ID NO 357.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1286
ID ADB31549 standard; cDNA; 697 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 70.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1287
ID ADS55917 standard; cDNA; 1386 BP.
DE Bacterial polynucleotide #7904.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 27.04% Mismatches: 78
Query Match: 8.13% Indels: 45
RESULT 1288
ID ABQ14764 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1355.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 8.13% Indels: 24
RESULT 1289
ID ABQ14765 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1356.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 8.13% Indels: 24
RESULT 1290
ID ABL25807 standard; DNA; 3381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28894.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.32% Mismatches: 41
Query Match: 8.13% Indels: 15
RESULT 1291
ID AAQ22986 standard; DNA; 3502 BP.
DE Sequence of ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBB-) WEBSTER A PTY LTD.
Best Local Similarity: 28.49% Mismatches: 58
Query Match: 8.13% Indels: 46
RESULT 1292
ID ADS49082 standard; cDNA; 3873 BP.
DE Bacterial polynucleotide #3825.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.12% Mismatches: 65
Query Match: 8.13% Indels: 66
RESULT 1293
ID ABL25806 standard; DNA; 5381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.32% Mismatches: 41
Query Match: 8.13% Indels: 15
RESULT 1294
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbmi68.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 28.68% Mismatches: 70
Query Match: 8.13% Indels: 15
RESULT 1295
ID ACA51121 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #32778.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 26.40% Mismatches: 44
Query Match: 8.09% Indels: 30
RESULT 1296
ID ABT42440 standard; DNA; 2636 BP.
DE Toxicity modelling related rat gene SEQ ID No 2142.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 36.84% Mismatches: 43
Query Match: 8.09% Indels: 11
RESULT 1297
ID AAA53800 standard; DNA; 7720 BP.
DE Genomic DNA encoding M68 TNF receptor related protein.
PN WO200046247-A1.
PD 10-AUG-2000.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 26.67% Mismatches: 80
Query Match: 8.09% Indels: 16
RESULT 1298
ID AAI21781 standard; DNA; 1075 BP.
DE Probe #11714 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1299
ID ABA66852 standard; DNA; 1075 BP.
DE Human foetal liver single exon nucleic acid probe #15157.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1300
ID AAI47064 standard; DNA; 1075 BP.
DE Probe #15750 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1301
ID ABA48937 standard; DNA; 1075 BP.
DE Human breast cell single exon nucleic acid probe #7632.
PN WO200157271-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1302
ID ABA33921 standard; DNA; 1075 BP.
DE Probe #12387 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1303
ID AAK41011 standard; DNA; 1075 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15568.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1304
ID AAK15288 standard; DNA; 1075 BP.
DE Human brain expressed single exon probe SEQ ID NO: 15279.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1305
ID ABS40603 standard; DNA; 1075 BP.
DE Human liver single exon probe, SEQ ID No 15593.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1306
ID AAI07466 standard; DNA; 1075 BP.
DE Probe #7457 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1307
ID ABS14983 standard; DNA; 1075 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14974.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1308
ID AAI12593 standard; DNA; 1403 BP.
DE Probe #2526 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1309
ID ABA54290 standard; DNA; 1403 BP.
DE Human foetal liver single exon nucleic acid probe #2595.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1310
ID AAI33941 standard; DNA; 1403 BP.
DE Probe #2627 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1311
ID ABA43834 standard; DNA; 1403 BP.
DE Human breast cell single exon nucleic acid probe #2529.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1312
ID ABA24047 standard; DNA; 1403 BP.
DE Probe #2513 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1313
ID AAK28010 standard; DNA; 1403 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2567.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1314
ID AAK02574 standard; DNA; 1403 BP.
DE Human brain expressed single exon probe SEQ ID NO: 2565.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1315
ID ABS27605 standard; DNA; 1403 BP.
DE Human liver single exon probe, SEQ ID No 2595.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1316
ID AAI02498 standard; DNA; 1403 BP.
DE Probe #2489 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1317
ID ABS02482 standard; DNA; 1403 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2473.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88%
Query Match: 8.04%
Mismatches: 44
Indels: 9
RESULT 1318
ID ADB58239 standard; DNA; 1548 BP.
DE Toxicity-related gene, SEQ ID 3265.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.17%
Query Match: 8.04%
Mismatches: 96
Indels: 88
RESULT 1319
ID ADB52767 standard; DNA; 1548 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3309.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Best Local Similarity: 21.17% Mismatches: 96
Query Match: 8.04% Indels: 88
RESULT 1320
ID ABT41946 standard; DNA; 1548 BP.
DE Toxicity modelling related rat gene SEQ ID No 1648.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.17% Mismatches: 96
Query Match: 8.04% Indels: 88
RESULT 1321
ID AAC51572 standard; DNA; 1626 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69007.
PN EP1033405-A2.
PD 06-SEP-2000.
Best Local Similarity: 21.58% Mismatches: 48
Query Match: 8.04% Indels: 31
RESULT 1322
ID ADG73739 standard; cDNA; 2059 BP.
DE Aspergillus niger Brsa-109 cDNA.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Best Local Similarity: 26.95% Mismatches: 65
Query Match: 8.04% Indels: 19
RESULT 1323
ID AAA81515 standard; DNA; 16878 BP.
DE N. meningitidis partial DNA sequence gnm_62 SEQ ID NO:62.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 18.25% Mismatches: 91
Query Match: 8.04% Indels: 87
RESULT 1324
Best Local Similarity: 18.25% Mismatches: 91
Query Match: 8.04% Indels: 87
RESULT 1325
ID AAF21609 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 18.25% Mismatches: 91
Query Match: 8.04% Indels: 87
RESULT 1326
ID AAF21608 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 18.25% Mismatches: 91
Query Match: 8.04% Indels: 87
RESULT 1327
ID ACA40155 standard; DNA; 1209 BP.
DE Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 22.39% Mismatches: 83
Query Match: 8.00% Indels: 46
RESULT 1328
ID ABL24493 standard; DNA; 1344 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.81% Mismatches: 72
Query Match: 8.00% Indels: 37
RESULT 1329
ID AAZ38579 standard; cDNA; 1608 BP.

DE D. farinae mite allergen protein (map) gene nDerf98-1608 coding strand.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1330
ID AAZ38580 standard; cDNA; 1608 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1608 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1331
ID ABK69575 standard; cDNA; 1608 BP.
DE Der HMW-map polynucleotide #5.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1332
ID ABK69576 standard; cDNA; 1608 BP.
DE Der HMW-map polynucleotide #6.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1333
ID AAZ38577 standard; cDNA; 1665 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1665 coding strand.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1334
ID AAZ38578 standard; cDNA; 1665 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1665 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1335
ID ABK69573 standard; cDNA; 1665 BP.
DE Der HMW-map polynucleotide #3.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1336
ID ABK69574 standard; cDNA; 1665 BP.
DE Der HMW-map polynucleotide #4.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1337
ID AAZ38576 standard; cDNA; 1752 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1752 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83% Mismatches: 91
Query Match: 8.00% Indels: 56
RESULT 1338
ID AAZ38575 standard; cDNA; 1752 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1752 coding strand.

PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83%
Query Match: 8.00%
RESULT 1339
ID ABK69572 standard; cDNA; 1752 BP.
DE Der HMW-map polynucleotide #2.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83%
Query Match: 8.00%
RESULT 1340
ID ABK69571 standard; cDNA; 1752 BP.
DE Der HMW-map polynucleotide #1.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.83%
Query Match: 8.00%
RESULT 1341
ID ADS48485 standard; cDNA; 3309 BP.
DE Bacterial polynucleotide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.53%
Query Match: 8.00%
RESULT 1342
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 24.10%
Query Match: 8.00%
RESULT 1343
ID AAQ81138 standard; cDNA; 1014 BP.
DE HPLA2-10 gene.
PN WO9502328-A1.
PD 26-JAN-1995.
PA (INDV) UNIV INDIANA FOUND.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 26.67%
Query Match: 7.96%
RESULT 1344
ID ACA42210 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #23867.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 24.90%
Query Match: 7.96%
RESULT 1345
ID ABX94893 standard; DNA; 1275 BP.
DE P. aureginosa PAO DNA variant SEQ ID 3.
PN WO2003022881-A2.
PD 20-MAR-2003.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
PA (TUEM/) TUENMLER B.
Best Local Similarity: 24.90%
Query Match: 7.96%
RESULT 1346
ID AAQ13620 standard; DNA; 1731 BP.
DE Nitrile hydratase L type gene from pNHJ20L.
PN EP445646-A.
PD 11-SEP-1991.
PA (NITT) NITTO CHEM IND CO LTD.

Best Local Similarity: 25.24%
Query Match: 7.96%
RESULT 1347
ID ABL24090 standard; DNA; 2198 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23743.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 31.03%
Query Match: 7.96%
RESULT 1348
ID ACA26621 standard; DNA; 2271 BP.
DE Prokaryotic essential gene #8278.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 25.36%
Query Match: 7.96%
RESULT 1349
ID AAA81473 standard; DNA; 92934 BP.
DE N. meningitidis partial DNA sequence gnm_21 SEQ ID NO:21.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 31.73%
Query Match: 7.96%
RESULT 1350
Best Local Similarity: 31.73%
Query Match: 7.96%
RESULT 1351
ID AAF21613 standard; DNA; 172325 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:114.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 31.73%
Query Match: 7.96%
RESULT 1352
ID ABL18125 standard; DNA; 1110 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5848.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 31.63%
Query Match: 7.91%
RESULT 1353
ID AAS82439 standard; cDNA; 1113 BP.
DE DNA encoding novel human diagnostic protein #18243.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 29.31%
Query Match: 7.91%
RESULT 1354
ID ABK69709 standard; cDNA; 1251 BP.
DE Human lysosomal associated membrane protein (LAMP-1) gene.
PN WO200228414-A1.
PD 11-APR-2002.
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
Best Local Similarity: 23.63%
Query Match: 7.91%
RESULT 1355
ID ADB67585 standard; cDNA; 1251 BP.
DE Human cDNA encoding lysosomal associated membrane protein.
PN US2003072767-A1.
PD 17-APR-2003.
PA (GAIG/) GAIGER A.
PA (MCNE/) MCNEILL P D.
PA (SMIT/) SMITHGALL M.
PA (MOUL/) MOULTON G.
PA (VEDV/) VEDVICK T S.

PA (SLEA/) SLEATH P R.		ID ADS63309 standard; cDNA; 1392 BP.	
PA (MOSS/) MOSSMAN S.		DE Bacterial polynucleotide #15296.	
PA (EVAN/) EVANS L.		PN US2003233675-A1.	
PA (SPIE/) SPIES A G.		PD 18-DEC-2003.	
PA (BOYD/) BOYDSTON J.		PA (CAOY/) CAO Y.	
Best Local Similarity: 23.63%	Mismatches: 63	PA (HINK/) HINKLE G J.	
Query Match: 7.91%	Indels: 52	PA (SLAT/) SLATER S C.	
RESULT 1356		PA (CHEN/) CHEN X.	
ID ADJ80818 standard; DNA; 1251 BP.		PA (GOLD/) GOLDMAN B S.	Mismatches: 70
DE Wilm's tumor antigen associated DNA #17.		Best Local Similarity: 22.56%	Indels: 41
PN WO2003037060-A2.		Query Match: 7.91%	
PD 08-MAY-2003.		RESULT 1365	
PA (CORI-) CORIXA CORP.		ID ADS63675 standard; cDNA; 1515 BP.	
PA (GAIG/) GAIGER A.		DE Bacterial polynucleotide #15662.	
Best Local Similarity: 23.63%	Mismatches: 63	PN US2003233675-A1.	
Query Match: 7.91%	Indels: 52	PD 18-DEC-2003.	
RESULT 1357		PA (CAOY/) CAO Y.	
ID ADJ83738 standard; DNA; 1251 BP.		PA (HINK/) HINKLE G J.	
DE Human lysosomal associated membrane protein 1 (LAMP-1) DNA.		PA (SLAT/) SLATER S C.	
PN US2003235557-A1.		PA (CHEN/) CHEN X.	
PD 25-DEC-2003.		PA (GOLD/) GOLDMAN B S.	
PA (CORI-) CORIXA CORP.		Best Local Similarity: 22.56%	Mismatches: 70
Best Local Similarity: 23.63%	Mismatches: 63	Query Match: 7.91%	Indels: 41
Query Match: 7.91%	Indels: 52	RESULT 1366	
RESULT 1358		ID ADS64066 standard; cDNA; 1515 BP.	
ID ADL57626 standard; cDNA; 1251 BP.		DE Bacterial polynucleotide #16053.	
DE Human lysosomal associated membrane protein, LAMP-1, cDNA.		PN US2003233675-A1.	
PN US2003215458-A1.		PD 18-DEC-2003.	
PD 20-NOV-2003.		PA (CAOY/) CAO Y.	
PA (CORI-) CORIXA CORP.		PA (HINK/) HINKLE G J.	
Best Local Similarity: 23.63%	Mismatches: 63	PA (SLAT/) SLATER S C.	
Query Match: 7.91%	Indels: 52	PA (CHEN/) CHEN X.	
RESULT 1359		PA (GOLD/) GOLDMAN B S.	
ID ADO09181 standard; DNA; 1251 BP.		Best Local Similarity: 22.56%	Mismatches: 70
DE Human lysosomal associated membrane protein-1, LAMP-1, DNA.		Query Match: 7.91%	Indels: 41
PN US2004018204-A1.		RESULT 1367	
PD 29-JAN-2004.		ID AAS89998 standard; cDNA; 1788 BP.	
PA (CORI-) CORIXA CORP.		DE DNA encoding novel human diagnostic protein #25802.	
Best Local Similarity: 23.63%	Mismatches: 63	PN WO200175067-A2.	
Query Match: 7.91%	Indels: 52	PD 11-OCT-2001.	
RESULT 1360		PA (HYSE-) HYSEQ INC.	
ID AAS76541 standard; cDNA; 1275 BP.		Best Local Similarity: 29.31%	Mismatches: 38
DE DNA encoding novel human diagnostic protein #12345.		Query Match: 7.91%	Indels: 30
PN WO200175067-A2.		RESULT 1368	
PD 11-OCT-2001.		ID AAS93927 standard; cDNA; 2019 BP.	
PA (HYSE-) HYSEQ INC.		DE DNA encoding novel human diagnostic protein #29731.	
Best Local Similarity: 24.12%	Mismatches: 87	PN WO200175067-A2.	
Query Match: 7.91%	Indels: 53	PD 11-OCT-2001.	
RESULT 1361		PA (HYSE-) HYSEQ INC.	
ID AAZ38628 standard; DNA; 1298 BP.		Best Local Similarity: 29.31%	Mismatches: 38
DE Human lysosomal membrane glycoprotein-1 (LAMP-1) DNA.		Query Match: 7.91%	Indels: 30
PN WO9958658-A2.		RESULT 1369	
PD 18-NOV-1999.		ID AAS84011 standard; cDNA; 2019 BP.	
PA (EPIM-) EPIMMUNE INC.		DE DNA encoding novel human diagnostic protein #19815.	
Best Local Similarity: 23.63%	Mismatches: 63	PN WO200175067-A2.	
Query Match: 7.91%	Indels: 52	PD 11-OCT-2001.	
RESULT 1362		PA (HYSE-) HYSEQ INC.	
ID AAS52636 standard; DNA; 1374 BP.		Best Local Similarity: 29.31%	Mismatches: 38
DE E. coli DNA for cellular proliferation protein #358.		Query Match: 7.91%	Indels: 30
PN WO200170955-A2.		RESULT 1370	
PD 27-SEP-2001.		ID AAS82441 standard; cDNA; 2244 BP.	
PA (ELIT-) ELITRA PHARM INC.		DE DNA encoding novel human diagnostic protein #18245.	
Best Local Similarity: 29.31%	Mismatches: 38	PN WO200175067-A2.	
Query Match: 7.91%	Indels: 30	PD 11-OCT-2001.	
RESULT 1363		PA (HYSE-) HYSEQ INC.	
ID ACA32668 standard; DNA; 1374 BP.		Best Local Similarity: 29.31%	Mismatches: 38
DE Prokaryotic essential gene #14325.		Query Match: 7.91%	Indels: 30
PN WO200277183-A2.		RESULT 1371	
PD 03-OCT-2002.		ID ADO07724 standard; cDNA; 2298 BP.	
PA (ELIT-) ELITRA PHARM INC.		DE Fly polynucleotide #24.	
Best Local Similarity: 29.31%	Mismatches: 38	PN US2004071700-A1.	
Query Match: 7.91%	Indels: 30	PD 15-APR-2004.	
RESULT 1364		PA (LIFE-) LIFE SCI DEV CORP.	

Best Local Similarity: 25.97% Mismatches: 51
Query Match: 7.91% Indels: 41
RESULT 1372
ID AAV19281 standard; DNA; 2409 BP.
DE H. insolens cellulase NC2 genomic sequence.
PN JP08126492-A.
PD 21-MAY-1996.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Best Local Similarity: 26.77% Mismatches: 45
Query Match: 7.91% Indels: 23
RESULT 1373
ID AAV19377 standard; DNA; 2409 BP.
DE Humicola insolens cellulase NCE2 gene.
PN WO9803667-A1.
PD 29-JAN-1998.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Best Local Similarity: 26.77% Mismatches: 45
Query Match: 7.91% Indels: 23
RESULT 1374
ID AAQ81966 standard; DNA; 2454 BP.
DE Human lysosomal membrane sialoglycoprotein lamp-1 DNA.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1375
ID ABK83772 standard; cDNA; 2455 BP.
DE Human cDNA differentially expressed in granulocytic cells #343.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1376
ID ADP65652 standard; DNA; 2455 BP.
DE Human lysosomal membrane glycoprotein-1 (LAMP1) mRNA, DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1377
ID ADP65085 standard; DNA; 2455 BP.
DE Human lysosomal-associated membrane protein 1 (LAMP1) DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1378
ID ADN03754 standard; cDNA; 2455 BP.
DE Antipsoriatic cDNA sequence #75.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1379
ID ADP03003 standard; cDNA; 2455 BP.
DE Human housekeeping gene cDNA #44.
PN JP2004135552-A.
PD 13-MAY-2004.
PA (NIGA) NGK INSULATORS LTD.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1380
ID ADP49319 standard; DNA; 2455 BP.
DE Human lysosomal associated membrane protein LAMP coding sequence #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.

Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1381
ID ADS88501 standard; cDNA; 2455 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:44.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIGA) NGK INSULATORS LTD.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1382
ID ADP23230 standard; cDNA; 2455 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:324.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 23.63% Mismatches: 63
Query Match: 7.91% Indels: 52
RESULT 1383
ID ABL18124 standard; DNA; 3183 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5845.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 31.63% Mismatches: 43
Query Match: 7.91% Indels: 16
RESULT 1384
ID AAT13688 standard; DNA; 675 BP.
DE ACNPV ORF 91, residues 78661-77987.
PN WO9601320-A2.
PD 18-JAN-1996.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
Best Local Similarity: 31.65% Mismatches: 33
Query Match: 7.87% Indels: 8
RESULT 1385
ID ADK58412 standard; DNA; 1047 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5795.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Best Local Similarity: 23.50% Mismatches: 70
Query Match: 7.87% Indels: 76
RESULT 1386
ID ADP29126 standard; DNA; 1053 BP.
DE Human secreted protein encoding sequence SEQ ID #1124.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Best Local Similarity: 19.53% Mismatches: 78
Query Match: 7.87% Indels: 126
RESULT 1387
ID ABD02026 standard; DNA; 1356 BP.
DE Pseudomonas aeruginosa polynucleotide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 20.68% Mismatches: 84
Query Match: 7.87% Indels: 95
RESULT 1388
ID AAA51962 standard; DNA; 2310 BP.
DE Modified HIV-1 Env gp160, Lys121-Val200; Asn425-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 24.15% Mismatches: 67
Query Match: 7.87% Indels: 78
RESULT 1389
ID AAA51954 standard; DNA; 2535 BP.
DE Modified HIV-1 Env gp160, Asn425-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.

Best Local Similarity: 24.15% Mismatches: 67
Query Match: 7.87% Indels: 78
RESULT 1390
ID ABL28110 standard; DNA; 2665 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35803.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 24.15% Mismatches: 66
Query Match: 7.87% Indels: 66
RESULT 1391
ID ABD02080 standard; DNA; 2955 BP.
DE Pseudomonas aeruginosa polynucleotide #684.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 20.68% Mismatches: 84
Query Match: 7.87% Indels: 95
RESULT 1392
ID ABD02123 standard; DNA; 3150 BP.
DE Pseudomonas aeruginosa polynucleotide #727.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 20.68% Mismatches: 84
Query Match: 7.87% Indels: 95
RESULT 1393
ID AAT13635 standard; DNA; 133894 BP.
DE AcNPV genomic DNA clone 6.
PN WO9601320-A2.
PD 18-JAN-1996.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
Best Local Similarity: 31.65% Mismatches: 33
Query Match: 7.87% Indels: 8
RESULT 1394
ID ADQ07766 standard; cDNA; 1701 BP.
DE Nucleotide sequence of serine protease INTP039.
PN WO2004053117-A2.
PD 24-JUN-2004.
PA (INPH-) INPHARMATICA LTD.
Best Local Similarity: 25.77% Mismatches: 54
Query Match: 7.82% Indels: 53
RESULT 1395
ID ABK99974 standard; cDNA; 1738 BP.
DE Human CADPKL cDNA #2.
PN WO200254939-A2.
PD 18-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1396
ID ABL12433 standard; cDNA; 1946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31781.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.26% Mismatches: 59
Query Match: 7.82% Indels: 52
RESULT 1397
ID AAS57123 standard; cDNA; 1946 BP.
DE cDNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.26% Mismatches: 59
Query Match: 7.82% Indels: 52
RESULT 1398
ID ADC35825 standard; cDNA; 1946 BP.
DE Drosophila G protein coupled receptor cDNA seq id 27.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 23.26% Mismatches: 59

Query Match: 7.82% Indels: 52
RESULT 1399
ID ADM01511 standard; cDNA; 1955 BP.
DE Human cDNA of the invention SEQ ID NO:196.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.31% Mismatches: 88
Query Match: 7.82% Indels: 78
RESULT 1400
ID AAI60703 standard; cDNA; 1956 BP.
DE Human polynucleotide SEQ ID NO 4692.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1401
ID AAI58917 standard; cDNA; 2165 BP.
DE Human polynucleotide SEQ ID NO 1120.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1402
ID ADQ99139 standard; cDNA; 2165 BP.
DE DNA encoding human GPCR-like protein seqid 809.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1403
ID ADB48899 standard; cDNA; 2165 BP.
DE Novel human cDNA SEQ ID NO 809.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1404
ID AAD36140 standard; DNA; 2447 BP.
DE Human calmodulin kinase, CAMK-X1 gene.
PN WO200224947-A2.
PD 28-MAR-2002.
PA (KINE-) KINETEK PHARM INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1405
ID ABL12432 standard; cDNA; 3946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31778.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.58% Mismatches: 91
Query Match: 7.82% Indels: 88
RESULT 1406
ID AAS57122 standard; DNA; 3946 BP.
DE DNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.58% Mismatches: 91
Query Match: 7.82% Indels: 88
RESULT 1407
ID ADC35824 standard; DNA; 3946 BP.
DE Drosophila G protein coupled receptor genomic DNA seq id 26.

PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 20.58% Mismatches: 91
Query Match: 7.82% Indels: 88
RESULT 1408
ID ADB53355 standard; DNA; 4238 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3897.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 25.23% Mismatches: 83
Query Match: 7.82% Indels: 50
RESULT 1409
ID ACC42734 standard; DNA; 6210 BP.
DE Geldanamycin PKS module 1 DNA sequence, SEQ ID 1.
PN WO2003013430-A2.
PD 20-FEB-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Best Local Similarity: 32.04% Mismatches: 47
Query Match: 7.82% Indels: 10
RESULT 1410
ID AAD61810 standard; DNA; 6210 BP.
DE Streptomyces geldanus polyketide synthase (PKS) gene #1.
PN US2003114450-A1.
PD 19-JUN-2003.
PA (SANT/) SANTI D.
PA (MYLE/) MYLES D C.
PA (TIAN/) TIAN Z.
PA (HUTC/) HUTCHINSON C R.
PA (JOHN/) JOHNSON R.
PA (ZHOU/) ZHOU Y.
PA (FENG/) FENG L.
Best Local Similarity: 32.04% Mismatches: 47
Query Match: 7.82% Indels: 10
RESULT 1411
ID ACA37577 standard; DNA; 31263 BP.
DE Prokaryotic essential gene #19234.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 28.21% Mismatches: 57
Query Match: 7.82% Indels: 60
RESULT 1412
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Best Local Similarity: 32.04% Mismatches: 47
Query Match: 7.82% Indels: 10
RESULT 1413
ID ABQ81845 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1101.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Best Local Similarity: 35.06% Mismatches: 35
Query Match: 7.82% Indels: 8
RESULT 1414
ID ADC72389 standard; DNA; 515 BP.
DE DNA Seq ID101 related to herbicide resistance and tolerance.
PN WO2003020956-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Best Local Similarity: 28.70% Mismatches: 32
Query Match: 7.78% Indels: 39
RESULT 1415
ID ADC76620 standard; DNA; 515 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1889.
PN WO2003020905-A2.
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.
Best Local Similarity: 28.70% Mismatches: 32
Query Match: 7.78% Indels: 39
RESULT 1416
ID ADK59253 standard; DNA; 515 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6636.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Best Local Similarity: 28.70% Mismatches: 32
Query Match: 7.78% Indels: 39
RESULT 1417
ID AAV53721 standard; cDNA; 759 BP.
DE The ORF of the cloned duplicate of human aggrecan G1-B domain.
PN EP861903-A1.
PD 02-SEP-1998.
PA (LANS/) LANSING M.
PA (UHLE/) UHLENKUEKEN J.
PA (SCHM/) SCHMIDT G.
Best Local Similarity: 21.02% Mismatches: 77
Query Match: 7.78% Indels: 36
RESULT 1418
ID AAV53720 standard; cDNA; 770 BP.
DE Cloned duplicate of human aggrecan G1-B domain.
PN EP861903-A1.
PD 02-SEP-1998.
PA (LANS/) LANSING M.
PA (UHLE/) UHLENKUEKEN J.
PA (SCHM/) SCHMIDT G.
Best Local Similarity: 21.02% Mismatches: 77
Query Match: 7.78% Indels: 36
RESULT 1419
ID ABD05199 standard; DNA; 795 BP.
DE Pseudomonas aeruginosa polynucleotide #3803.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.30% Mismatches: 74
Query Match: 7.78% Indels: 58
RESULT 1420
ID ABQ80359 standard; DNA; 1149 BP.
DE A. fumigatus AfPGU3 DNA.
PN WO2003012071-A2.
PD 13-FEB-2003.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 23.24% Mismatches: 74
Query Match: 7.78% Indels: 76
RESULT 1421
ID AAX27948 standard; DNA; 1422 BP.
DE H. insolens Cel6A fungal cellulase coding sequence.
PN WO9901544-A1.
PD 14-JAN-1999.
PA (NOVO) NOVO-NORDISK AS.
Best Local Similarity: 27.66% Mismatches: 43
Query Match: 7.78% Indels: 8
RESULT 1422
ID AAX27958 standard; DNA; 1437 BP.
DE H. insolens Cel6A fungal cellulase coding sequence.
PN WO9901544-A1.
PD 14-JAN-1999.
PA (NOVO) NOVO-NORDISK AS.
Best Local Similarity: 27.66% Mismatches: 43
Query Match: 7.78% Indels: 8
RESULT 1423
ID ADG76370 standard; cDNA; 1471 BP.
DE Human Incyte cDNA encoding an enzyme (SeqID 62).
PN WO2003083082-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 22.04% Mismatches: 57
Query Match: 7.78% Indels: 59
RESULT 1424

ID ABD05240 standard; DNA; 1623 BP.
DE Pseudomonas aeruginosa polynucleotide #3844.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.30% Mismatches: 74
Query Match: 7.78% Indels: 58
RESULT 1425
ID ADQ85383 standard; cDNA; 2529 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2197.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 26.44% Mismatches: 77
Query Match: 7.78% Indels: 30
RESULT 1426
ID ADI21801 standard; cDNA; 2539 BP.
DE Novel human protein cDNA #60.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 26.44% Mismatches: 77
Query Match: 7.78% Indels: 30
RESULT 1427
ID AAL42738 standard; DNA; 2578 BP.
DE Human membrane protein coding sequence.
PN JP2002085074-A.
PD 26-MAR-2002.
PA (KIRI) KIRIN BREWERY KK.
Best Local Similarity: 26.44% Mismatches: 77
Query Match: 7.78% Indels: 30
RESULT 1428
ID ABD05062 standard; DNA; 4167 BP.
DE Pseudomonas aeruginosa polynucleotide #3666.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 24.30% Mismatches: 74
Query Match: 7.78% Indels: 58
RESULT 1429
ID AAV26962 standard; cDNA to mRNA; 5275 BP.
DE Bovine parathyroid calcium receptor 1 gene 5Kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Best Local Similarity: 22.75% Mismatches: 113
Query Match: 7.78% Indels: 49
RESULT 1430
ID AAZ25053 standard; cDNA to mRNA; 5275 BP.
DE Bovine parathyroid calcium receptor 1 nucleotide sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Best Local Similarity: 22.75% Mismatches: 113
Query Match: 7.78% Indels: 49
RESULT 1431
ID AAV82483 standard; cDNA to mRNA; 5275 BP.
DE Bovine parathyroid calcium receptor BOPCar 1 encoding cDNA.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Best Local Similarity: 22.75% Mismatches: 113
Query Match: 7.78% Indels: 49
RESULT 1432
ID AAZ89296 standard; cDNA to mRNA; 5275 BP.
DE Bovine calcium receptor BOPCar1 cDNA.
PN US6031003-A.
PD 29-FEB-2000.

PA (NPSP-) NPS PHARM INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Best Local Similarity: 22.75% Mismatches: 113
Query Match: 7.78% Indels: 49
RESULT 1433
ID AAI72120 standard; cDNA to mRNA; 5275 BP.
DE cDNA encoding BOPCar1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSP-) NPS PHARM INC.
Best Local Similarity: 22.75% Mismatches: 113
Query Match: 7.78% Indels: 49
RESULT 1434
ID AAX91461 standard; DNA; 867 BP.
DE T. gondii nTG867 reverse complement sequence.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1435
ID AAX91460 standard; DNA; 867 BP.
DE T. gondii immunogenic protein encoding DNA.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1436
ID AAS42783 standard; cDNA; 867 BP.
DE T. gondii cDNA encoding immunogenic protein PTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1437
ID AAS42784 standard; cDNA; 867 BP.
DE Reverse complement of T. gondii cDNA nTg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1438
ID ADG17392 standard; DNA; 867 BP.
DE T. gondii protein DNA #86.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1439
ID ADG17390 standard; cDNA; 867 BP.
DE T. gondii protein cDNA #6.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1440
ID AAS92828 standard; cDNA; 1200 BP.
DE DNA encoding novel human diagnostic protein #28632.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 22.22% Mismatches: 77
Query Match: 7.73% Indels: 40
RESULT 1441
ID ADS57193 standard; cDNA; 1272 BP.
DE Bacterial polynucleotide #9180.
PN US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 28.12% Mismatches: 56
Query Match: 7.73% Indels: 40
RESULT 1442
ID ADN11029 standard; DNA; 1359 BP.
DE Clostridium botulinum neurotoxin A light chain nucleic acid.
PN WO2004031355-A2.
PD 15-APR-2004.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
Best Local Similarity: 25.85% Mismatches: 61
Query Match: 7.73% Indels: 69
RESULT 1443
ID AAX91462 standard; DNA; 1397 BP.
DE T. gondii immunogenic protein encoding DNA.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1444
ID AAX91463 standard; DNA; 1397 BP.
DE T. gondii nTGl397 reverse complement sequence.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1445
ID AAS42786 standard; cDNA; 1397 BP.
DE Reverse complement of T. gondii cDNA nTGl397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1446
ID AAS42785 standard; cDNA; 1397 BP.
DE T. gondii cDNA encoding immunogenic protein PTgl397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1447
ID ADG17395 standard; DNA; 1397 BP.
DE T. gondii protein DNA #87.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1448
ID ADG17393 standard; cDNA; 1397 BP.
DE T. gondii protein cDNA #7.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Best Local Similarity: 29.67% Mismatches: 47
Query Match: 7.73% Indels: 6
RESULT 1449
ID ADF44597 standard; cDNA; 1493 BP.
DE Corn fructokinase cDNA #1.
PN US2003088882-A1.
PD 08-MAY-2003.
PA (HARV/) HARVELL L T.
PA (RAGG/) RAGGHIANI J J.
Best Local Similarity: 28.68% Mismatches: 49
Query Match: 7.73% Indels: 33
RESULT 1450

ID ADR85486 standard; DNA; 1536 BP.
DE Aspergillus fumigatus essential gene open reading frame #123.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 25.00% Mismatches: 63
Query Match: 7.73% Indels: 51
RESULT 1451
ID AAS89605 standard; cDNA; 1750 BP.
DE DNA encoding novel human diagnostic protein #25409.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.97% Mismatches: 79
Query Match: 7.73% Indels: 18
RESULT 1452
ID AAC41495 standard; DNA; 2469 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 32093.
PN EP1033405-A2.
PD 06-SEP-2000.
Best Local Similarity: 21.57% Mismatches: 62
Query Match: 7.73% Indels: 32
RESULT 1453
ID AAQ02831 standard; DNA; 2716 BP.
DE Sequence encoding tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Best Local Similarity: 23.63% Mismatches: 64
Query Match: 7.73% Indels: 52
RESULT 1454
ID ADL90420 standard; DNA; 3393 BP.
DE Clostridial neurotoxin nucleotide sequence SEQ ID NO:138.
PN WO2004024909-A2.
PD 25-MAR-2004.
PA (HEAL-) HEALTH PROTECTION AGENCY.
Best Local Similarity: 23.25% Mismatches: 76
Query Match: 7.73% Indels: 65
RESULT 1455
ID ABL16368 standard; DNA; 7417 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 577.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 37.50% Mismatches: 28
Query Match: 7.73% Indels: 23
RESULT 1456
ID ABL07608 standard; cDNA; 12713 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17306.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.13% Mismatches: 76
Query Match: 7.73% Indels: 45
RESULT 1457
ID ABV94393 standard; cDNA; 813 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:384.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Best Local Similarity: 27.52% Mismatches: 41
Query Match: 7.69% Indels: 23
RESULT 1458
ID ADR47322 standard; DNA; 1297 BP.
DE Periconia gene encoding a serine protease.
PN WO2004072279-A2.
PD 26-AUG-2004.
PA (NOVO) NOVOZYMES AS.
Best Local Similarity: 25.13% Mismatches: 62
Query Match: 7.69% Indels: 62
RESULT 1459
ID AAN91235 standard; DNA; 1368 BP.

DE DNA sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Best Local Similarity: 30.77% Mismatches: 44
Query Match: 7.69% Indels: 5
RESULT 1460
ID ACA26216 standard; DNA; 1629 BP.
DE Prokaryotic essential gene #7873.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 24.31% Mismatches: 93
Query Match: 7.69% Indels: 40
RESULT 1461
ID ABZ41778 standard; DNA; 1728 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 8145.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1462
ID AAZ54260 standard; DNA; 1731 BP.
DE Neisseria gonorrhoeae ORF 730 partial DNA sequence SEQ ID NO:2469.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1463
ID ADA71387 standard; DNA; 1815 BP.
DE Rice gene, SEQ ID 4710.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 28.39% Mismatches: 43
Query Match: 7.69% Indels: 50
RESULT 1464
ID ABZ39678 standard; DNA; 1815 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 3945.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1465
ID ABD11870 standard; DNA; 1929 BP.
DE Pseudomonas aeruginosa polynucleotide #10474.
PN US6551795-B1. .
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 23.85% Mismatches: 77
Query Match: 7.69% Indels: 63
RESULT 1466
ID ADA48491 standard; DNA; 2015 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 28.39% Mismatches: 43
Query Match: 7.69% Indels: 50
RESULT 1467
ID AAA51960 standard; DNA; 2322 BP.
DE Modified HIV-1 Env gp160, Arg426-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 23.73% Mismatches: 70
Query Match: 7.69% Indels: 76
RESULT 1468
ID ADS57996 standard; cDNA; 2328 BP.

DE Bacterial polynucleotide #9983.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.69% Mismatches: 48
Query Match: 7.69% Indels: 51
RESULT 1469
ID AAA51953 standard; DNA; 2541 BP.
DE Modified HIV-1 Env gp160, Arg426-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 23.73% Mismatches: 70
Query Match: 7.69% Indels: 76
RESULT 1470
ID ABL16369 standard; DNA; 2607 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 580.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.93% Mismatches: 34
Query Match: 7.69% Indels: 9
RESULT 1471
ID AAX60539 standard; DNA; 4435 BP.
DE C. trachomatis LGV L2 HMW protein encoding DNA.
PN WO9917741-A1.
PD 15-APR-1999.
PA (ANTE-) ANTEX BIOLOGICS INC.
Best Local Similarity: 23.36% Mismatches: 61
Query Match: 7.69% Indels: 79
RESULT 1472
ID ABK91474 standard; DNA; 6658 BP.
DE Modified HIV protein-encoding plasmid DNA #26.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1473
ID ABK91509 standard; DNA; 6730 BP.
DE Modified HIV protein-encoding plasmid DNA #61.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1474
ID ABK91468 standard; DNA; 6736 BP.
DE Modified HIV protein-encoding plasmid DNA #20.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1475
ID ABK91503 standard; DNA; 6808 BP.
DE Modified HIV protein-encoding plasmid DNA #55.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1476
ID ABK91489 standard; DNA; 7909 BP.
DE Modified HIV protein-encoding plasmid DNA #41.

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PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1477
ID ABK91483 standard; DNA; 7987 BP.
DE Modified HIV protein-encoding plasmid DNA #35.
PD WO200232943-A2.
PN 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1478
Best Local Similarity: 23.36% Mismatches: 61
Query Match: 7.69% Indels: 79
RESULT 1479
Best Local Similarity: 23.42% Mismatches: 83
Query Match: 7.69% Indels: 19
RESULT 1480
ID ABQ34166 standard; DNA; 593 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20757.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 27.52% Mismatches: 36
Query Match: 7.64% Indels: 28
RESULT 1481
ID ABQ34167 standard; DNA; 593 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20758.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 27.52% Mismatches: 36
Query Match: 7.64% Indels: 28
RESULT 1482
ID ADR85331 standard; DNA; 1110 BP.
DE Aspergillus fumigatus essential gene with introns #555.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 23.56% Mismatches: 85
Query Match: 7.64% Indels: 58
RESULT 1483
ID ABT06525 standard; DNA; 1150 BP.
DE HOXA5 gene promoter sequence.
PN WO200259347-A2.
PD 01-AUG-2002.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1484
ID ADM83708 standard; DNA; 1150 BP.
DE Human homeobox gene A5 (HOXA5) promoter DNA #1.
PN US2003138783-A1.
PD 24-JUL-2003.
PA (SUKU/) SUKUMAR S.
PA (EVRO/) EVRON E.
PA (DOOL/) DOOLEY W C.
PA (SACC/) SACCHI N.
PA (DAVI/) DAVIDSON N.
PA (FACK/) FACKLER M J.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1485
ID ADR83433 standard; DNA; 1332 BP.
DE Human homeo box A5 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1486
ID ADB69782 standard; DNA; 1371 BP.
DE C. neoformans open reading frame SEQ ID NO:2187.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 24.51% Mismatches: 37
Query Match: 7.64% Indels: 20
RESULT 1487
ID ADA69648 standard; DNA; 1518 BP.
DE Rice gene, SEQ ID 2971.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 23.58% Mismatches: 78
Query Match: 7.64% Indels: 71
RESULT 1488
ID ADQ25471 standard; DNA; 1544 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8291.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1489
ID AAL26527 standard; cDNA; 1574 BP.
DE Human breast cancer expressed polynucleotide 18984.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1490
ID AAL26465 standard; cDNA; 1574 BP.
DE Human breast cancer expressed polynucleotide 18922.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1491
ID AAL26532 standard; cDNA; 1574 BP.
DE Human breast cancer expressed polynucleotide 18989.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1492
ID ADF81842 standard; DNA; 1636 BP.
DE Leukaemia-related DNA sequence #2398.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1493
ID ADF38056 standard; cDNA; 2089 BP.
DE Synchronised tobacco BY2 cDNA sequence SEQ ID NO:115.
PN WO2003085115-A2.
PD 16-OCT-2003.
PA (CROP-) CROPDESIGN NV.
Best Local Similarity: 23.63% Mismatches: 104
Query Match: 7.64% Indels: 47
RESULT 1494
ID ACN41796 standard; cDNA; 2167 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:671.
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PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 32.14% Mismatches: 41
Query Match: 7.64% Indels: 8
RESULT 1495
ID ACN41509 standard; cDNA; 2167 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:384.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 32.14% Mismatches: 41
Query Match: 7.64% Indels: 8
RESULT 1496
ID ADA70158 standard; DNA; 2664 BP.
DE Rice gene, SEQ ID 3481.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 26.87% Mismatches: 51
Query Match: 7.64% Indels: 28
RESULT 1497
ID ADR84744 standard; DNA; 3110 BP.
DE Aspergillus fumigatus essential gene genomic sequence #555.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 23.56% Mismatches: 85
Query Match: 7.64% Indels: 58
RESULT 1498
ID ABL27410 standard; DNA; 3289 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33703.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 24.12% Mismatches: 60
Query Match: 7.64% Indels: 70
RESULT 1499
ID ABZ09895 standard; DNA; 3523 BP.
DE Human 5' and/or regulatory region of HOXA5 DNA SEQ ID NO:35.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14
RESULT 1500
ID ADE84042 standard; DNA; 6523 BP.
DE 5' regulatory region of human gene HOXA5.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 32.91% Mismatches: 27
Query Match: 7.64% Indels: 14

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 16:31:30 ; Search time 4154.4 Seconds
 (without alignments)
 2950.295 Million cell updates/sec

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 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_htc:
 4: gb_est3:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_gss1:
 9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description

1	1657	100.0	1091 1	AL550279
2	1657	100.0	1781 3	CR598862
3	1657	100.0	1786 3	CR614245
4	1657	100.0	1797 3	CR604450
5	1657	100.0	1820 3	CR612000
6	1657	100.0	1898 3	CR597409
7	1657	100.0	1911 3	CR614790
8	1657	100.0	1925 3	CR595979
9	1657	100.0	1945 3	CR605021

1	1657	100.0	1091 1	AL550279
2	1657	100.0	1781 3	CR598862
3	1657	100.0	1786 3	CR614245
4	1657	100.0	1797 3	CR604450
5	1657	100.0	1820 3	CR612000
6	1657	100.0	1898 3	CR597409
7	1657	100.0	1911 3	CR614790
8	1657	100.0	1925 3	CR595979
9	1657	100.0	1945 3	CR605021

10	1510.5	91.2	1045	1	AL550621
11	1480	89.3	965	1	AL552299
12	1476.5	89.1	1090	1	AL546669
13	1439	86.8	1043	1	AL551020
14	1347.5	81.3	1823	3	CR599107
15	1323.5	79.9	946	1	AL553858
16	1316	79.4	845	5	BX459046
17	1283	77.4	977	5	BX366718
18	1278	77.1	1023	1	AL550911
19	1275	76.9	922	1	AL549512
20	1264	76.3	855	1	AL543874
21	1262	76.2	1056	1	AL547774
22	1253	75.6	1059	1	AL552127
23	1243.5	75.0	1036	5	BX402505
24	1243	75.0	1017	1	AL544430
25	1235	74.5	973	5	BX366589
26	1230	74.2	1033	1	AL552661
27	1225.5	74.0	1064	1	AL550829
28	1213	73.2	769	1	AL546217
29	1207.5	72.9	998	1	AL546623
30	1200	72.4	896	1	AL550615
31	1168	70.5	961	1	AL552777
32	1160	70.0	863	4	BI761420
33	1142	68.9	836	1	AL545331
34	1103	66.6	2607	3	AK004726
35	1054.5	63.6	760	6	CB959809
36	1019	61.5	583	5	BP291949
37	1019	61.5	746	6	CD238639
38	1000	60.4	846	5	BX418211
39	970	58.5	743	1	AL598709
40	961	58.0	580	5	BP339718
41	935.5	56.5	801	4	BG483354
42	929	56.1	1018	1	AL553712
43	926	55.9	794	4	BG566260
44	925	55.8	582	5	BP198472
45	923	55.7	1765	3	CR622723
46	909.5	54.9	898	5	BP159588
47	905	54.6	1023	6	BY704927
48	901	54.4	596	1	AA046671
49	892	53.8	911	5	BX366791
50	874.5	52.8	802	6	CB994314
51	844	50.9	1070	1	AL546565
52	826	49.8	751	7	CO737890
53	822.5	49.6	757	6	CB229605
54	820	49.5	580	5	BP341529
55	812	49.0	581	5	BP197816
56	807	48.7	877	4	BI763579
57	795.5	48.0	964	5	BU504417
58	778	47.0	581	5	BP197366
59	771	46.5	582	5	BP320362
60	766	46.2	895	1	AL553920
61	737	44.5	487	6	CA407758
62	733.5	44.3	1298	7	CF110966
63	732	44.2	696	7	CV111589
64	725.5	43.8	910	6	CA786491
65	712.5	43.0	974	6	CB988195
66	690	41.6	465	7	H69328
67	675	40.7	841	4	BI730362
68	660.5	39.9	670	2	BB611620
69	635.5	38.4	682	5	BP434862
70	634	38.3	584	5	BP345245
71	627	37.8	581	5	BP320205
72	612.5	37.0	579	1	AI391129
73	605	36.5	793	9	AY411057
74	603.5	36.4	556	5	BM935573
75	587	35.4	368	4	BG012717
76	576.5	34.8	499	2	BE198670
77	573	34.6	872	4	BG541447
78	567.5	34.2	1070	6	CB989089
79	564	34.0	473	6	CB269023
80	563	34.0	790	9	AY411058
81	562.5	33.9	581	5	BP344636
82	560	33.8	535	2	BE756611

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84	530	32.0	1130	1	AL574194	AL574194
85	523.5	31.6	411	7	H02823	Yj4lh11.r1
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87	511.5	30.9	455	1	AI006667	ue16b07.y
88	511.5	30.9	883	5	BU239567	
89	509	30.7	409	2	AW961536	EST373608
90	503	30.4	707	7	CK836545	
91	481.5	29.1	380	1	AA081350	zn33h09.r
92	472.5	28.5	813	5	BU388030	
93	470.5	28.4	474	7	CF791146	
94	470	28.4	581	5	BP338802	
95	466.5	28.2	437	1	AJ686473	
96	450	27.2	865	6	CD106276	
97	447	27.0	675	7	CK958011	
98	445	26.9	444	7	T96904	
99	443	26.7	673	7	CK949504	
100	438	26.4	776	7	CO567156	
101	434.5	26.2	540	5	BQ417943	
102	430	26.0	871	4	BG173551	
103	423	25.5	415	1	AA463325	zx71f04.r
104	417	25.2	656	4	BM426481	
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106	406.5	24.5	366	7	R24376	
107	397.5	24.0	479	2	BE847124	
108	387	23.4	328	1	AA297240	
109	386.5	23.3	800	9	AY411059	
110	382	23.1	807	5	BU125818	
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112	378	22.8	371	2	BE684197	
113	371.5	22.4	747	5	BU324601	
114	360.5	21.8	745	7	CF520494	
115	353.5	21.3	385	7	W29485	
116	351	21.2	1007	1	AL552625	
117	347.5	21.0	469	2	BF471572	
118	343.5	20.7	993	1	AL575633	
119	333.5	20.1	449	2	BF041814	BP250014B
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121	318	19.2	1010	1	AL571871	
122	315.5	19.0	351	6	CB780898	
123	315	19.0	779	7	CK773274	
124	298.5	18.0	353	5	BY318491	
125	291.5	17.6	354	5	BY107653	
126	288	17.4	529	6	CD671330	
127	285	17.2	948	1	AL573693	
128	275.5	16.6	1006	1	AL571928	
129	275	16.6	540	4	BM253102	
130	275	16.6	751	7	CK775586	
131	274.5	16.6	652	7	CF250037	esa007.f1
132	259	15.6	974	7	CK404422	AUF_ifHdk
133	254.5	15.4	801	7	CK030244	
134	253	15.3	895	6	CA474635	
135	250.5	15.1	627	5	BU241066	
136	249	15.0	960	1	AL575514	
137	248	15.0	811	7	CF285506	
138	245	14.8	906	7	CF546586	
139	241	14.5	723	7	CF547545	
140	240	14.5	242	2	AW318386	
141	239.5	14.5	924	1	AL550876	
142	238	14.4	390	7	H78909	
143	233.5	14.1	405	6	BY766304	
144	233	14.1	305	1	AV749159	
145	233	14.1	318	7	R71437	
146	233	14.1	337	7	R81462	
147	232.5	14.0	576	5	BQ400750	
148	231.5	14.0	913	7	CK410366	AUF_ipHdk
149	228.5	13.8	600	6	CB512734	
150	228	13.8	868	7	CF379047	AGENCOURT
151	226	13.6	2851	3	AK045226	Mus muscu
152	225.5	13.6	599	6	CB515759	ssalrgb51
153	224	13.5	759	7	CF285642	
154	224	13.5	827	7	CK471875	AGENCOURT
155	224	13.5	833	6	CD361163	AGENCOURT

c	156	222.5	13.4	954	5	BX418210
	157	220.5	13.3	431	4	BG657011
	158	218.5	13.2	423	2	AW419846
	159	218.5	13.2	599	6	CB582683
	160	218.5	13.2	763	7	CO570158
	161	218.5	13.2	810	7	CK476032
	162	216	13.0	774	5	BP169122
	163	216	13.0	905	5	BP166057
	164	215.5	13.0	766	5	BP167565
	165	215	13.0	825	5	BP157524
	166	214.5	12.9	289	5	BY145458
	167	214	12.9	598	6	CA367101
	168	212	12.8	1876	3	CR596847
	169	212	12.8	1955	3	CR621045
	170	211	12.7	721	7	CF763972
	171	210	12.7	563	5	BQ566621
	172	208	12.6	793	7	CN823883
	173	207	12.5	1906	3	AK087472
	174	206.5	12.5	838	7	CF727499
	175	206	12.4	642	6	CB442342
	176	206	12.4	821	6	CA846294
	177	206	12.4	824	7	CK791054
	178	204.5	12.3	828	5	EX078167
	179	204	12.3	499	6	CD285349
	180	203.5	12.3	810	6	CB314546
	181	203	12.3	706	7	CN823877
	182	202.5	12.2	592	7	CN660471
	183	202.5	12.2	615	7	CF907877
	184	202.5	12.2	619	5	BQ393883
	185	202.5	12.2	623	7	CN661635
	186	202.5	12.2	623	7	CN661701
	187	202.5	12.2	638	7	CK624682
	188	202.5	12.2	647	6	CA572928
	189	202.5	12.2	650	7	CF909697
	190	202.5	12.2	666	6	BY731449
	191	202.5	12.2	670	4	BI328140
	192	202	12.2	828	4	BG170766
	193	201.5	12.2	1085	5	BM913991
	194	201	12.1	867	5	BU184888
	195	201	12.1	1085	4	BM550721
	196	200.5	12.1	864	5	BQ690615
	197	200	12.1	820	4	BG760275
	198	200	12.1	916	5	BU166171
	199	200	12.1	1024	5	BM904914
c	201	199.5	12.0	750	6	CD467776
	202	199	12.0	578	4	BI008726
	203	199	12.0	627	5	BP280494
	204	198.5	12.0	834	5	BU150725
	205	198.5	12.0	630	2	AW732334
	206	198.5	12.0	658	6	CD466155
	207	198.5	12.0	749	6	CD470595
	208	198.5	12.0	750	6	CD466893
	209	198	11.9	775	7	CN218866
	210	197.5	11.9	821	6	CD559300
	211	197.5	11.9	582	2	BB611006
	212	197.5	11.9	677	6	BY744790
	213	197.5	11.9	735	7	CN347081
	214	197.5	11.9	791	1	AL548444
	215	197	11.9	831	4	BI856036
	216	197	11.9	886	7	CF251786
	217	197	11.9	976	4	BM562794
	218	196.5	11.9	976	5	BQ957776
	219	196.5	11.9	658	6	CD469720
	220	196.5	11.9	660	6	CD469535
	221	196.5	11.9	669	6	CD470836
	222	196.5	11.9	796	4	BG868920
	223	196.5	11.9	819	4	BI333992
	224	196.5	11.9	851	4	BG750268
	225	196	11.8	925	2	BF311255
	226	196	11.8	588	4	BM744218
	227	196	11.8	636	7	CV026388
	228	196	11.8	654	7	CN347082
		196		666	7	CN347074

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CB582683	AMGNNUC:N
CO570158	AGENCOURT
CK476032	AGENCOURT
BP169122	BP169122
BP166057	BP166057
BP167565	BP167565
BP157524	BP157524
BY145458	BY145458
CA367101	642837 NC
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AK087472	Mus muscu
CF727499	UI-M-HB0-
CB442342	692918 MA
CA846294	haa12a06.
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CN661701	A0722G02-
CK624682	mi24a09.y
CA572928	K0542E07-
CF909697	A0540A04-
BY731449	BY731449
BI328140	602979293
BG170766	602323885
BM913991	AGENCOURT
BU184888	AGENCOURT
BM550721	AGENCOURT
BQ690615	AGENCOURT
BG760275	602716678
BU166171	AGENCOURT
BM904914	AGENCOURT
CD467776	Leukos1_6
BI008726	QV3-RT007
BP280494	BP280494
BU150725	AGENCOURT
AW732334	bb03a02.y
CD466155	Leukon2_2
CD470595	Leukos4_5
CD466893	Leukon2_8
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CN347081	170004249
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CD469720	Leukos2_8
CD469535	Leukos2_4
CD470836	Leukos5_2
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BG750268	602709071
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229	196	11.8	698	7	CN347073	CN347073	170005325	302	191.5	11.6	582	7	CF256984	pha005_c0
230	196	11.8	699	4	BM763301	BM763301	K-EST0044	303	191.5	11.6	608	7	CF257313	pha009_f1
231	196	11.8	709	4	BG539893	BG539893	602563781	304	191.5	11.6	660	6	CD468968	LeukoS3_8
232	196	11.8	728	4	BI769128	BI769128	603053720	305	191.5	11.6	739	1	AJ450624	AJ450624
233	196	11.8	730	7	CN347080	CN347080	170004708	306	191.5	11.6	855	7	CF257095	pha006_g0
234	196	11.8	743	6	CB318661	CB318661	AGENCOURT	307	191.5	11.6	859	7	CF257757	pha015_a1
235	196	11.8	764	4	BG759720	BG759720	602711117	308	191.5	11.6	881	7	CF251803	hdm004_e0
236	196	11.8	791	4	BG485676	BG485676	602505976	309	191	11.5	393	7	CF144025	UI-HF_BP0
237	196	11.8	827	4	BI833320	BI833320	603087916	310	191	11.5	515	4	BM753415	K-EST0030
238	196	11.8	858	5	BQ223902	BQ223902	AGENCOURT	311	191	11.5	536	5	BP162646	BP162646
239	196	11.8	864	1	AL548999	AL548999	AL548999	312	191	11.5	565	5	BP267691	BP267691
240	196	11.8	879	5	BQ962000	BQ962000	AGENCOURT	313	191	11.5	582	5	BP278066	BP278066
241	196	11.8	885	7	CF257093	CF257093	pha006_f1	314	191	11.5	582	5	BP356315	BP356315
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243	196	11.8	890	5	BU158569	BU158569	AGENCOURT	316	191	11.5	598	5	BP279982	BP279982
244	196	11.8	894	5	BQ880928	BQ880928	AGENCOURT	317	191	11.5	602	5	BP279073	BP279073
245	196	11.8	903	6	CA455121	CA455121	AGENCOURT	318	191	11.5	625	2	AW732339	bb03b02.Y
246	196	11.8	906	5	BU149945	BU149945	AGENCOURT	319	191	11.5	697	4	BG912337	602806886
247	196	11.8	923	5	BQ946450	BQ946450	AGENCOURT	320	190.5	11.5	820	4	BM051234	BM051234
248	196	11.8	940	4	BG747697	BG747697	602705169	321	190.5	11.5	951	4	BG119674	6023347092
249	196	11.8	985	5	BU168480	BU168480	AGENCOURT	322	190.5	11.5	973	4	BI820251	BI820251
250	196	11.8	985	5	BX356719	BX356719	BX356719	323	190	11.5	512	4	BM744870	BM744870
251	196	11.8	1004	5	BX439725	BX439725	BX439725	324	190	11.5	545	6	CB135807	CB135807
252	196	11.8	1010	1	AL552534	AL552534	AL552534	325	190	11.5	550	5	BP377364	BP377364
253	195.5	11.8	801	2	BE570280	BE570280	601332944	326	190	11.5	553	4	BM846600	BM846600
254	195.5	11.8	832	4	BG114530	BG114530	602284857	327	190	11.5	555	4	BM753425	BM753425
255	195.5	11.8	984	5	BQ677018	BQ677018	AGENCOURT	328	190	11.5	556	6	CB141325	CB141325
256	195.5	11.8	1054	5	BM918483	BM918483	AGENCOURT	329	190	11.5	556	6	CB141372	CB141372
257	195	11.8	476	2	AW501445	AW501445	UI-HF-BP0	330	190	11.5	558	7	CN482614	hw22e06.Y
258	195	11.8	579	5	BP268197	BP268197	BP268197	331	190	11.5	561	4	BM743702	BM743702
259	195	11.8	738	5	BU195946	BU195946	AGENCOURT	332	190	11.5	563	4	BM840881	BM840881
260	195	11.8	928	5	BQ683148	BQ683148	AGENCOURT	333	190	11.5	569	4	BM848299	BM848299
261	195	11.8	1067	1	AL544334	AL544334	AL544334	334	190	11.5	569	4	BM853235	BM853235
262	194.5	11.7	503	6	CA573126	CA573126	K0546C07-	335	190	11.5	573	1	AU280746	AU280746
263	194.5	11.7	504	5	BQ562475	BQ562475	H4076B11-	336	190	11.5	576	5	BP279188	BP279188
264	194.5	11.7	509	2	AW761944	AW761944	ur51f10.Y	337	190	11.5	578	4	BM742678	BM742678
265	194.5	11.7	519	6	CA570202	CA570202	K0503C08-	338	190	11.5	579	5	BP363851	BP363851
266	194.5	11.7	521	6	CA570891	CA570891	K0513B10-	339	190	11.5	580	5	BP236550	BP236550
267	194.5	11.7	522	6	CA873377	CA873377	K0924G02-	340	190	11.5	580	5	BP272835	BP272835
268	194.5	11.7	546	6	CA883079	CA883079	B0101A04-	341	190	11.5	581	4	BI824066	BI824066
269	194.5	11.7	581	6	CA896005	CA896005	B0196A07-	342	190	11.5	581	5	BP206044	BP206044
270	194.5	11.7	883	5	BQ877431	BQ877431	AGENCOURT	343	190	11.5	581	5	BP221857	BP221857
271	194	11.7	574	4	BM742230	BM742230	K-EST0015	344	190	11.5	581	5	BP221889	BP221889
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275	194	11.7	662	5	BQ109366	BQ109366	imageqc_6	348	190	11.5	581	5	BP237035	BP237035
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285	194	11.7	913	4	BG327238	BG327238	602426190	358	190	11.5	581	5	BP354214	BP354214
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527	183	11.0	582	5	BP235338	BP235338	600	174	10.5	905	4	BG251812	602364427
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533	182	11.0	321	7	CO261322	CO261322 4133483 B	606	172	10.4	581	5	BP208292	BP208292
534	182	11.0	511	4	BM848382	BM848382 K-EST0128	607	172	10.4	582	5	BP215537	BP215537
535	182	11.0	576	5	BP206244	BP206244	608	172	10.4	583	5	BP349577	BP349577
536	182	11.0	579	5	BP334408	BP334408	609	172	10.4	589	5	BP354144	BP354144
537	182	11.0	937	4	BG325414	BG325414 602424105	610	171.5	10.4	698	4	BG748079	BG748079 602705577
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541	181	10.9	679	6	CB135879	CB135879 K-EST0188	614	170.5	10.3	442	7	CF166420	B0770E04 -
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548	179	10.8	576	6	CD472209	CD472209 LeukoS6_1	621	170	10.3	1336	3	CR660524	Tetraodon
549	179	10.8	582	5	BP278062	BP278062	622	169.5	10.2	598	5	BP280260	BP280260
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552	178	10.7	591	5	BP336010	BP336010	625	169	10.2	582	5	BP364971	BP364971
553	178	10.7	592	5	BP363850	BP363850	626	169	10.2	583	5	BP354393	BP354393
554	178	10.7	838	4	BG704722	BG704722 602688329	627	169	10.2	811	4	BI856520	603385622
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556	177.5	10.7	503	2	BB867301	BB867301	629	168.5	10.2	1243	5	BQ230605	AGENCOURT
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561	177	10.7	580	5	BP299494	BP299494	634	167	10.1	582	5	BP315724	BP315724
562	177	10.7	581	5	BP305097	BP305097	635	167	10.1	582	5	BP354763	BP354763
563	177	10.7	581	5	BP324616	BP324616	636	166.5	10.0	457	2	BB862318	BB862318
564	177	10.7	581	5	BP353795	BP353795	637	166.5	10.0	463	6	CB120042	K-EST0167
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566	177	10.7	581	5	BP363831	BP363831	639	166.5	10.0	480	6	CB139711	K-EST0192
567	177	10.7	581	5	BP365172	BP365172	640	166.5	10.0	482	4	BM752546	K-EST0029
568	177	10.7	582	5	BP279349	BP279349	641	166	10.0	582	5	BP236892	BP236892
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570	177	10.7	582	5	BP279865	BP279865	643	166	10.0	770	6	CD559302	AGENCOURT
571	177	10.7	582	5	BP279956	BP279956	644	165.5	10.0	464	2	BE127204	DEPA0953
572	177	10.7	582	5	BP299760	BP299760	645	165	10.0	550	5	BP279159	BP279159
573	177	10.7	582	5	BP359628	BP359628	646	165	10.0	582	5	BP339224	BP339224
574	177	10.7	582	5	BP366132	BP366132	647	165	10.0	583	5	BP255503	BP255503
575	177	10.7	583	5	BP279259	BP279259	648	165	10.0	748	2	BE546472	601077647
576	177	10.7	583	5	BP279567	BP279567	649	164.5	9.9	452	4	BM742492	K-EST0015
577	177	10.7	583	5	BP365496	BP365496	650	164	9.9	448	4	BM797335	BM797335 K-EST0080
578	177	10.7	583	5	BP379517	BP379517	651	164	9.9	583	5	BP366227	BP366227
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581	177	10.7	596	5	BP365383	BP365383	654	162.5	9.8	433	5	BY252039	BY252039
582	177	10.7	603	5	BP279828	BP279828	655	162.5	9.8	446	4	BI960888	BI960888 MONQ1_2_B
583	177	10.7	603	5	BP280025	BP280025	656	162.5	9.8	476	6	CD465241	LeukoN1_2
584	177	10.7	607	5	BP279866	BP279866	657	162.5	9.8	915	5	BQ432026	AGENCOURT
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586	176	10.6	581	5	BP322120	BP322120	659	161.5	9.7	450	7	CK613064	CK613064 LPSi_H05
587	176	10.6	583	5	BP333904	BP333904	660	161	9.7	582	5	BP323917	BP323917
588	176	10.6	592	5	BP281049	BP281049	661	160.5	9.7	693	4	BI557680	BI557680 603237040
589	176	10.6	696	2	BE274840	BE274840 601122795	662	160	9.7	887	4	BG528427	BG528427 602579863
590	176	10.6	804	2	BE618977	BE618977 601472779	663	159.5	9.6	332	6	CD584497	CD584497 RK025A2G1
591	175	10.6	486	4	BM847024	BM847024 K-EST0126	664	159.5	9.6	420	2	BE767810	CM3-GN004
592	175	10.6	581	5	BP364418	BP364418	665	159.5	9.6	459	7	CF137888	UI-HF-BN0
593	175	10.6	582	5	BP356350	BP356350	666	159.5	9.6	492	4	BM824519	K-EST0096

667 159.5 9.6 765 7 CN347077 CN347077 170004177
668 158.5 9.6 483 5 BU661013 c168b03.z
669 158 9.5 549 1 AA282906 zt14h05.r
670 158 9.5 998 2 BE616364
671 157 9.5 570 5 BP369857 BP369857
672 157 9.5 592 5 BP280439 BP280439
673 157 9.5 676 6 CD528831 Leukon3_5
674 156.5 9.4 628 5 BP278601 BP278601
675 156.5 9.4 744 4 BG250382 602362532
676 156.5 9.4 785 5 BX915863 BX915863
677 156.5 9.4 931 7 CN321916 AGENCOURT
678 156 9.4 583 5 BP278490 BP278490
679 155.5 9.4 287 6 CB140504 K-EST0193
680 155.5 9.4 449 6 CB120078 K-EST0167
681 155.5 9.4 459 6 CD469110 Leukos2_1
682 155 9.4 583 5 BP363547 BP363547
683 155 9.4 815 9 BX188005 Danio rer
684 154.5 9.3 582 5 BP361203 BP361203
685 154.5 9.3 952 1 AL570563 AL570563
686 154 9.3 1003 5 BX380694 BX380694
687 153.5 9.3 432 4 BM764097 K-EST0045
688 153.5 9.3 438 4 BM785480 K-EST0063
689 153.5 9.3 444 4 BM826025 K-EST0097
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691 153.5 9.3 641 6 BY726835 BY726835
692 153.5 9.3 879 5 BQ962151 AGENCOURT
693 152.5 9.2 573 6 CD535920 Leukon5_5
694 152 9.2 3454 3 AK028441 Mus muscu
695 151.5 9.1 422 5 BU428717 UI-HF-BN0
696 151.5 9.1 509 4 BM088473 501959 MA
697 151.5 9.1 717 7 CV221259 Le_mx0_46
698 151 9.1 758 5 BQ227807 AGENCOURT
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706 149 9.0 608 7 CF371082 TgESTzyj6
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708 149 9.0 850 2 BE735557 601304365
709 148.5 9.0 572 5 BP333480 BP333480
710 148.5 9.0 719 6 CA342417 672284_NC
711 148 8.9 574 5 BP278877 BP278877
712 147.5 8.9 514 4 BG684702 BG684702
713 147.5 8.9 831 6 CA473822 AGENCOURT
714 147.5 8.9 1110 7 CK028468 AGENCOURT
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716 147 8.9 588 5 BP336450 BP336450
717 147 8.9 625 6 CD471271 Leukos5_1
718 147 8.9 702 7 CN347076 170004248
719 146.5 8.8 767 4 BG822533 BG822533
720 146.5 8.8 1073 2 BE904427 BE904427
721 146 8.8 331 1 AA363579 AA363579
722 146 8.8 577 9 AY421183 Pan trogl
723 146 8.8 1122 7 CK028027 CK028027 AGENCOURT
724 145.5 8.8 444 2 BB860365 BB860365
725 145.5 8.8 468 6 CA389865 CA389865
726 145.5 8.8 582 5 BP205440 BP205440
727 145.5 8.8 587 7 CV029518 8335_Full1
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730 145.5 8.8 834 9 AY421182 Homo sapi
731 145.5 8.8 1001 1 AL540999 AL540999
732 145 8.8 545 5 BX480271 DKFZp6860
733 145 8.8 557 4 BI467634 BI467634
734 145 8.8 582 5 BP194641 BP194641
735 145 8.8 583 5 BP204751 BP204751
736 145 8.8 691 7 CO132920 EST00003
737 145 8.8 744 5 BU376182 603808158
738 145 8.8 760 7 CV079185 AGENCOURT
739 145 8.8 866 7 CO390036 AGENCOURT

740 145 8.8 868 5 BQ230041 BQ230041
741 144.5 8.7 432 6 CB128106 K-EST0177
742 144.5 8.7 500 1 AL544354 AL544354
743 144.5 8.7 589 4 BI342110 369784_MA
744 144.5 8.7 673 6 CD772495 AGENCOURT
745 144.5 8.7 680 6 CD465458 Leukon1_4
746 144 8.7 450 2 BE855266 ux28a10.y
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753 144 8.7 585 5 BP289867 BP289867
754 144 8.7 599 1 AV593707 AV593707
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756 144 8.7 688 6 CD469382 Leukos2_3
757 144 8.7 796 2 BF031320 601559076
758 144 8.7 828 9 AY421184 Mus muscu
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761 143.5 8.7 417 4 BM743706 K-EST0016
762 143.5 8.7 1090 5 BM908074 AGENCOURT
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765 143 8.6 2368 3 BC019712 Mus muscu
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767 142.5 8.6 582 5 BP227819 BP227819
768 142.5 8.6 606 6 CA347334 678437_NC
769 142 8.6 227 1 AA029420 AA029420 ze96c11.r
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771 142 8.6 649 7 CN980729 48731_126
772 142 8.6 678 7 CN969354 16851_123
773 141.5 8.5 378 7 W68991 T2873_MVAT4
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777 140 8.4 428 5 BQ133343 BQ133343 fz40d02.y
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785 140 8.4 905 7 CN510906 AGENCOURT
786 139.5 8.4 387 6 CD471434 Leukos5_5
787 139 8.4 388 2 AW435659 AW435659 74622_MAR
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792 139 8.4 674 7 CK685212 ZF101-P00
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794 138 8.3 946 5 BQ720761 AGENCOURT
795 136.5 8.2 595 9 FR0036223 FR0036223
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797 136 8.2 808 6 CD512219 AGENCOURT
798 136 8.2 3085 3 AK034522 AK034522 Mus muscu
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800 135.5 8.2 2661 9 AY402614 Mus muscu
801 135 8.1 466 5 BY153109 BY153109
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803 134.5 8.1 694 6 CA376384 CA376384 654727_NC
804 134.5 8.1 986 5 BX390379 BX390379
805 134.5 8.1 3025 3 BC049247 Mus muscu
806 134 8.1 582 5 BP363410 BP363410
807 133.5 8.1 729 7 CN056501 Salamande
808 133 8.0 245 1 AA360733 EST70005
809 133 8.0 291 1 AA347120 EST53364
810 133 8.0 669 5 BU631966 UI-H-FE1-
811 132.5 8.0 878 6 CD359001 AGENCOURT
812 132 8.0 327 7 W40210 zc83b06.r1

813	132	8.0	770	5	BU749989	BU749989 CH3#030_C	886	121.5	7.3	790	1	AV704163
814	132	8.0	781	1	AL669025	AL669025 AL669025	887	121	7.3	492	1	AV671084
815	131.5	7.9	860	4	BG541514	BG541514 602570961	888	121	7.3	526	5	BQ565916
816	131.5	7.9	874	2	BF582542	BF582542 602094513	889	121	7.3	557	4	BM254894
817	131	7.9	784	4	BG866546	BG866546 602785510	890	121	7.3	683	5	BW300493
818	131	7.9	2736	9	AY402612	AY402612 Homo sapi	c 891	121	7.3	688	6	CA308497
819	131	7.9	2759	3	BC029313	BC029313 Homo sapi	892	121	7.3	703	5	BW301620
820	131	7.9	3270	3	BC035457	BC035457 Homo sapi	893	120.5	7.3	353	5	BY016053
821	130.5	7.9	362	5	BY019901	BY019901 BY019901	894	120.5	7.3	738	2	BF346219
822	130.5	7.9	584	5	BP217677	BP217677 BP217677	c 895	120.5	7.3	1071	5	BX447415
823	130.5	7.9	706	2	AW954379	AW954379 EST366449	896	120	7.2	223	5	BQ132939
824	130.5	7.9	906	1	AA717936	AA717936 vt09f11.r	897	120	7.2	366	5	BY324757
825	130	7.8	329	7	W93163	W93163 zd93d04.r1	898	120	7.2	366	6	BY767081
826	130	7.8	582	5	BP301774	BP301774 BP301774	899	120	7.2	380	5	BY011815
827	130	7.8	640	2	BE371133	BE371133 601218624	c 900	120	7.2	534	1	AV605303
828	129.5	7.8	446	2	B8840038	B8840038 B8840038	901	120	7.2	736	7	CF457207
829	128.5	7.8	416	5	BY208234	BY208234 BY208234	902	120	7.2	875	2	BF531009
830	128	7.7	643	5	BX114551	BX114551 BX114551	903	119.5	7.2	367	5	BY330481
831	127.5	7.7	384	5	BY172775	BY172775 BY172775	904	119.5	7.2	382	6	BY772496
832	127.5	7.7	581	5	BP250869	BP250869 BP250869	905	119.5	7.2	395	6	CB140481
833	127.5	7.7	1832	3	CR613805	CR613805 full-leng	906	119.5	7.2	398	6	CD465668
834	127.5	7.7	1844	3	AY037161	AY037161 Homo sapi	907	119.5	7.2	582	5	BP289784
835	127.5	7.7	2485	3	BC023209	BC023209 Homo sapi	908	119.5	7.2	848	7	CK236600
836	127.5	7.7	3105	3	BC053689	BC053689 Homo sapi	909	119	7.2	235	6	CA946461
837	127.5	7.7	3295	3	BC029348	BC029348 Homo sapi	910	119	7.2	362	6	BY766890
838	127	7.7	377	5	BY075544	BY075544 BY075544	911	119	7.2	364	5	BY171892
839	127	7.7	422	1	AV670072	AV670072 AV670072	912	119	7.2	654	6	CB056916
840	127	7.7	642	7	CV078311	CV078311 AGENCOURT	913	119	7.2	841	2	BF528870
841	127	7.7	732	7	CK805674	CK805674 AGENCOURT	914	119	7.2	931	5	BQ876201
842	127	7.7	938	7	CK799651	CK799651 AGENCOURT	915	118.5	7.2	389	5	BY165009
843	127	7.7	964	4	BI222267	BI222267 602939755	916	118.5	7.2	491	6	CB153314
844	126.5	7.6	750	7	CK699945	CK699945 ZF101-P00	917	118.5	7.2	515	6	CB153421
c 845	126	7.6	1079	9	CNS05DEJ	AL332308 Tetraodon	918	118.5	7.2	582	5	BP310145
846	125.5	7.6	572	7	CNS32870	CNS32870 UI-M-HO0-	919	118.5	7.2	696	2	BF529489
847	125.5	7.6	648	5	BP765140	BP765140 BP765140	920	118.5	7.2	792	7	CF456942
848	125.5	7.6	765	7	CNS08989	CNS08989 AGENCOURT	921	118	7.1	290	1	AA374988
849	125.5	7.6	885	6	CA496501	CA496501 AGENCOURT	922	118	7.1	520	4	BM798170
850	125.5	7.6	2189	3	AK003582	AK003582 Mus muscu	923	118	7.1	562	5	BQ130854
851	125.5	7.6	2194	3	AK048107	AK048107 Mus muscu	924	118	7.1	788	4	BG912617
852	125.5	7.6	2876	3	AK032750	AK032750 Mus muscu	925	118	7.1	2273	3	AK034871
853	125	7.5	683	4	BJ523352	BJ523352 BJ523352	926	118	7.1	2448	3	AK014525
854	125	7.5	2809	3	BC021652	BC021652 Mus muscu	927	118	7.1	6914	9	AY418553
855	124.5	7.5	445	2	BB840170	BB840170 BB840170	928	117.5	7.1	382	7	CN484304
856	124.5	7.5	504	7	N24337	N24337 Yx24f11.r1	929	117.5	7.1	592	5	BP235883
857	124	7.5	572	6	CB268774	CB268774 1007680 H	930	117.5	7.1	932	5	BU438823
858	124	7.5	690	2	BF342700	BF342700 602013653	931	117	7.1	361	9	CG502350
c 859	124	7.5	915	5	BX748376	BX748376 BX748376	932	117	7.1	408	5	BY314612
860	123.5	7.5	800	7	CK028357	CK028357 AGENCOURT	933	117	7.1	457	1	AA305495
861	123	7.4	229	1	AA347305	AA347305 EST53585	934	117	7.1	624	5	BX390371
862	123	7.4	324	7	CN661075	CN661075 A0714A10-	935	117	7.1	639	4	BJ010521
863	123	7.4	371	6	BY767768	BY767768 BY767768	c 936	117	7.1	669	2	AW188198
864	123	7.4	377	5	BY352647	BY352647 BY352647	937	117	7.1	888	5	BU468347
865	123	7.4	381	5	BY164785	BY164785 BY164785	c 938	117	7.1	1204	9	CL104582
866	123	7.4	392	7	R93568	R93568 Yq34e10.r1	c 939	117	7.1	1320	9	CL104648
867	123	7.4	524	5	BQ259314	BQ259314 fz97g05.Y	940	116.5	7.0	558	4	BG896846
868	123	7.4	562	4	BM254875	BM254875 516445 MA	941	116	7.0	444	5	BY155496
869	123	7.4	568	2	BE200989	BE200989 fk84e04.Y	942	115.5	7.0	431	5	BY226451
870	123	7.4	591	5	BQ093786	BQ093786 fz51h01.Y	943	115.5	7.0	588	5	BM949590
871	123	7.4	758	7	CF998236	CF998236 AGENCOURT	c 944	115.5	7.0	1023	1	AL526824
872	123	7.4	780	7	CF348306	CF348306 AGENCOURT	945	115	6.9	375	2	BF175470
873	123	7.4	814	7	CK030082	CK030082 AGENCOURT	c 946	115	6.9	642	9	CE016545
874	123	7.4	822	7	CN510127	CN510127 AGENCOURT	947	115	6.9	707	4	BG770063
875	123	7.4	840	7	CNS06106	CNS06106 AGENCOURT	948	115	6.9	714	4	BG760615
876	123	7.4	868	7	CK018837	CK018837 AGENCOURT	949	114.5	6.9	461	2	BB858159
877	122.5	7.4	567	2	BE016734	BE016734 fk68b07.Y	950	114.5	6.9	722	2	BF529219
878	122.5	7.4	724	4	BI755270	BI755270 603022711	951	114.5	6.9	819	5	BX717115
879	122	7.4	373	5	BY134672	BY134672 BY134672	952	114.5	6.9	1473	9	CL976219
880	122	7.4	497	4	BI326214	BI326214 fr29d09.Y	953	114	6.9	638	2	BB590171
881	122	7.4	513	2	AW343039	AW343039 fi72f05.Y	954	114	6.9	2143	3	AK040503
882	122	7.4	583	5	BP230565	BP230565 BP230565	955	113.5	6.8	385	6	BY770884
883	122	7.4	721	4	BG764304	BG764304 602736181	956	113.5	6.8	584	5	BP250707
884	122	7.4	894	5	BX431647	BX431647 BX431647	957	113	6.8	358	5	BY320846
885	121.5	7.3	436	7	CF371048	CF371048 TgESTzyj6	958	113	6.8	362	5	BY173073

AV704163	AV704163	AV704163
AV671084	AV671084	AV671084
BQ565916	gi47g06.Y	gi47g06.Y
BM254894	516470 MA	516470 MA
BW300493	BW300493	BW300493
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BW301620	BW301620	BW301620
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BF346219	602017695	602017695
BX447415	BX447415	BX447415
BQ132939	fz35g10.Y	fz35g10.Y
BY324757	BY324757	BY324757
BY767081	BY767081	BY767081
BY011815	BY011815	BY011815
AV605303	AV605303	AV605303
CF457207	AGENCOURT	AGENCOURT
BF531009	602072338	602072338
BY330481	BY330481	BY330481
BY772496	BY772496	BY772496
CB140481	K-EST0193	K-EST0193
CD465668	LeukonL_6	LeukonL_6
BP289784	BP289784	BP289784
CK236600	AGENCOURT	AGENCOURT
CA946461	ni06c11.x	ni06c11.x
BY766890	BY766890	BY766890
BY171892	BY171892	BY171892
CB056916	NISC_jj22	NISC_jj22
BF528870	602043330	602043330
BQ876201	AGENCOURT	AGENCOURT
BY165009	BY165009	BY165009
CB153314	K-EST0210	K-EST0210
CB153421	K-EST0210	K-EST0210
BP310145	BP310145	BP310145
BF529489	602043246	602043246
CF456942	AGENCOURT	AGENCOURT
AA374988	EST87204	EST87204
BM798170	K-EST0081	K-EST0081
BQ130854	ij88f05.Y	ij88f05.Y
BG912617	602808055	602808055
AK034871	Mus muscu	Mus muscu
AK014525	Mus muscu	Mus muscu
AY418553	Mus muscu	Mus muscu
CN484304	hw45d01.Y	hw45d01.Y
BP235883	BP235883	BP235883
BU438823	603209228	603209228
CG502350	OST47179	OST47179
BY314612	BY314612	BY314612
AA305495	EST176742	EST176742
BX390371	BX390371	BX390371
BJ010521	BJ010521	BJ010521
AW188198	xj93f03.x	xj93f03.x
BU468347	603372362	603372362
CL104582	ISB1-43D1	ISB1-43D1
CL104648	ISB1-43F1	ISB1-43F1
BG896846	HOA50-1-H	HOA50-1-H
BY155496	BY155496	BY155496
BY226451	BY226451	BY226451
BM949590	UI-M-EGOp	UI-M-EGOp
AL526824	AL526824	AL526824
BF175470	MYE5034 M	MYE5034 M
CE016545	tigr-gs-	tigr-gs-
BG770063	602745189	602745189
BG760615	602717366	602717366
BB858159	BB858159	BB858159
BF529219	602041665	602041665
BX717115	BX717115	BX717115
CL976219	ObIFCC028	ObIFCC028
BB590171	BB590171	BB590171
AK040503	Mus muscu	Mus muscu
BY770884	BY770884	BY770884
BP250707	BP250707	BP250707
BY320846	BY320846	BY320846
BY173073	BY173073	BY173073

959	113	6.8	713	7	CN312058	CN312058	170005318
960	113	6.8	723	5	BU410657	BU410657	603158435
961	113	6.8	7102	9	AY418551	AY418551	Homo sapi
c	962	6.8	611	2	AW593307	hg12h10.x	
	963	6.8	748	7	CK138733	AGENCOURT	
	964	6.8	883	7	CN019296	AGENCOURT	
	965	6.8	372	4	BM743705	K-EST0016	
966	112	6.8	629	7	CN4112529	CN412529	170005325
c	967	6.8	648	6	CB442867	693703	MA
	968	6.8	669	9	DR49F8T	AL976731	Danio rer
969	112	6.8	721	4	B1219897	602936347	
970	112	6.8	961	6	BY717654	BY717654	
971	111.5	6.7	357	5	BY019919	BY019919	
972	111.5	6.7	552	5	BQ472599	HB09A18T	
973	111.5	6.7	570	2	BE233224	139315	MA
c	974	6.7	652	5	BQ211047	UI-R-DY1-	
	975	6.7	680	5	BQ191492	UI-R-DY0-	
c	976	6.7	776	7	CO387930	AGENCOURT	
	977	6.7	783	5	BU479797	BU479797	603841693
978	111.5	6.7	850	9	CR198040	Forward s	
979	111.5	6.7	911	2	BF339458	602039113	
980	111.5	6.7	977	4	B1857845	603388405	
	981	111	360	6	CD471311	LeukoS5.1	
982	111	6.7	433	1	AL589309	DKFZp451H	
c	983	111	585	4	BM812126	fx14f12.y	
	984	110.5	741	4	BG966850	602834350	
985	110.5	6.7	857	9	BX996872	Forward s	
986	110	6.6	630	6	CB044799	NISC_gc06	
c	987	110	584	6	CA414871	UI-H-EZ0-	
	988	110	781	9	AY418556	Mus muscu	
989	110	6.6	794	7	CK458738	923144	MA
	990	110	846	7	CK457667	921992	MA
991	109.5	6.6	640	4	BM637828	170006875	
992	109.5	6.6	672	4	BM577341	170006871	
993	109.5	6.6	694	4	BM620184	170006874	
994	109.5	6.6	697	2	BF528688	602043443	
	995	109.5	891	5	BU484122	603471770	
c	996	109.5	1362	4	B1524385	603052277	
	997	109	491	6	CA353467	624978	NC
998	109	6.6	589	4	BM769767	K-EST0053	
999	109	6.6	748	5	BX882021	BX882021	
c1000	109	6.6	759	5	BQ574012	UI-H-EZ0-	
	1001	109	783	5	BU479065	603843018	
1002	109	6.6	789	9	CL688941	PR1014d_F	
1003	109	6.6	825	6	CA317002	UI-M-FW0-	
1004	109	6.6	877	6	CD253524	AGENCOURT	
1005	109	6.6	913	5	BX929008	BX929008	
1006	108.5	6.5	282	5	BU973380	HB24L19r	
1007	108.5	6.5	308	1	AA296020	EST10183	
c1008	108.5	6.5	1116	1	AL571513	AL571513	
	1009	108	233	2	AW839650	RC6-LT007	
1010	108	6.5	406	1	AA880234	vx39d06.r	
1011	108	6.5	508	4	BI671638	fs50h08.Y	
1012	108	6.5	563	1	AL874048	AL874048	
1013	108	6.5	574	6	CA346211	677050	NC
1014	108	6.5	654	4	BM697249	UI-E-DX0-	
c1015	108	6.5	659	7	CO872953	BovGen_01	
	1016	108	701	6	CD354133	UI-M-GM0-	
1017	108	6.5	756	7	CO738793	SlLE04C21	
1018	108	6.5	775	9	AY418554	Homo sapi	
c1019	108	6.5	778	6	CA411964	UI-H-EZ0-	
	1020	108	824	9	CC551496	CH240_436	
1021	108	6.5	839	7	CV490818	AGENCOURT	
1022	108	6.5	1029	1	AL539422	AL539422	
1023	108	6.5	1042	2	BF527690	602040687	
1024	108	6.5	1161	4	BM467077	BM467077	AGENCOURT
1025	108	6.5	1278	3	CR597704	full-leng	
1026	108	6.5	1383	3	AK017865	Mus muscu	
1027	108	6.5	1433	3	AK016123	Mus muscu	
1028	108	6.5	1630	3	CR605965	full-leng	
1029	107.5	6.5	639	1	AV734145	AV734145	
c1030	107.5	6.5	686	7	CF179894	814933	MA
	1031	107	353	5	BY135479	BY135479	

6.5	107	354	5	BY132505	BY132505	BY132505
6.5	107	355	5	BY312652	BY312652	BY312652
6.5	107	379	6	CB139630	CB139630	K-EST0192
6.5	107	383	6	CD471716	LeukoS6_4	
6.5	107	561	2	BF527166	602039844	
6.5	107	598	5	BU400752	603485038	
6.5	107	680	5	BU249879	603403239	
6.5	107	681	2	BF347167	602020964	
6.5	107	700	4	BG910156	602805533	
6.5	107	716	7	CF536406	UI-M-G10-	
6.5	107	745	7	CF723087	UI-M-GV0-	
6.5	107	763	5	BU410360	603158087	
6.5	107	785	4	BG911337	602807633	
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6.5	107	979	5	BU410188	602955232	
6.5	107	1158	5	BU409151	603158151	
6.5	107	2248	3	AK081264	Mus muscu	
6.4	106.5	362	5	BY173138	BY173138	
6.4	106.5	457	7	CN153458	940572	MA
6.4	106.5	555	6	CD180838	MS1-0027T	
6.4	106.5	755	7	CN155571	942876	MA
6.4	106.5	808	4	BG887918	EST513769	
6.4	106.5	824	5	BU369144	603596992	
6.4	106.5	888	2	BF581527	602101046	
6.4	106.5	1040	5	BQ714183	AGENCOURT	
6.4	106	378	2	AW486980	78517	MAR
6.4	106	681	6	CA138598	SCEQRT202	
6.4	106	848	5	BU410207	603159488	
6.4	106	873	5	BU427310	603232069	
6.4	106	962	2	BF300451	602032375	
6.4	106	1799	2	BF683675	602139925	
6.4	106	2736	9	AY402613	Pan trogl	
6.4	105.5	371	6	CA599565	waw1c.pk0	
6.4	105.5	626	9	CG005573	ZUABW77TV	
6.4	105.5	698	1	AA941503	LD25669.5	
6.4	105.5	791	6	CB998003	AGENCOURT	
6.4	105.5	948	9	BX989560	Reverse s	
6.3	105	372	4	BM757210	K-EST0035	
6.3	105	499	5	BU534446	AGENCOURT	
6.3	105	756	6	CB327411	UI-R-FS0-	
6.3	104.5	444	2	BF389806	UI-R-BS2-	
6.3	104.5	649	6	CD312012	StrPu691.	
6.3	104.5	690	6	CD294616	StrPu691.	
6.3	104.5	699	9	CC745777	ZMMBBb012	
6.3	104.5	714	2	BE454951	HVSMeh009	
6.3	104.5	749	8	BZ637147	OGCCJ87TC	
6.3	104.5	823	7	CK147509	AGENCOURT	
6.3	104.5	955	2	BE039709	OC02G02_O	
6.3	104.5	999	5	BX446538	BX446538	
6.3	1019	5	5	BU523320	AGENCOURT	
6.3	104.5	1253	5	BQ884322	AGENCOURT	
6.3	104	456	7	H93850	yv08a03.r1	
6.3	104	503	5	BU480294	603844970	
6.3	104	663	7	CN368025	170005999	
6.3	104	664	1	AJ637165	AJ637165	
6.3	104	668	1	AJ637187	AJ637187	
6.3	104	893	2	BF303297	602030211	
6.3	104	896	5	BU160160	AGENCOURT	
6.3	104	952	3	CNS08HPM	BX012374	Single re
6.3	104	1070	5	BX359755	BX359755	
6.3	104	7102	9	AY418552	Pan trogl	
6.2	103.5	259	2	BB570771	BB570771	
6.2	103.5	353	5	BY337424	BY337424	
6.2	103.5	357	5	BY131735	BY131735	
6.2	103.5	357	5	BY310928	BY310928	
6.2	103.5	522	5	BW588971	BW588971	
6.2	103.5	657	7	CK494148	rswba0_00	
6.2	103.5	672	5	BQ263492	faa23e07.	
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6.2	103.5	708	2	BE193339	HVSMeh008	

BY132505	BY132505	BY132505
BY312652	BY312652	BY312652
CB139630	CB139630	K-EST0192
CD471716	CD471716	LeukoS6_4
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BU400752	BU400752	603485038
BU249879	BU249879	603403239
BF347167	BF347167	602020964
BG910156	BG910156	602805533
CF536406	CF536406	UI-M-G10-
CF723087	CF723087	UI-M-GV0-
BU410360	BU410360	603158087
BG911337	BG911337	602807633
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BU409087	BU409087	603158870
BU410188	BU410188	602955232
BU409151	BU409151	603158151
AK081264	AK081264	Mus muscu
BY173138	BY173138	BY173138
CN153458	CN153458	940572 MA
CD180838	CD180838	MS1-0027T
CN155571	CN155571	942876 MA
BG887918	BG887918	EST513769
BU369144	BU369144	603596992
BF581527	BF581527	602101046
BQ714183	BQ714183	AGENCOURT
AW486980	AW486980	78517 MAR
CA138598	CA138598	SCEQRT202
BU410207	BU410207	603159488
BU427310	BU427310	603232069
BF300451	BF300451	602032375
BF683675	BF683675	602139925
AY402613	AY402613	Pan trogl
CA599565	CA599565	waw1c.pk0
CG005573	CG005573	ZUABW77TV
AA941503	AA941503	LD25669.5
CB998003	CB998003	AGENCOURT
BX989560	BX989560	Reverse s
BM757210	BM757210	K-EST0035
BU534446	BU534446	AGENCOURT
CB327411	CB327411	UI-R-FS0-
BF389806	BF389806	UI-R-BS2-
CD312012	CD312012	StrPu691.
CD294616	CD294616	StrPu691.
CC745777	CC745777	ZMMBBb012
BE454951	BE454951	HVSMeh009
BZ637147	BZ637147	OGCCJ87TC
CK147509	CK147509	AGENCOURT
BE039709	BE039709	OC02G02_O
BX446538	BX446538	BX446538
BU523320	BU523320	AGENCOURT
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BU480294	BU480294	603844970
CN368025	CN368025	170005999
AJ637165	AJ637165	AJ637165
AJ637187	AJ637187	AJ637187
BF303297	BF303297	602030211
BU160160	BU160160	AGENCOURT
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BX359755	BX359755	BX359755
AY418552	AY418552	Pan trogl
BB570771	BB570771	BB570771
BY337424	BY337424	BY337424
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1117 102.5 6.2 495 6 CA343718 CA343718 673899 NC
1118 102.5 6.2 507 2 AV952258 AV952258
1119 102.5 6.2 558 4 BG637332 BG637332 SD15266.5
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1125 102.5 6.2 611 1 AA736027 AA736027 GM10804.5
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1132 102.5 6.2 633 4 BI585810 BI585810 RH25484.5
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1179 101 6.1 898 4 BI819191 BI819191 603034603
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1242 100 6.0 572 6 CA859090 CA859090 EST633584
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1247 100 6.0 643 6 CA859175 CA859175 EST633669
1248 100 6.0 667 7 CF176921 CF176921 805349_MA
1249 100 6.0 675 6 CA905790 CA905790 PCSC20838
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BI819191 603034603
CK272793 EST718871
BX030163 Single_re
AA285261 PMY0643_K
BE474876 sp69f02.y
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BG791104 sae57d02.
BG725909 sae10f02.
CA937287 sav16f01.
BE022330 sm73e06.y
BF069689 st55c09.y
BG882222 sae97e03.
AW309843 sf25e02.x
AW395001 sh38c03.y
BM525239 sal21d11.
BG405102 sac48b07.
BG790894 sae71c08.
BU081838 sar01c01.
AL909801
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BM525281 sal21h12.
BE022314 sm73c11.y
BE347125 sp35c06.y
BG790733 sae76b09.
BI972116 sag87d09.
BI701219 sag56b06.
BQ080152 san06c12.
AI900434 sc05g01.y
BM527444 sal61h10.
AW234664 sf17h02.y
BQ610888 sap52b03.
BE329814 so70a04.y
CA820060 sau83h12.
BM524565 sal17b11.
BQ610696 sap49e12.
BM522788 sam97e09.
BU084364 sar18e10.
BM087557 500346_MA
CK494474 rswbb0_00
AW704274 sk18h12.y
CA800135 sat78c07.
BU760691 sas57b04.
CD7770921 AGENCOURT
CF806326 psHB008xO
CF806539 psHB013xF
CF806378 psHB010xB
BE661120 7-G11_Gma
CL923142 OA_ABa002
CF806583 psHB013xP
CF069769 EST670490
CA783649 sat51c12.
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CD459095 Fg08_04g0
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CA983981 AGENCOURT
BF133111 601645537
BF580970 602100673
CL445616 ZMMBBb046
CR623874 full-leng
AK090118 Mus_muscu
AW417692 54636_MAR
BM742648 K-EST0015
CA905778 PCS04511
CA859090 EST633584
CF430580 NIT1_3_F0
AI973128 wr47h08.x
CB937331 IpCGJx13
BQ246369 Tae15012F
CA859175 EST633669
CF176921 805349_MA
CA905790 PCSC20838
CA412730 UI-H-EZ0-

c1251	100	6.0	733	1	AJ721352	AJ721352	AJ721352
1252	100	6.0	754	4	BI155142	602903113	BI155142
c1253	100	6.0	885	3	CNS08EMW	Single re	CR703693
1254	100	6.0	1200	3	CR703693	Tetraodon	AK033574
1255	100	6.0	2453	3	AK033574	Mus muscu	CA998062
1256	99.5	6.0	563	6	CA998062	S234X_H10	CB584777
c1257	99.5	6.0	592	6	CB584777	AMGNNUC:U	BI578851
1258	99.5	6.0	598	4	BI578851	RE72782.5	CB582909
c1259	99.5	6.0	598	6	CB582909	AMGNNUC:U	BG576172
c1260	99.5	6.0	616	4	BG576172	602597149	AI950438
c1261	99.5	6.0	652	1	AI950438	wq35d10.x	BE979942
c1262	99.5	6.0	713	2	BE979942	UI-M-BG2-	CD349219
1263	99.5	6.0	722	6	CD349219	UI-M-FY0-	BJ778009
c1264	99.5	6.0	727	4	BJ778009	BJ778009	BJ811105
c1265	99.5	6.0	731	4	BJ811105	BJ811105	EX012540
c1266	99.5	6.0	872	3	CNS08HU8	Single re	EX012539
1267	99.5	6.0	941	3	CNS08HU7	Single re	BF582640
1268	99.5	6.0	972	2	BF582640	602094031	BF527687
1269	99.5	6.0	1116	2	BF527687	602040683	CR690035
1270	99.5	6.0	1148	3	CR690035	Tetraodon	AU281355
1271	99	6.0	447	1	AU281355	AU281355	CB743206
1272	99	6.0	449	6	CB743206	AMGNNUC:N	CA859348
1273	99	6.0	451	6	CA859348	EST633842	BE655314
c1274	99	6.0	507	2	BE655314	UI-M-BH0-	AU265139
1275	99	6.0	532	1	AU265139	AU265139	BG367700
1276	99	6.0	553	4	BG367700	HVSMEI001	BW347955
1277	99	6.0	569	5	BW347955	BW347955	CD369984
c1278	99	6.0	652	6	CD369984	UI-H-FT1-	CO520360
1279	99	6.0	669	7	CO520360	3530_1_13	CD535240
1280	99	6.0	686	6	CD535240	LeukO5_1	CF435137
1281	99	6.0	706	7	CF435137	EST671482	CD193256
c1282	99	6.0	711	6	CD193256	MS1-0078G	CO738752
1283	99	6.0	836	7	CO738752	SLLE04c21	BQ949185
1284	99	6.0	922	5	BQ949185	AGENCOURT	EX034585
1285	99	6.0	1002	3	CNS08YUL	Single re	BM552398
1286	99	6.0	1018	4	BM552398	AGENCOURT	BC024540
1287	99	6.0	1025	3	BC024540	Mus muscu	AY417461
1288	99	6.0	1233	9	AY417461	Mus muscu	AK032047
1289	99	6.0	2777	3	AK032047	Mus muscu	AK032126
1290	99	6.0	4634	3	AK032126	Mus muscu	AA448801
1291	98.5	5.9	419	1	AA448801	zx10g02.r	CN282071
1292	98.5	5.9	441	7	CN282071	170005329	BU764674
1293	98.5	5.9	514	5	BU764674	sas04h12.	CO876287
1294	98.5	5.9	548	7	CO876287	BovGen_04	BF695021
1295	98.5	5.9	582	2	BF695021	602083052	CR455030
c1296	98.5	5.9	585	7	CR455030	CR455030	AI850361
c1297	98.5	5.9	588	1	AI850361	UI-M-BG1-	CD084905
c1298	98.5	5.9	597	6	CD084905	MC1-0013T	BF586321
c1299	98.5	5.9	624	4	BF586321	FM1_27_D1	BG052018
c1300	98.5	5.9	638	4	BG052018	RHI22_7_H	CG868310
1301	98.5	5.9	653	9	CG868310	ZMMBB036	AU205000
1302	98.5	5.9	654	1	AU205000	AU205000	BE211661
1303	98.5	5.9	673	2	BE211661	so64f04.y	CA362129
1304	98.5	5.9	725	6	CA362129	636116_NC	BE195429
1305	98.5	5.9	803	2	BE195429	HVSMEh008	AL203832
c1306	98.5	5.9	865	9	CNS02M9R	Tetraodon	CO920977
1307	98.5	5.9	872	7	CO920977	AGENCOURT	EX053747
1308	98.5	5.9	922	3	CNS09DMV	Single re	BC023911
1309	98.5	5.9	977	3	CNS09KPQ	Single re	BY776755
1310	98.5	5.9	1441	3	BC023911	Mus muscu	BF461115
1311	98	5.9	357	6	BY776755	BY776755	BF461115
1312	98	5.9	487	2	BF461115	UI-M-CGOp	CN748475
1313	98	5.9	518	7	BN748475	SAL_US028	BE956860
c1314	98	5.9	581	2	BE956860	UI-M-BG2-	CD812957
1315	98	5.9	608	6	CD812957	BN15.001B	CD819254
1316	98	5.9	612	6	CD819254	BN20.048F	CK662434
1317	98	5.9	615	7	CK662434	LP22658.5	CD813302
1318	98	5.9	622	6	CD813302	BN15.019C	CD823378
1319	98	5.9	649	6	CD823378	BN25.048J	CD823460
1320	98	5.9	653	6	CD823460	BN25.048N	CD817436
1321	98	5.9	663	6	CD817436	BN20.041O	CD812642
1322	98	5.9	668	6	CD812642	BN10.021N	CD823049
1323	98	5.9	670	6	CD823049	BN25.047H	

1324	98	5.9	672	6	CD824112	CD824112
1325	98	5.9	678	6	CD824097	CD824097
1326	98	5.9	737	6	CD823558	BN25.049C
1327	98	5.9	786	4	BG866550	602785516
c1328	98	5.9	794	6	CB326761	UI-R-D20-
1329	98	5.9	801	6	CD794302	EST665663
1330	98	5.9	835	5	BW467001	BW467001
1331	98	5.9	837	1	AU119529	AU119529
1332	98	5.9	886	5	BX458405	BX458405
1333	98	5.9	889	7	CR582578	CR582578
1334	98	5.9	921	3	CR622952	full-leng
1335	98	5.9	999	4	BG964505	602832171
1336	98	5.9	1134	5	BX396679	BX396679
1337	98	5.9	1343	3	CR675256	Tetraodon
1338	98	5.9	1734	2	BF539725	BF539725
c1339	97.5	5.9	510	5	BW076358	BW076358
1340	97.5	5.9	513	5	BW211988	BW211988
1341	97.5	5.9	558	5	BQ264294	faa49f06.
c1342	97.5	5.9	581	2	AW123236	UI-M-BH2.
1343	97.5	5.9	592	5	BQ309048	MRO-BT450
1344	97.5	5.9	669	9	CR329616	Medicago
1345	97.5	5.9	706	7	CF865978	CF865978
c1346	97.5	5.9	707	4	BM594363	170006874
1347	97.5	5.9	713	5	BU408855	603158450
1348	97.5	5.9	719	2	BE602747	HVSMEh010
1349	97.5	5.9	728	7	CF865730	tric0002xo
1350	97.5	5.9	737	7	CF867310	tric010xn
1351	97.5	5.9	738	7	CF867311	tric010xn
1352	97.5	5.9	742	5	BU427200	603234473
1353	97.5	5.9	751	7	CF867101	tric0009x1
1354	97.5	5.9	751	7	CO892908	BovGen_21
1355	97.5	5.9	761	6	CB895920	tric004xe
1356	97.5	5.9	783	6	CB895647	tric002xo
1357	97.5	5.9	793	6	CB897342	tric010xn
1358	97.5	5.9	794	6	CB897341	tric010xn
1359	97.5	5.9	807	6	CB897114	tric0009x1
1360	97.5	5.9	835	1	AJ816579	AJ816579
1361	97.5	5.9	836	1	AJ816601	AJ816601
c1362	97.5	5.9	870	9	CL968328	OSIFCC040
1363	97.5	5.9	919	5	BQ960367	AGENCOURT
1364	97.5	5.9	956	6	CA077209	SCQAM104
1365	97.5	5.9	977	3	CNS08E4C	Single re
1366	97.5	5.9	995	2	BE602834	HVSMEh010
1367	97	5.9	419	7	CF136553	UI-HF-BN0
c1368	97	5.9	538	4	BJ047143	BJ047143
1369	97	5.9	577	7	CO149290	EST824343
1370	97	5.9	601	2	AV999537	AV999537
c1372	97	5.9	631	4	BG365929	HVSMEI000
1373	97	5.9	648	6	BY705907	BY705907
1374	97	5.9	655	6	CD816943	BN20.040D
1375	97	5.9	665	4	BJ234010	BJ234010
1376	97	5.9	716	2	BE455072	HVSMEh009
1377	97	5.9	719	9	CL912807	OA_ABa001
1378	97	5.9	792	4	BI161403	602865847
c1379	97	5.9	876	4	BG769059	602743307
c1380	97	5.9	930	9	CC690926	OGUKT69TV
1381	97	5.9	1250	3	AK005742	Mus muscu
1382	96.5	5.8	1518	3	CNS0ACU8	Arabidops
1383	96.5	5.8	461	6	CA915486	PCSC06693
c1384	96.5	5.8	506	6	CD820013	BN20.050N
1385	96.5	5.8	517	6	CD201750	MS1-0129T
1386	96.5	5.8	522	5	BW307716	BW307716
1387	96.5	5.8	525	2	BE603039	HVSMEh010
1388	96.5	5.8	534	9	CE558576	tigr-gss-
1389	96.5	5.8	548	5	BQ240384	TaE05018C
c1390	96.5	5.8	569	5	BQ180668	UI-M-EX0-
1391	96.5	5.8	593	9	CL924200	OA_ABa002
1392	96.5	5.8	597	6	CA727188	wdelf.pk0
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1395	96.5	5.8	600	5	BU923862	7072-38_M
1396	96.5	5.8	603	2	AW180870	MGA1041f
	96.5	5.8	633	6	CA325011	UI-M-FY0-

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CB326761	UI-R-D20-
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BW467001	BW467001
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BX458405	BX458405
CR582578	CR582578
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BX396679	BX396679
CR675256	Tetraodon
BF539725	602049936
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CR329616	Medicago
CF865978	CF865978
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BU408855	603158450
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CF867310	tric010xn
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BU427200	603234473
CF867101	tric0009x1
CO892908	BovGen_21
CB895920	tric004xe
CB895647	tric002xo
CB897342	tric010xn
CB897341	tric010xn
CB897114	tric0009x1
AJ816579	AJ816579
AJ816601	AJ816601
CL968328	OSIFCC040
BQ960367	AGENCOURT
CA077209	SCQAM104
EX007720	Single re
BE602834	HVSMEh010
CF136553	UI-HF-BN0
BJ047143	BJ047143
CO149290	EST824343
AV999537	AV999537
BG365929	HVSMEI000
BY705907	BY705907
CD816943	BN20.040D
BJ234010	BJ234010
BE455072	HVSMEh009
CL912807	OA_ABa001
BI161403	602865847
BG769059	602743307
CC690926	OGUKT69TV
AK005742	Mus muscu
BX814927	Arabidops
CA915486	PCSC06693
CD820013	BN

1397	96.5	5.8	640	2	BE427257	PSR6175 I
1398	96.5	5.8	642	4	BI180567	LRH13H9 L
1399	96.5	5.8	659	6	CA226780	SCRLF300
1400	96.5	5.8	659	6	CA734124	wde2f.pk0
1401	96.5	5.8	665	7	CO395103	AGENCOURT
1402	96.5	5.8	686	6	CD052359	EST1618 Z
1403	96.5	5.8	695	5	BX505525	DKFZp686K
1404	96.5	5.8	699	5	BW375317	BW375317
1405	96.5	5.8	743	7	CF488034	POL1 47 H
1406	96.5	5.8	750	6	CA285922	SCEZSD108
1407	96.5	5.8	813	7	CK791708	AGENCOURT
1408	96.5	5.8	844	9	CR076237	Reverse s
1409	96.5	5.8	852	6	CA978035	AGENCOURT
1410	96.5	5.8	860	4	BI951090	HVSME1002
1411	96.5	5.8	926	8	AZ546537	ENTDQ33TF
1412	96.5	5.8	939	4	BG365940	HVSME1000
1413	96.5	5.8	1059	2	BE739579	601556547
1414	96.5	5.8	1120	7	CK208889	
1415	96.5	5.8	1139	5	BQ963823	
1416	96.5	5.8	1229	5	BU511494	
1417	96.5	5.8	1324	3	CR727933	Tetraodon
1418	96.5	5.8	3065	9	AY412874	Mus muscu
1419	96.5	5.8	3463	3	AK036983	Mus muscu
1420	96.5	5.8	3465	3	AK011754	Mus muscu
1421	96.5	5.8	3471	3	AK030619	Mus muscu
1422	96.5	5.8	3779	3	AK050265	Mus muscu
1423	96.5	5.8	3965	3	AK028317	Mus muscu
1424	96.5	5.8	5387	3	AK029840	Mus muscu
1425	96	5.8	421	5	BX321310	BX321310
1426	96	5.8	515	6	CA915483	PCSC05960
1427	96	5.8	516	6	CA915481	PCS04166
1428	96	5.8	518	6	CA915482	PCS05618
1429	96	5.8	532	4	BJ374459	BJ374459
1430	96	5.8	538	6	CA915489	PCSC09473
1431	96	5.8	543	6	CA898165	PCEP04609
1432	96	5.8	571	6	CA898166	PCEP04668
1433	96	5.8	584	6	CA915502	PCSC15104
1434	96	5.8	586	4	BJ412922	BJ412922
1435	96	5.8	598	4	BI170501	RE11976.5
1436	96	5.8	607	2	AW956729	EST368799
1437	96	5.8	612	6	CB054443	NISC_gm04
1438	96	5.8	622	6	CA905789	PCSC19922
1439	96	5.8	648	4	BG765571	602738208
1440	96	5.8	653	6	CA915499	PCSC14281
1441	96	5.8	655	6	CA915504	PCSC15991
1442	96	5.8	658	6	CA915471	PCS00339X
1443	96	5.8	671	6	CD819579	BN20.049H
1444	96	5.8	676	6	CA915497	PCSC14054
1445	96	5.8	696	6	CA915498	PCSC14091
1446	96	5.8	709	7	CF406012	CSECS062F
1447	96	5.8	726	7	CO044877	UI-M-AK0-
1448	96	5.8	727	5	BU384897	603856373
1449	96	5.8	732	5	BW028799	BW028799
1450	96	5.8	746	7	CF343215	AGENCOURT
1451	96	5.8	753	7	CK949012	4074228 B
1452	96	5.8	761	2	BF540045	602050677
1453	96	5.8	780	4	BG165260	602344152
1454	96	5.8	807	9	CG206127	PUIBB90TD
1455	96	5.8	857	7	CR426830	CR426830
1456	96	5.8	857	9	CC979138	ZUAGY20TH
1457	96	5.8	865	9	CG384578	OG3CS02TH
1458	96	5.8	878	7	CR580595	CR580595
1459	96	5.8	885	7	CF590051	AGENCOURT
1460	96	5.8	897	7	CR580597	CR580597
1461	96	5.8	900	5	BQ686613	AGENCOURT
1462	96	5.8	915	7	CF593205	AGENCOURT
1463	96	5.8	926	4	BG108043	602279969
1464	96	5.8	1599	3	CR643518	Tetraodon
1465	95.5	5.8	280	5	BU971558	HB17P20r
1466	95.5	5.8	297	5	BU984229	HF03F16r
1467	95.5	5.8	529	6	CB155742	K-EST0214
1468	95.5	5.8	531	2	BE429535	TAS001.B0
1469	95.5	5.8	537	2	BF193254	244772 MA

CL1470	95.5	5.8	538	6	CD183315	CD183315 MS1-0038U
CL1471	95.5	5.8	544	1	AI816980	AI816980 wJ59a06.x
1472	95.5	5.8	552	4	BI468944	BI468944 sai05c11.
1473	95.5	5.8	554	1	AI425582	AI425582 md19b07.y
1474	95.5	5.8	566	5	BW3334508	BW3334508 BW3334508
1475	95.5	5.8	583	5	BP207390	BP207390 BP207390
1476	95.5	5.8	600	6	CA643574	CA643574 wreln.pk0
1477	95.5	5.8	601	4	BJ058236	BJ058236 BJ058236
CL1478	95.5	5.8	615	6	CD084873	CD084873 MCL-0013T
CL1479	95.5	5.8	651	4	BM267850	BM267850 MEST373-A
CL1480	95.5	5.8	653	9	AG106165	AG106165 Pan trogl
1481	95.5	5.8	663	7	CF333111	CF333111 JMT--01-O
1482	95.5	5.8	666	2	AW917101	AW917101 EST348405
1483	95.5	5.8	689	6	BY706595	BY706595 BY706595
CL1484	95.5	5.8	691	9	CC7112206	CC7112206 OGTAI31TC
CL1485	95.5	5.8	707	8	BZ725029	BZ725029 OEGCG59TM
1486	95.5	5.8	723	9	CC712210	CC712210 OGTAI31TM
1487	95.5	5.8	745	9	CG440326	CG440326 OGVGS61TH
1488	95.5	5.8	780	4	BG368072	BG368072 HVSMEi001
1489	95.5	5.8	798	8	BZ725025	BZ725025 OEGCG59TC
CL1490	95.5	5.8	824	9	CG440337	CG440337 OGVGS61TV
1491	95.5	5.8	830	7	CR292477	CR292477 CR292477
1492	95.5	5.8	839	4	BG914162	BG914162 602810407
1493	95.5	5.8	847	5	BP160594	BP160594 BP160594
1494	95.5	5.8	885	7	CF377799	CF377799 AGENCOURT
1495	95.5	5.8	888	5	BU480079	BU480079 603845914
CL1496	95.5	5.8	891	3	CNS080UPM	BX029222 Single re
1497	95.5	5.8	901	1	AL666250	AL666250 AL666250
1498	95.5	5.8	913	6	CD106887	CD106887 AGENCOURT
CL1499	95.5	5.8	925	9	CG285818	CG285818 OG2BC41TV
1500	95.5	5.8	926	7	CK017503	CK017503 AGENCOURT

ALIGNMENTS

RESULT 1

AL550279

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL550279 1091 bp mRNA linear EST 25-MAR-2004
AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI039YJ06 5-PRIME, mRNA sequence.
AL550279
AL550279.3 GI:45750655
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1091)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272096.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DI039DE03QPlkc=5952.r>.

FEATURES

source

Location/Qualifiers
1..1091
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI039YJ06"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:	
Pred. No.:	5,17e-160
Score:	1657.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	1
Length:	1091
Matches:	322
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-063-670-6 (1-322) x AL550279 (1-1091)

Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	59	ATGGCCAGGTGCTTTCAGCCTGGTGTGGTCTTCACTTCCATCTCGACACGAGGCTCCTG	118
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	119	GTCCAAGSGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG	178
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	179	ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAAGCTAAGGAGGCC	238
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	239	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCT	298
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
Db	299	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCTCTAGGATT	358
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	359	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAAAGTTTCCAGTG	418
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	419	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCATT	478
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	479	CCAGAAATATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACACAAACA	538
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	539	GAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	598
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	599	CCTACTACTACTCCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	658
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	659	TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	718
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	719	GAAAAATAAGCAGCATTCAGAATGAAGCTCTGGGTTTGGAGGTGTCCCCACGGCTCTG	778
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	779	CTAGTGCTTGCTCTCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	838
Qy	261	ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	839	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC	898
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300

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Db 239 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 298
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 299 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTTGATCTCTAGGATT 358
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 359 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTGGAAGGTTCCAGTG 418
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 419 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 478
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 479 CCAGAAATTATCACCCACCAAGATCCCATATTTCAACTCAAACTGCAACACAAACA 538
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db 539 GAATTTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 598
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 599 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGGAGAAAAAATTGATT 658
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 659 TGTGTCACAGAAGTTTTTATGGAACCTAGCACCATGCTACAGAAACTGAACCATTTGTT 718
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
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Db 719 GAAATATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 778
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db 779 CTAGTGCTTGCTCCTCTCTCTTTGTTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 838
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 839 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 898
QY 281 LysValValLysGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db 899 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 958
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 959 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCTTGGAGCT 1018
QY 321 GluVal 322
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Db 1019 GAAGTT 1024

RESULT 3
CR614245
LOCUS full-length cDNA clone CS0DI029YJ09 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
1786 bp mRNA linear HTC 21-JUL-2004
CR614245
ACCESSION
VERSION CR614245.1 GI:50495052
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1786)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue
2 (bases 1 to 1786)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1..1786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YJ09"
/tissue type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.07e-159 Length: 1786
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-063-670-6 (1-322) x CR614245 (1-1786)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 64 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCTG 123
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db 124 GTCCAAGGCTCTTTCGCTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 183
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db 184 ATCACCTTGTGAGCAAAAAGGGCAACCCAGCAGCTGAATTCACAGAAAGCTAAGAGGCC 243
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 244 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGACCAAGTTTGAACAGCCTTGAAAGCT 303
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 304 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTTGATCTCTAGGATT 363
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 364 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 423
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 424 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 483
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 484 CCAGAAATTATCACCCACCAAGATCCCATATTTCAACTCAAACTGCAACACAAACA 543
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db 544 GAATTTATTGTGAGTACAGTACCTACTACGTTGGCATCCCTTACTCTACAATACCTGCC 603
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 604 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCACGGGAGAAAAAATTGATT 663
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 664 TGTGTCACAGAGTTTATGGAACTAGACCATGTCTACAGAACTGAACCATTTGTT 723
QY 221 GluAsnLysAlaIaPheLysAsnGluAlaIaGlyPheGlyGlyValProThrAlaLeu 240
Db 724 GAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 783
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaIaGlyLeuGlyPheCysTyrValLys 260
Db 784 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTTGGATTTCATGTCAAA 843
QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 844 AGGTATGTGAAGGCTTCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 903
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 904 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 963
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 964 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1023
QY 321 GluVal 322
Db 1024 GAAGTT 1029

RESULT 4
CR604450
LOCUS
DEFINITION
full-length cDNA clone CS0DI065YD17 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR604450
VERSION
CR604450.1 GI:50485257
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1797)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 1797)
REFERENCE
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1. .1797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI065YD17"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 1.08e-159 Length: 1797
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0
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Db 94 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 153
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 154 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTATGCAGAATTATGGGG 213
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 214 ATCACCTTGTGAGCAAAAAGGCCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 273
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 274 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 333
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 334 AGCTTTGAAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 393
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 394 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 453
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
Db 454 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACCTGGACTAACTCGTGCAAT 513
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 514 CCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA 573
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 574 GAATTTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACTGCC 633
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 634 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 693
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 694 TGTGTCACAGAAGTTTATTGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 753
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 754 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 813
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaIaGlyLeuGlyPheCysTyrValLys 260
Db 814 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTTGGATTTCATGTCAAA 873
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 874 AGGTATGTGAAGGCTTCCTTTTACAAAACAAGAATCAGCAGAAGGAATGATCGAAACC 933
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 934 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 993
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 994 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1053
QY 321 GluVal 322
Db 1054 GAAGTT 1059
RESULT 5

CR612000
LOCUS
DEFINITION CR612000 1820 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI069YN02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612000
VERSION CR612000.1 GI:50492807
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1820)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1820)
REFERENCE 2 (bases 1 to 1820)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1820
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.1e-159 Length: 1820
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-063-670-6 (1-322) x CR612000 (1-1820)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 98 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTTCACTTCCATCTGGACCAGGCTCCTG 157
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 158 GTCCAAGGCTCTTTTGC GTG CAG AAG AGCTTTCCATCCAGGTGTCATGCAGAAFTATGGGG 217
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 218 ATCACCTTGTGAGCAAAAGCGCAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 277
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 337
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 338 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 397
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 398 AGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTCTCTGTGATTGGAAGGTTCCAGTG 457

QY 121 SerArgGlnPheAlaAlaTyrCystTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 458 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 517
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 518 CCAGAAATTATCACCAAAAGATCCCATATTCACACTCAAACCTGCAACACAAACAACA 577
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 578 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACTGCC 637
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 638 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 697
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 698 TGTGTCACAGAAGTTTATTGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 757
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 758 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCCGCTCTG 817
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db 818 CTAGTGCTTGCTCTCCTCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 877
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 878 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 937
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db 938 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAGAAAAACT 997
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 998 GATAAAACCCCAAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1057
QY 321 GluVal 322
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Db 1058 GAAGTT 1063
RESULT 6
CR597409
LOCUS CR597409 1898 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI067YG15 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR597409
VERSION CR597409.1 GI:50478216
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1898)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1898)
REFERENCE 2 (bases 1 to 1898)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1. .1898

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI067YG15"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-063-670-6 (1-322) x CR597409 (1-1898)

QY

1

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db

190

ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGAGGCTCCTG 249

QY

21

ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db

250

GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 309

QY

41

IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db

310

ATCACCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 369

QY

61

CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db

370

TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 429

QY

81

SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db

430

AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTGGTCATCTCTAGGATT 489

QY

101

SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db

490

AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCCTGATTTGGAAGGTTCCAGTG 549

QY

121

SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db

550

AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTAACTCGTGCAAT 609

QY

141

ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db

610

CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 669

QY

161

GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db

670

GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 729

QY

181

ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db

730

CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 789

QY

201

CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db

790

TGTGTACAGAAAGTTTTTATGGAAGACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 849

QY

221

GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db

850

GAAAAATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 909

QY

241

LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db

910

CTAGTGTCTGCTCTCTCTCTCTTTGGTGCTGCAGCTGGTCTTTGGATTTTGTATGTCAA 969

FEATURES

source

division of Invitrogen.

Location/Qualifiers

1. .1898

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI067YG15"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-063-670-6 (1-322) x CR614790 (1-1911)

QY

1

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db

171

ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 230

QY

21

ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db

231

GTCCAAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 290

QY

261

ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db

970

AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAAAGAAATGATCGAAACC 1029

QY

281

LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db

1030

AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1089

QY

301

AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db

1090

GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1149

QY

321

GluVal 322

Db

1150

GAAGTT 1155

RESULT 7

CR614790

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .1911

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI018YG12"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-063-670-6 (1-322) x CR614790 (1-1911)

QY

1

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db

171

ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 230

QY

21

ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db

231

GTCCAAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 290


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QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 730 CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 789
|||||
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||
Db 790 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 849
|||||
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
Db 850 GAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 909
|||||
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 910 CTAGTGCTTGCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTGCTATGTCAA 969
|||||
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 970 AGGTATGTGAAGGCTTCCCTTTTACAAACACAGAATCAGCAGAAGGAATGATCGAAACC 1029
|||||
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 1030 AAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1089
|||||
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||
Db 1090 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1149
|||||
QY 321 GluVal 322
|||||
Db 1150 GAAGTT 1155

RESULT 9
CR605021
LOCUS
DEFINITION full-length cDNA clone CS0DI029YM23 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR605021
VERSION CR605021.1 GI:50485828
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1945)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1945)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source 1..1945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YM23"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
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Alignment Scores:
Pred. No.: 1.21e-159 Length: 1945
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-063-670-6 (1-322) x CR605021 (1-1945)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 222 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 281
|||||
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 282 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTGATGCAGAAATTAATGGGG 341
|||||
QY 41 IleThrIeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 342 ATCACCTTGTGAGCAAAAAGCGAAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 401
|||||
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 402 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 461
|||||
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 462 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTCACTCTTAGGATT 521
|||||
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 522 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGTCTTGATTGGGAAGGTTCCAGTG 581
|||||
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 582 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCATT 641
|||||
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 642 CCAGAAATATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAAACAACA 701
|||||
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 702 GAATTTATGTGAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 761
|||||
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 762 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTGATT 821
|||||
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||
Db 822 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 881
|||||
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
Db 882 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 941
|||||
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 942 CTAGTGCTTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCATATGTCAA 1001
|||||
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 1002 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGAGAAATGATCGAAACC 1061
|||||
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 1062 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATAGGAATCAAAGAAACT 1121
|||||
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||
Db 1122 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1181
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QY      321 GluVal 322
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Db      1182 GAAGTT 1187

RESULT 10
AL550621
LOCUS
DEFINITION AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI058YN14 5-PRIME, mRNA sequence.
ACCESSION AL550621
VERSION AL550621.3 GI:45750987
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1045)
JOURNAL Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31272438.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI058DG07QP1&c=5952.r.
FEATURES
source
1..1045
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI058YN14"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 6.33e-145 Length: 1045
Score: 1510.50 Matches: 296
Percent Similarity: 95.53% Conservative: 3
Best Local Similarity: 94.57% Mismatches: 11
Query Match: 91.16% Indels: 3
DB: 1 Gaps: 1

US-10-063-670-6 (1-322) x AL550621 (1-1045)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
      |||||
Db      94 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCACTCCATCTGGACCACGAGGCTCCTG 153

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||||
Db      154 GTCCAAGGCTCTTTGCGTCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 213

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||||
Db      214 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 273

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||||
Db      274 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT 333
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QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||||
Db      334 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 393

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||||
Db      394 AGCCCAAAACCCCAAGTGTGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 453

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||||
Db      454 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTAACTCGTGCAAT 513

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||||
Db      514 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAACAACA 573

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      ::|||
Db      574 AAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 633

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||||
Db      634 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 693

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
      |||||
Db      694 TGTGTCAAGAGTCTTTATGGAAACTAGACCATGTCTACAGAAACTGAACCATTTGTT 753

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||||
Db      754 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTGGAGGTGTCCCACGGCTCTG 813

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||||
Db      814 CTAGTGCTTGCTCTCTCTCTCTTTGGTGCTGCAGCTGGTCTTTGGATTTTGTATGTCAAA 873

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||||
Db      874 AGGTATGTGAAGGCTTCCCTTTTACAAAMAARAATCAGCMGAAGGAAATGWTGADACC 933

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||
Db      934 MAAGTAGTAAAGCAGGAGAGGCAATGATWASCACCCCYAATGAGGGATCAAAGAAAAACT 993

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThr 313
      |||||
Db      994 GWTAAAACCCCG-----AAGAGTCCAGAGTCMAGC 1023

RESULT 11
AL552299
LOCUS
DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION AL552299.3 GI:45857087
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 965)
JOURNAL Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31274114.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
```

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DI069DG01QPl&c=5952.r.

FEATURES

source
1. .965
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.89e-142 Length: 965
Score: 1480.00 Matches: 288
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.32% Indels: 0
DB: 1 Gaps: 0

US-10-063-670-6 (1-322) x AL5522299 (1-965)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
DB 94 ATGGCCAGGTGCTTCAGCTGGTGTGTTCTCTCACTCCATCTGGACCACGAGGCTCCTG 153

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
DB 154 GTCCAAGGCTCTTTGCGTCGAGAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 213

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
DB 214 ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAGAAGCTAAGGAGCC 273

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
DB 274 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 333

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
DB 334 AGCTTTGAACCTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTGCATCTCTAGGATT 393

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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DB 394 AGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 453

QY 121 SerArgGlnPheAlaAlaTyrcysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
DB 454 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 513

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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DB 514 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 573

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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DB 574 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 633

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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DB 634 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 693

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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DB 694 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 753

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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DB 754 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTG 813

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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DB 814 CTAGTGCTTGCTCTCCTCTCTCTTCTTGGTGTGCAGCTGGTCTTGGATTTGCTATGTCAA 873

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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DB 874 AGGTATGTGAAGGCCTTCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 933

QY 281 LysValValLysGluGluLysAla 288
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DB 934 AAAGTAGTAAAGGAGGAGGAGGCC 957

RESULT 12

AL546669
LOCUS AL546669 Homo sapiens 1090 bp mRNA linear EST 25-MAR-2004
DEFINITION clone CS0DI029YJ09 5-PRIME, mRNA sequence.
ACCESSION AL546669
VERSION AL546669.3 GI:45747132
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1090)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31268502.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DI029CE05QP1&c=5952.r.

FEATURES

source
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/clone="CS0DI029YJ09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 2.17e-141 Length: 1090
Score: 1476.50 Matches: 302
Percent Similarity: 96.24% Conservative: 5
Best Local Similarity: 94.67% Mismatches: 11
Query Match: 89.11% Indels: 5
DB: 1 Gaps: 1

US-10-063-670-6 (1-322) x AL546669 (1-1090)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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DB 64 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 123

Db	511	GAATTTATTGTAGTACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	
Db	571	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	
Db	631	TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	
Db	691	GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTG	
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	
Db	751	CTAGTGCTTGCTCTCTCTCTTTTGGTGTGTCAGCTGGTCTTGGATTTTGCTATGTCAA	
QY	261	ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	
Db	811	AGGTATGTGAAGGC-TTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACC	
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	
Db	870	AAGTA-GTAAAGDGGAGAGGGC-AATGATAGCAA-CCTAATGAGGA-TCAAAGAAAACT	
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu	
Db	926	GATAAAACC---AGAAGAGTCAAGAGTCCAGCAAACTACGKG---CGATGCTKGCAG	
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CR599107			
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DEFINITION			
ACCESSION			
VERSION			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:			

Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
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QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
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QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	247	GTCCAAGGCTCTTTGCGTGCAGAAAGGTAGTTCTTTTATAGCTCTGTGTTCTTTCAGCA	306
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	307	ATAGAGATG-----AAGCCTTCTAATCAT-----	330
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	331	-----	333
QY	81	Ser-PheGluThrCys-----SerTyrGlyTrpValGlyAspGlyPheValVa	96
Db	334	TCTGTTCAACTAGTGTGATTCTTTTACAGCTATGGCTGGGTGGAGATGGATTCTGTGGT	393
QY	96	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTr	116
Db	394	CATCTCTAGGATTAGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTGTCCTGATTTG	453
QY	116	pLysValProValSerArgGlnPheAlaAlaTyrCystyrAsnSerSerAspThrTrpTh	136
Db	454	GAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGAC	513
QY	136	rAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAl	156
Db	514	TAACTCGTGCATTCCAGAAATTATCACCACCAAAAGATCCCATAATTCAAACACTCAA	573
QY	156	aThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSe	176
Db	574	AACACAAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCCTTACTC	633
QY	176	rThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgAr	196
Db	634	TACAATACCTGCCCTACTACTACTCTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAG	693
QY	196	gLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluTh	216
Db	694	AAAAAATTGATTGTGTACAGAAAGTTTATTATGGAAACTAGCACCATGTCTACAGAAAC	753
QY	216	rGluPropheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyVa	236
Db	754	TGAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGT	813
QY	236	lProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPh	256
Db	814	CCCCACGGCTCTGTAGTGTGCTTCTCTCTCTCTTCTTTTGGTGTGCTGAGCTGGTCTTGGATT	873
QY	256	eCystyrValLysArgTyrValLysAlaPhePropheThrAsnLysAsnGlnLysGl	276
Db	874	TTGCTATGTCAAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGA	933
QY	276	uMetIleGluThrLysValLysGluLysAlaAsnAspSerAsnProAsnGluGl	296
Db	934	AATGATCGAAACCAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGA	993
QY	296	uSerLysLysThrAspLysAsnProGluGluSerLysSerProSerLysThrThrValAr	316
Db	994	ATCAAAAGAAAACTGATAAAAAACCCCAAGAGTCCCAAGAGTCCCAAGCAAAACTACCGTGCG	1053
QY	316	gCysLeuGluAlaGluVal	322

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RESULT 15
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AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI077YJ17 5-PRIME, mRNA sequence.
ACCESSION
AL553858
VERSION
AL553858.3 GI:45858623
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 946)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
AUTHORS
Full-length cDNA libraries and normalization
TITLE
Unpublished (2001)
JOURNAL
COMMENT
On Feb 15, 2001 this sequence version replaced gi:31275672.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI077CE09QPl&c=5952.r.
FEATURES
source
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/clone="CSODI077YJ17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.07e-125 Length: 946
Score: 1323.50 Matches: 272
Percent Similarity: 98.55% Conservative: 0
Best Local Similarity: 98.55% Mismatches: 4
Query Match: 79.87% Indels: 4
DB: 1 Gaps: 0
US-10-063-670-6 (1-322) x AL553858 (1-946)
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Search completed: October 8, 2005, 22:44:56
Job time : 4259.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 22:45:22 ; Search time 860.456 Seconds
 (without alignments)
 2606.386 Million cell updates/sec

Perfect score: 1657
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Searched: 8443130 seqs, 3482420727 residues

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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1657	100.0	2029	15	US-10-079-111-2	Sequence 2, Appli
2	1657	100.0	2029	22	US-10-820-474A-198	Sequence 198, App
5	1657	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
94	1657	100.0	2372	15	US-10-223-085-31	Sequence 31, Appl
95	1657	100.0	2372	15	US-10-223-084-31	Sequence 31, Appl
96	1657	100.0	2372	15	US-10-223-088-31	Sequence 31, Appl
97	1657	100.0	2372	15	US-10-223-090-31	Sequence 31, Appl
99	1657	100.0	2372	15	US-10-223-087-31	Sequence 31, Appl
102	1657	100.0	2372	15	US-10-223-083-31	Sequence 31, Appl
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108	1657	100.0	2372	16	US-10-299-976-200	Sequence 200, App
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235	1657	100.0	2372	17	US-10-425-447-200	Sequence 200, App
236	1657	100.0	2372	18	US-10-081-056-31	Sequence 31, Appl
238	1657	100.0	2372	19	US-10-215-371-200	Sequence 200, App
239	1657	100.0	2372	19	US-10-771-187-200	Sequence 200, App
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241	1657	100.0	2372	21	US-10-963-467-200	Sequence 200, App
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243	1657	100.0	2372	22	US-10-797-366-200	Sequence 200, App
244	1657	100.0	2372	22	US-10-970-823-200	Sequence 200, App
245	1657	100.0	2436	22	US-10-756-149-3836	Sequence 3836, Ap
246	1657	100.0	2667	20	US-10-723-860-7823	Sequence 7823, Ap
247	1654	99.8	2324	18	US-10-276-774-999	Sequence 999, App
248	1651	99.6	2313	15	US-10-291-634-1	Sequence 1, Appli
249	1651	99.6	2369	17	US-10-264-237-1260	Sequence 1260, Ap
250	1638	98.9	2313	20	US-10-723-860-3908	Sequence 3908, Ap
251	1638	98.9	2313	22	US-10-287-436A-215	Sequence 215, App
252	1511.5	91.2	1127	17	US-10-138-588-1	Sequence 1, Appli
253	1103	66.6	1896	10	US-09-866-050A-595	Sequence 595, App
254	1103	66.6	1896	14	US-10-152-661-595	Sequence 595, App
255	673	40.6	411	10	US-09-918-995-8107	Sequence 8107, Ap
256	627.5	37.9	531	21	US-10-696-639-2768	Sequence 2768, Ap
257	595.5	35.9	559	15	US-10-079-111-3	Sequence 3, Appli
258	440	26.6	486	10	US-09-918-995-10116	Sequence 10116, A
259	386	23.3	279	15	US-10-079-111-4	Sequence 4, Appli
260	354	21.4	492	15	US-10-291-634-12	Sequence 12, Appl
261	349	21.1	466	15	US-10-291-634-13	Sequence 13, Appl
262	306	18.5	469	9	US-09-864-761-2325	Sequence 2325, Ap
263	286.5	17.3	498	15	US-10-291-634-15	Sequence 15, Appl
264	281.5	17.0	457	9	US-09-864-761-15431	Sequence 15431, A
265	233.5	14.1	1089	22	US-10-024-607-25	Sequence 25, Appl
266	231	13.9	2747	9	US-09-917-800A-1588	Sequence 1588, Ap
267	231	13.9	2747	22	US-10-024-607-7	Sequence 7, Appli
268	229.5	13.9	1177	22	US-10-024-607-24	Sequence 24, Appl
269	223	13.5	1992	15	US-10-101-510-436	Sequence 436, App
270	222	13.4	141	9	US-09-864-761-19060	Sequence 19060, A
271	215	13.0	1354	11	US-09-836-544-31	Sequence 31, Appl
272	213	12.9	1794	15	US-10-007-926A-376	Sequence 376, App
273	213	12.9	1794	21	US-10-482-029-254	Sequence 254, App
274	213	12.9	1794	21	US-10-852-335A-36	Sequence 36; Appl
275	213	12.9	1794	21	US-10-956-157-443	Sequence 443, App
276	213	12.9	4335	19	US-10-741-601-56	Sequence 56, Appl
277	213	12.9	4335	21	US-10-741-600-220	Sequence 220, App
278	212	12.8	1083	22	US-10-505-769-1	Sequence 1, Appli
279	212	12.8	1981	15	US-10-084-817-180	Sequence 180, App
280	212	12.8	4365	16	US-10-247-671-72	Sequence 72, Appl
281	212	12.8	5165	10	US-09-814-353-20099	Sequence 20099, A

282	210	12.7	1297	18	US-10-641-643-876	Sequence 876, App	355	145.5	8.8	7840	18	US-10-634-574-15	Sequence 15, Appl
283	210	12.7	1297	22	US-10-024-607-23	Sequence 23, Appl	c 356	145	8.8	351	14	US-10-060-036-880	Sequence 880, App
284	209.5	12.6	5452	19	US-10-741-601-57	Sequence 57, Appl	357	145	8.8	466	17	US-10-242-535A-58386	Sequence 58386, A
285	209.5	12.6	5452	21	US-10-741-600-219	Sequence 219, App	358	145	8.8	466	18	US-10-085-783A-58386	Sequence 58386, A
286	205.5	12.4	3091	22	US-10-783-271-86	Sequence 86, Appl	359	145	8.8	1414	9	US-09-799-118-1	Sequence 1, Appli
287	205.5	12.4	3091	22	US-10-287-436A-196	Sequence 196, App	360	143.5	8.7	396	10	US-09-918-995-17767	Sequence 17767, A
288	205.5	12.4	3091	22	US-10-287-436A-807	Sequence 807, App	361	143.5	8.7	431	18	US-10-424-599-106015	Sequence 106015,
289	205.5	12.4	4633	19	US-10-741-601-61	Sequence 61, Appl	362	142.5	8.6	8444	17	US-10-028-248A-1	Sequence 1, Appli
290	205.5	12.4	4633	21	US-10-741-600-224	Sequence 224, App	363	142.5	8.6	8444	17	US-10-107-782-1	Sequence 1, Appli
291	205	12.4	4723	19	US-10-741-601-53	Sequence 53, Appl	364	141.5	8.5	3625	22	US-10-667-723-17	Sequence 17, Appl
292	205	12.4	4723	21	US-10-741-600-217	Sequence 217, App	365	141.5	8.5	8495	17	US-10-028-248A-3	Sequence 3, Appli
293	204.5	12.3	3083	21	US-10-690-880-18	Sequence 18, Appl	366	141.5	8.5	8495	17	US-10-107-782-3	Sequence 3, Appli
294	203	12.3	3091	21	US-10-741-600-226	Sequence 226, App	367	138.5	8.4	1411	9	US-09-765-231A-44	Sequence 44, Appl
295	203	12.3	5468	19	US-10-741-601-60	Sequence 60, Appl	368	137	8.3	3260	17	US-10-028-248A-210	Sequence 210, App
296	203	12.3	5468	21	US-10-741-600-225	Sequence 225, App	369	137	8.3	3260	17	US-10-107-782-210	Sequence 210, App
297	203	12.3	5674	19	US-10-741-601-54	Sequence 54, Appl	370	137	8.3	4576	9	US-09-842-930A-24	Sequence 24, Appl
298	203	12.3	5674	21	US-10-741-600-218	Sequence 218, App	371	137	8.3	4576	21	US-10-990-844-24	Sequence 24, Appl
299	203	12.3	5739	19	US-10-741-601-55	Sequence 55, Appl	372	137	8.3	4642	15	US-10-133-172-3	Sequence 3, Appli
300	203	12.3	5739	21	US-10-741-600-221	Sequence 221, App	373	137	8.3	4962	15	US-10-133-172-19	Sequence 19, Appl
301	199.5	12.0	1737	21	US-10-505-680-474	Sequence 474, App	374	136	8.2	4706	9	US-09-842-930A-1	Sequence 1, Appli
302	199.5	12.0	1737	22	US-10-024-607-22	Sequence 22, Appl	375	136	8.2	4706	15	US-10-133-172-1	Sequence 1, Appli
303	199.5	12.0	1824	21	US-10-486-226-1	Sequence 1, Appli	376	136	8.2	4706	21	US-10-990-844-1	Sequence 1, Appli
304	199.5	12.0	2100	15	US-10-012-969C-1	Sequence 1, Appli	377	135.5	8.2	3153	10	US-09-759-130B-343	Sequence 343, App
305	199.5	12.0	2100	22	US-10-505-769-3	Sequence 3, Appli	378	135.5	8.2	3153	14	US-10-189-123-73	Sequence 73, Appl
306	199.5	12.0	2308	11	US-09-836-544-33	Sequence 33, Appl	379	135.5	8.2	3153	16	US-10-188-495-73	Sequence 73, Appl
307	199.5	12.0	2316	10	US-09-983-000A-15	GENERAL INFORMATI	380	135.5	8.2	3153	19	US-10-741-790-343	Sequence 343, App
308	199.5	12.0	2316	21	US-10-652-981-15	Sequence 15, Appl	381	132.5	8.0	2160	17	US-10-104-047-1824	Sequence 1824, Ap
309	199.5	12.0	4674	9	US-09-974-298-22	Sequence 22, Appl	382	131.5	7.9	2652	14	US-10-195-970-4	Sequence 4, Appli
310	199.5	12.0	4674	10	US-09-971-429B-51	Sequence 51, Appl	383	131.5	7.9	2652	17	US-10-453-420-4	Sequence 4, Appli
311	199.5	12.0	4674	15	US-10-084-817-181	Sequence 181, App	384	131	7.9	2013	10	US-09-759-130B-330	Sequence 330, App
312	199.5	12.0	4675	22	US-10-765-700-97	Sequence 97, Appl	385	131	7.9	2013	14	US-10-189-123-60	Sequence 60, Appl
313	198	11.9	5053	19	US-10-741-601-52	Sequence 52, Appl	386	131	7.9	2013	16	US-10-188-495-60	Sequence 60, Appl
314	198	11.9	5053	21	US-10-741-600-216	Sequence 216, App	387	131	7.9	2013	19	US-10-741-790-330	Sequence 330, App
315	197	11.9	2097	22	US-10-505-769-5	Sequence 5, Appli	388	131	7.9	2730	10	US-09-759-130B-329	Sequence 329, App
316	197	11.9	2263	21	US-10-956-157-4279	Sequence 4279, Ap	389	131	7.9	2730	14	US-10-189-123-59	Sequence 59, Appl
317	197	11.9	2265	21	US-10-696-639-33	Sequence 33, Appl	390	131	7.9	2730	16	US-10-188-495-59	Sequence 59, Appl
318	197	11.9	2387	19	US-10-648-593-41	Sequence 41, Appl	391	131	7.9	2730	19	US-10-741-790-329	Sequence 329, App
319	197	11.9	2387	22	US-10-783-271-67	Sequence 67, Appl	392	131	7.9	3438	18	US-10-312-352-60	Sequence 60, Appl
320	197	11.9	2905	13	US-10-044-090-495	Sequence 495, App	401	131	7.9	3476	14	US-10-237-535-51	Sequence 51, Appl
321	197	11.9	3474	9	US-09-981-353-9	Sequence 9, Appli	410	131	7.9	3476	21	US-10-936-626-11	Sequence 11, Appl
322	197	11.9	4874	19	US-10-741-601-59	Sequence 59, Appl	501	131	7.9	3476	21	US-10-938-061-11	Sequence 11, Appl
323	197	11.9	4874	21	US-10-741-600-223	Sequence 223, App	502	131	7.9	3476	21	US-10-195-970-5	Sequence 5, Appli
324	196	11.8	1735	21	US-10-956-157-4281	Sequence 4281, Ap	503	130.5	7.9	2652	14	US-10-453-420-5	Sequence 5, Appli
325	191.5	11.6	339	21	US-10-487-620-5	Sequence 5, Appli	504	130.5	7.9	2652	17	US-10-956-157-562	Sequence 1320, Ap
326	191	11.5	1760	21	US-10-956-157-4280	Sequence 4280, Ap	505	130.5	7.9	3681	17	US-10-264-237-1320	Sequence 562, App
327	190	11.5	336	21	US-10-487-620-1	Sequence 1, Appli	506	130.5	7.9	7137	21	US-10-956-157-562	Sequence 235, App
328	188	11.3	336	21	US-10-487-620-7	Sequence 7, Appli	507	130.5	7.9	7137	22	US-10-287-436A-235	Sequence 1, Appli
329	186	11.2	336	21	US-10-487-620-9	Sequence 9, Appli	508	130	7.8	7879	21	US-10-497-991-1	Sequence 5739, Ap
330	184	11.1	336	21	US-10-487-620-11	Sequence 11, Appl	509	130	7.8	8038	20	US-10-723-860-5739	Sequence 2294, Ap
331	182	11.0	336	21	US-10-487-620-3	Sequence 3, Appli	510	127.5	7.7	488	10	US-09-918-995-2294	Sequence 328, App
332	180.5	10.9	2764	22	US-10-450-763-17058	Sequence 17058, A	511	127.5	7.7	1365	13	US-10-098-841-328	Sequence 328, App
333	179	10.8	2273	22	US-10-450-763-17062	Sequence 17062, A	512	127.5	7.7	1925	20	US-10-723-860-6530	Sequence 6530, Ap
334	170	10.3	106	9	US-09-864-761-31946	Sequence 31946, A	515	127.5	7.7	1985	9	US-09-905-291A-212	Sequence 212, App
335	166.5	10.0	399	10	US-09-918-995-36412	Sequence 36412, A	1045	127.5	7.7	1985	16	US-10-174-587-27	Sequence 27, Appl
c 336	165	10.0	820	15	US-10-079-111-5	Sequence 5, Appli	1080	127.5	7.7	1985	16	US-10-299-976-212	Sequence 212, App
337	164.5	9.9	444	21	US-10-696-639-1827	Sequence 1827, Ap	1082	127.5	7.7	1985	16	US-10-299-937-212	Sequence 212, App
338	158	9.5	549	15	US-10-101-510-85	Sequence 85, Appl	1092	127.5	7.7	1985	17	US-10-298-993-212	Sequence 212, App
339	158	9.5	549	21	US-10-505-680-476	Sequence 476, App	1097	127.5	7.7	1985	17	US-10-448-923-212	Sequence 212, App
340	153.5	9.3	270	10	US-09-927-463-7	Sequence 7, Appli	1098	127.5	7.7	1985	17	US-10-449-656-212	Sequence 212, App
341	153.5	9.3	270	20	US-10-837-671-7	Sequence 7, Appli	1099	127.5	7.7	1985	17	US-10-448-713-212	Sequence 212, App
342	151	9.1	2863	17	US-10-104-047-610	Sequence 610, App	1101	127.5	7.7	1985	17	US-10-425-447-212	Sequence 212, App
343	148.5	9.0	425	10	US-09-918-995-35733	Sequence 35733, A	1109	127.5	7.7	1985	19	US-10-215-371-212	Sequence 212, App
c 344	148.5	9.0	836	13	US-10-027-632-148987	Sequence 35733, A	1110	127.5	7.7	1985	19	US-10-771-187-212	Sequence 212, App
c 345	148.5	9.0	836	17	US-10-027-632-148987	Sequence 148987,	1111	127.5	7.7	1985	21	US-10-963-467-212	Sequence 212, App
346	145.5	8.8	1144	13	US-10-044-090-446	Sequence 446, App	1112	127.5	7.7	1985	21	US-10-978-255-212	Sequence 212, App
347	145.5	8.8	1144	16	US-10-247-671-124	Sequence 124, App	1113	127.5	7.7	1985	22	US-10-797-366-212	Sequence 212, App
348	145.5	8.8	1422	17	US-10-295-027-291	Sequence 291, App	1117	127.5	7.7	1985	22	US-10-970-823-212	Sequence 212, App
349	145.5	8.8	1430	17	US-10-295-027-1020	Sequence 1020, Ap	1118	127.5	7.7	2558	10	US-09-983-000A-13	GENERAL INFORMATI
350	145.5	8.8	1440	20	US-10-723-860-4325	Sequence 4325, Ap	1119	127.5	7.7	2558	21	US-10-652-981-13	Sequence 13, Appl
351	145.5	8.8	1440	21	US-10-278-698-280	Sequence 280, App	1120	127.5	7.7	2558	21	US-10-936-626-12	Sequence 12, Appl
352	145.5	8.8	1440	21	US-10-278-698-794	Sequence 794, App	1121	127.5	7.7	2558	21	US-10-938-061-12	Sequence 12, Appl
c 353	145.5	8.8	1461	20	US-10-723-860-8161	Sequence 8161, Ap	1122	127.5	7.7	2558	21	US-10-852-335A-1	Sequence 1, Appli
354	145.5	8.8	1728	13	US-10-044-090-445	Sequence 445, App	1123	127.5	7.7	2878	17	US-10-453-420-7	Sequence 7, Appli

1124	127.5	7.7	2878	17	US-10-295-027-259	Sequence 259, App	1197	111	6.7	1720	10	US-09-148-545-53	Sequence 53, Appl
1125	127	7.7	2465	9	US-09-917-800A-500	Sequence 500, App	1198	111	6.7	1720	22	US-10-979-111-53	Sequence 53, Appl
1126	126.5	7.6	2753	10	US-09-774-639-12	Sequence 12, App1	1199	110.5	6.7	434	18	US-10-424-599-41662	Sequence 41662, A
1127	126.5	7.6	2753	10	US-09-969-730-13	Sequence 13, App1	1200	110	6.6	1308	10	US-09-948-820-14	Sequence 14, Appl
1128	126.5	7.6	2753	17	US-10-621-363-13	Sequence 13, App1	1201	110	6.6	1308	20	US-10-613-076-14	Sequence 14, Appl
1129	126	7.6	201	21	US-10-741-600-7000	Sequence 7000, Ap	1202	110	6.6	2343	19	US-10-437-963-46994	Sequence 46994, A
1130	125	7.5	201	19	US-10-741-601-1565	Sequence 1565, Ap	1203	109.5	6.6	1466	19	US-10-437-963-51867	Sequence 51867, A
1131	125	7.5	201	19	US-10-741-601-1575	Sequence 1575, Ap	1204	109	6.6	6310	9	US-09-795-651-45	Sequence 45, Appl
1132	125	7.5	201	19	US-10-741-601-1591	Sequence 1591, Ap	1205	109	6.6	6310	15	US-10-241-220-26	Sequence 26, Appl
1133	125	7.5	201	19	US-10-741-601-1608	Sequence 1608, Ap	1206	109	6.6	6310	17	US-10-295-027-261	Sequence 261, App
1134	125	7.5	201	19	US-10-741-601-1617	Sequence 1617, Ap	1207	109	6.6	6310	20	US-10-872-992-26	Sequence 26, Appl
1135	125	7.5	201	19	US-10-741-601-1632	Sequence 1632, Ap	1208	109	6.6	6310	20	US-10-872-991-26	Sequence 26, Appl
1136	125	7.5	201	19	US-10-741-601-1648	Sequence 1648, Ap	1209	109	6.6	6310	22	US-10-698-190-17	Sequence 17, Appl
1137	125	7.5	201	19	US-10-741-601-1663	Sequence 1663, Ap	1210	108	6.5	1492	18	US-10-120-907A-27	Sequence 27, Appl
1138	125	7.5	201	19	US-10-741-601-1672	Sequence 1672, Ap	1211	108	6.5	1492	21	US-10-956-157-722	Sequence 722, App
1139	125	7.5	201	21	US-10-741-600-6878	Sequence 6878, Ap	1212	108	6.5	1640	9	US-09-764-853-249	Sequence 249, App
1140	125	7.5	201	21	US-10-741-600-6888	Sequence 6888, Ap	1213	108	6.5	1640	14	US-10-091-438-33	Sequence 33, Appl
1141	125	7.5	201	21	US-10-741-600-6904	Sequence 6904, Ap	1214	108	6.5	1641	9	US-09-764-853-420	Sequence 420, App
1142	125	7.5	201	21	US-10-741-600-6920	Sequence 6920, Ap	1215	108	6.5	1641	14	US-10-091-438-94	Sequence 94, Appl
1143	125	7.5	201	21	US-10-741-600-6927	Sequence 6927, Ap	c1216	108	6.5	1790	15	US-10-311-455-2348	Sequence 2348, Ap
1144	125	7.5	201	21	US-10-741-600-6943	Sequence 6943, Ap	1217	108	6.5	1957	18	US-10-120-907A-2	Sequence 2, Appli
1145	125	7.5	201	21	US-10-741-600-6961	Sequence 6961, Ap	1218	108	6.5	1957	18	US-10-120-907A-6	Sequence 6, Appli
1146	125	7.5	201	21	US-10-741-600-6971	Sequence 6971, Ap	1219	108	6.5	1957	18	US-10-120-907A-8	Sequence 8, Appli
1147	125	7.5	201	21	US-10-741-600-6986	Sequence 6986, Ap	1220	108	6.5	1957	18	US-10-120-907A-10	Sequence 10, Appl
1148	125	7.5	1414	11	US-09-968-007A-208	Sequence 208, App	1221	108	6.5	1957	18	US-10-120-907A-12	Sequence 12, Appl
1149	125	7.5	1414	17	US-10-133-937-18	Sequence 18, App1	1222	108	6.5	1957	18	US-10-120-907A-14	Sequence 14, Appl
1150	125	7.5	1414	17	US-10-295-027-293	Sequence 293, App	1223	108	6.5	1957	18	US-10-120-907A-16	Sequence 16, Appl
1151	125	7.5	1414	17	US-10-159-563-18	Sequence 18, App1	1224	108	6.5	1957	18	US-10-120-907A-18	Sequence 18, Appl
1152	125	7.5	1414	19	US-10-755-889-117	Sequence 117, App	1225	108	6.5	1957	18	US-10-120-907A-20	Sequence 20, Appl
1153	125	7.5	1414	21	US-10-278-698-79	Sequence 79, App1	1226	108	6.5	1957	18	US-10-120-907A-26	Sequence 26, Appl
1154	125	7.5	1414	21	US-10-278-698-593	Sequence 593, App	1227	108	6.5	1957	18	US-10-120-907A-26	Sequence 26, Appl
1155	125	7.5	1414	21	US-10-843-641A-6678	Sequence 6678, Ap	1228	108	6.5	1957	18	US-10-120-907A-62	Sequence 62, Appl
1156	124	7.5	474	10	US-09-918-995-32777	Sequence 32777, A	1229	108	6.5	2166	18	US-10-120-907A-4	Sequence 4, Appli
c1157	121.5	7.3	2694	14	US-10-050-704-40	Sequence 40, Appl	1230	108	6.5	2166	18	US-10-120-907A-61	Sequence 61, Appl
c1158	121.5	7.3	2694	19	US-10-798-512-40	Sequence 40, App1	1231	108	6.5	2166	18	US-10-120-907A-63	Sequence 63, Appl
1159	121	7.3	1587	21	US-10-314-942-19	Sequence 19, App1	1232	108	6.5	2538	20	US-10-723-860-6874	Sequence 6874, Ap
1160	118.5	7.2	1783	18	US-10-112-944-153	Sequence 153, App	1233	107.5	6.5	6279	24	US-11-097-143-8399	Sequence 8399, Ap
1161	118.5	7.2	11185	9	US-09-880-107-3311	Sequence 3311, Ap	c1234	107	6.5	600	22	US-10-972-079-42389	Sequence 42389, A
1162	118.5	7.2	11185	10	US-09-873-367C-1039	Sequence 1039, Ap	1235	107	6.5	1851	17	US-10-257-021-144	Sequence 144, App
1163	118.5	7.2	11185	16	US-10-269-909-12	Sequence 12, App1	1236	107	6.5	2011	22	US-10-667-723-3	Sequence 3, Appli
1164	118.5	7.2	11185	17	US-10-159-563-100	Sequence 100, App	1237	107	6.5	3858	19	US-10-741-601-58	Sequence 58, Appl
1165	118.5	7.2	11185	21	US-10-843-641A-1039	Sequence 1039, Ap	1238	107	6.5	3858	21	US-10-741-600-222	Sequence 222, App
1166	118.5	7.2	11185	22	US-10-631-467-315	Sequence 315, App	1239	107	6.5	4614	9	US-09-801-368-103	Sequence 103, App
1167	118.5	7.2	11214	17	US-10-062-674-1454	Sequence 1454, Ap	1240	107	6.5	4614	17	US-10-369-493-25085	Sequence 25085, A
1168	118.5	7.2	12319	16	US-10-240-965-240	Sequence 240, App	1241	107	6.5	5259	22	US-10-698-190-23	Sequence 23, Appl
1169	118	7.1	1627	19	US-10-437-963-14608	Sequence 14608, A	1242	107	6.5	5388	24	US-11-097-143-36209	Sequence 36209, A
1170	118	7.1	7375	22	US-10-631-467-1178	Sequence 1178, Ap	1243	107	6.5	5864	21	US-10-324-035-16	Sequence 16, Appl
1171	115.5	7.0	410	10	US-09-918-995-16642	Sequence 16642, A	c1244	107	6.5	7782	24	US-11-097-143-36208	Sequence 36208, A
1172	115.5	7.0	7291	21	US-10-741-600-348	Sequence 348, App	c1245	106.5	6.4	1174	20	US-10-363-345A-29077	Sequence 29077, A
1173	115.5	7.0	7358	21	US-10-741-600-350	Sequence 350, App	1246	106.5	6.4	1174	20	US-10-363-345A-29078	Sequence 29078, A
1174	115.5	7.0	12553	21	US-10-741-600-344	Sequence 344, App	c1247	106.5	6.4	1174	21	US-10-363-483A-29077	Sequence 29077, A
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1176	114.5	6.9	5191	18	US-10-152-319A-1928	Sequence 1928, Ap	1249	106.5	6.4	1482	17	US-10-305-720-230	Sequence 230, App
1177	114.5	6.9	5191	22	US-10-698-190-21	Sequence 21, App1	1250	106	6.4	201	19	US-10-741-601-1560	Sequence 1560, Ap
1178	114	6.9	8924	24	US-11-097-143-8398	Sequence 8398, Ap	1251	106	6.4	201	19	US-10-741-601-1570	Sequence 1570, Ap
1179	113	6.8	2087	20	US-10-270-253-1	Sequence 1, Appli	1252	106	6.4	201	19	US-10-741-601-1580	Sequence 1580, Ap
1180	113	6.8	4330	21	US-10-741-600-346	Sequence 346, App	1253	106	6.4	201	19	US-10-741-601-1597	Sequence 1597, Ap
1181	113	6.8	7182	14	US-10-116-802-207	Sequence 207, App	1254	106	6.4	201	19	US-10-741-601-1614	Sequence 1614, Ap
1182	113	6.8	8224	15	US-10-177-293-89	Sequence 89, App1	1255	106	6.4	201	19	US-10-741-601-1622	Sequence 1622, Ap
1183	113	6.8	8224	18	US-10-240-425-1534	Sequence 1534, Ap	1256	106	6.4	201	19	US-10-741-601-1643	Sequence 1643, Ap
1184	113	6.8	8224	21	US-10-482-029-193	Sequence 193, App	1257	106	6.4	201	19	US-10-741-601-1653	Sequence 1653, Ap
1185	113	6.8	8224	21	US-10-852-335A-90	Sequence 90, App1	1258	106	6.4	201	19	US-10-741-601-1667	Sequence 1667, Ap
1186	113	6.8	9592	21	US-10-741-600-349	Sequence 349, App	1259	106	6.4	201	21	US-10-741-600-6873	Sequence 6873, Ap
1187	113	6.8	9647	14	US-10-198-846-11006	Sequence 11006, A	1260	106	6.4	201	21	US-10-741-600-6883	Sequence 6883, Ap
1188	113	6.8	9659	21	US-10-741-600-347	Sequence 347, App	1261	106	6.4	201	21	US-10-741-600-6893	Sequence 6893, Ap
c1189	113	6.8	12644	14	US-10-161-803-45	Sequence 45, App1	1262	106	6.4	201	21	US-10-741-600-6910	Sequence 6910, Ap
1190	112.5	6.8	972	9	US-09-764-853-156	Sequence 156, App	1263	106	6.4	201	21	US-10-741-600-6924	Sequence 6924, Ap
1191	112	6.8	340	17	US-10-242-535A-49165	Sequence 49165, A	1264	106	6.4	201	21	US-10-741-600-6932	Sequence 6932, Ap
1192	112	6.8	340	18	US-10-085-783A-49165	Sequence 49165, A	1265	106	6.4	201	21	US-10-741-600-6956	Sequence 6956, Ap
1193	112	6.8	105550	19	US-10-741-601-5630	Sequence 5630, Ap	1266	106	6.4	201	21	US-10-741-600-6966	Sequence 6966, Ap
1194	112	6.8	105550	21	US-10-741-600-17620	Sequence 17620, A	1267	106	6.4	201	21	US-10-741-600-6976	Sequence 6976, Ap
1195	111.5	6.7	1209	17	US-10-282-122A-28025	Sequence 28025, A	1268	106	6.4	201	21	US-10-741-600-6998	Sequence 6998, Ap
1196	111	6.7	1720	9	US-09-981-876-53	Sequence 53, App1	1269	106	6.4	1534	19	US-10-437-963-14663	Sequence 14663, A

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1271	105	6.3	36604	21	US-10-494-364-5	Sequence 5, Appli	c1344	97.5	5.9	814	13	US-10-027-632-168872	Sequence 168872,
1272	104.5	6.3	538	16	US-10-029-386-12772	Sequence 12772, A	c1345	97.5	5.9	814	13	US-10-027-632-168873	Sequence 168873,
1273	104.5	6.3	172569	13	US-10-087-192-1366	Sequence 1366, Ap	c1346	97.5	5.9	814	17	US-10-027-632-168872	Sequence 168872,
1274	104	6.3	484	17	US-10-172-118-144	Sequence 144, App	c1347	97.5	5.9	814	17	US-10-027-632-168873	Sequence 168873,
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1276	104	6.3	4767	11	US-09-973-278-731	Sequence 731, App	c1349	97.5	5.9	1195	20	US-10-363-345A-12097	Sequence 12097, A
1277	104	6.3	4768	11	US-09-973-278-730	Sequence 730, App	1350	97.5	5.9	1195	20	US-10-363-345A-12098	Sequence 12098, A
c1278	104	6.3	5430	14	US-10-091-438-279	Sequence 279, App	c1351	97.5	5.9	1195	21	US-10-363-483A-12097	Sequence 12097, A
1279	104	6.3	86941	18	US-10-461-194-2	Sequence 2, Appli	1352	97.5	5.9	1195	21	US-10-363-483A-12098	Sequence 12098, A
c1280	103.5	6.2	8433	24	US-11-097-143-37921	Sequence 37921, A	1353	97.5	5.9	1767	17	US-10-376-947-9	Sequence 9, Appli
c1281	103	6.2	1962	9	US-09-981-876-111	Sequence 111, App	1354	97.5	5.9	16878	22	US-10-915-740A-62	Sequence 62, Appli
c1282	103	6.2	1962	10	US-09-148-545-111	Sequence 111, App	c1355	97.5	5.9	2242716	22	US-10-915-740A-1068	Sequence 1068, Ap
c1283	103	6.2	1962	22	US-10-979-111-111	Sequence 111, App	1356	97	5.9	304	17	US-10-242-535A-18394	Sequence 18394, A
1284	103	6.2	3146	18	US-10-424-599-70993	Sequence 70993, A	1357	97	5.9	304	18	US-10-085-783A-18394	Sequence 18394, A
1285	103	6.2	35167	19	US-10-645-794-5	Sequence 5, Appli	1358	97	5.9	334	16	US-10-029-386-26472	Sequence 26472, A
1286	103	6.2	35167	19	US-10-645-883A-1	Sequence 1, Appli	c1359	97	5.9	738	20	US-10-363-345A-20561	Sequence 20561, A
1287	102.5	6.2	1341	19	US-10-481-179-43	Sequence 43, Appl	1360	97	5.9	738	21	US-10-363-483A-20561	Sequence 20561, A
1288	102.5	6.2	1372	24	US-11-097-143-24752	Sequence 24752, A	1362	97	5.9	738	21	US-10-363-483A-20562	Sequence 20562, A
c1289	102.5	6.2	4492	24	US-11-097-143-24751	Sequence 24751, A	c1363	97	5.9	1347	20	US-10-363-345A-28465	Sequence 28465, A
1290	102	6.2	201	19	US-10-741-601-11249	Sequence 11249, A	1364	97	5.9	1347	20	US-10-363-345A-28466	Sequence 28466, A
1291	102	6.2	201	21	US-10-741-600-28711	Sequence 28711, A	1364	97	5.9	1347	21	US-10-363-483A-28465	Sequence 28465, A
c1292	102	6.2	593	22	US-10-972-079-42390	Sequence 42390, A	c1365	97	5.9	1347	21	US-10-363-483A-28466	Sequence 28466, A
1293	102	6.2	1323	18	US-10-425-114-13953	Sequence 13953, A	1366	97	5.9	1347	21	US-10-363-483A-28466	Sequence 28466, A
1294	102	6.2	2256646	19	US-10-470-565-1	Sequence 1, Appli	c1367	97	5.9	2085	17	US-10-282-122A-18735	Sequence 18735, A
c1295	101.5	6.1	1276	20	US-10-363-345A-27853	Sequence 27853, A	1368	97	5.9	2751	17	US-10-094-749-624	Sequence 624, App
1296	101.5	6.1	1276	20	US-10-363-345A-27854	Sequence 27854, A	1369	97	5.9	1230025	17	US-10-289-762-1	Sequence 1, Appli
c1297	101.5	6.1	1276	21	US-10-363-483A-27853	Sequence 27853, A	1370	96.5	5.8	1381	18	US-10-424-599-56763	Sequence 56763, A
1298	101.5	6.1	1276	21	US-10-363-483A-27854	Sequence 27854, A	c1371	96.5	5.8	3161	24	US-11-097-143-39133	Sequence 39133, A
1299	101.5	6.1	2607	10	US-09-991-053-11	Sequence 11, Appl	1372	96.5	5.8	3684	17	US-10-369-493-38962	Sequence 38962, A
1300	101.5	6.1	2607	10	US-09-957-187-11	Sequence 11, Appl	1373	96	5.8	2070	19	US-10-437-963-93608	Sequence 93608, A
1301	101.5	6.1	2607	24	US-11-058-709-11	Sequence 11, Appl	1374	96	5.8	2238	15	US-10-156-761-3861	Sequence 3861, Ap
c1302	101.5	6.1	6112	15	US-10-172-086-34	Sequence 34, Appl	c1375	96	5.8	4562	17	US-10-398-221-3772	Sequence 3772, Ap
c1303	101.5	6.1	6112	19	US-10-311-507-66	Sequence 66, Appl	1376	96	5.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
c1304	101.5	6.1	6112	20	US-10-480-846-34	Sequence 34, Appl	1377	95.5	5.8	1131	9	US-09-801-368-205	Sequence 205, App
c1305	101	6.1	871	18	US-10-425-114-4960	Sequence 4960, Ap	1378	95.5	5.8	1798	21	US-10-868-381-95	Sequence 95, Appl
c1306	101	6.1	2313	17	US-10-243-552-681	Sequence 681, App	c1379	95.5	5.8	2404	19	US-10-437-963-16578	Sequence 16578, A
1307	101	6.1	3175	17	US-10-104-047-1332	Sequence 1332, Ap	1380	95.5	5.8	3654	19	US-10-437-963-81408	Sequence 81408, A
1308	101	6.1	4011	18	US-10-263-929-49	Sequence 49, Appl	c1381	95.5	5.8	4435	18	US-10-701-844-1	Sequence 1, Appli
c1309	101	6.1	33302	21	US-10-741-600-17866	Sequence 17866, A	1382	95.5	5.8	4435	19	US-10-766-711-1	Sequence 1, Appli
1310	101	6.1	72691	21	US-10-741-600-17712	Sequence 17712, A	1383	95.5	5.8	4435	21	US-10-931-779-1	Sequence 1, Appli
1311	100.5	6.1	1209	18	US-10-257-174-23	Sequence 23, Appl	c1384	95.5	5.8	12781	18	US-10-221-714A-107	Sequence 107, App
c1312	100.5	6.1	1241	19	US-10-729-807-33	Sequence 33, Appl	c1385	95.5	5.8	12781	18	US-10-240-589C-37	Sequence 37, Appl
1313	100.5	6.1	1475	17	US-10-343-953-1	Sequence 1, Appli	1386	95.5	5.8	65140	19	US-10-203-295-1	Sequence 1, Appli
c1314	100.5	6.1	1612	19	US-10-437-963-92511	Sequence 92511, A	1387	95	5.7	1380	21	US-10-203-295-35	Sequence 35, Appl
c1315	100.5	6.1	1825	19	US-10-437-963-93701	Sequence 93701, A	1388	95	5.8	125401	19	US-10-203-295-1	Sequence 10, Appl
1316	100.5	6.1	2865	18	US-10-424-599-24135	Sequence 24135, A	1389	95	5.7	1380	21	US-10-847-918-10	Sequence 301, App
1317	100.5	6.1	4140	24	US-11-097-143-33611	Sequence 33611, A	c1390	95	5.7	1440	17	US-10-295-027-301	Sequence 3, Appli
1318	100.5	6.1	7596	16	US-10-004-113-57	Sequence 57, Appl	1391	95	5.7	1440	17	US-10-282-122A-17996	Sequence 17996, A
1319	100.5	6.1	8064	16	US-10-004-113-56	Sequence 56, Appl	c1392	95	5.7	2211	24	US-11-097-143-16301	Sequence 16301, A
c1320	100	6.0	618	22	US-10-756-149-3813	Sequence 3813, Ap	1393	95	5.7	2304	17	US-10-104-047-1752	Sequence 1752, Ap
c1321	100	6.0	645	20	US-10-363-345A-695	Sequence 695, App	c1394	95	5.7	2450	19	US-10-437-963-2523	Sequence 2523, Ap
1322	100	6.0	645	20	US-10-363-345A-696	Sequence 696, App	c1395	95	5.7	2803	17	US-10-094-749-1364	Sequence 1364, Ap
c1323	100	6.0	645	21	US-10-363-483A-695	Sequence 695, App	c1396	95	5.7	4678	24	US-11-097-143-16300	Sequence 16300, A
1324	100	6.0	645	21	US-10-363-483A-696	Sequence 696, App	c1397	95	5.7	109519	11	US-09-758-759-1	Sequence 1, Appli
c1325	100	6.0	1386	17	US-10-369-493-31591	Sequence 31591, A	c1398	94.5	5.7	632	19	US-10-437-963-40393	Sequence 40393, A
1326	100	6.0	9487	19	US-10-788-792-43	Sequence 43, Appl	1399	94.5	5.7	936	18	US-10-425-114-23361	Sequence 23361, A
1327	99.5	6.0	2622	20	US-10-481-698-48	Sequence 48, Appl	c1400	94.5	5.7	1026	20	US-10-363-345A-7171	Sequence 7171, Ap
1328	99	6.0	438	17	US-10-242-535A-7137	Sequence 7137, Ap	1401	94.5	5.7	1026	20	US-10-363-345A-7172	Sequence 7172, Ap
1329	99	6.0	438	18	US-10-085-783A-7137	Sequence 7137, Ap	c1402	94.5	5.7	1026	21	US-10-363-483A-7171	Sequence 7171, Ap
1330	99	6.0	2663	19	US-10-437-963-24639	Sequence 24639, A	1403	94.5	5.7	1026	21	US-10-363-483A-7172	Sequence 7172, Ap
1331	99	6.0	4287	24	US-11-097-143-37922	Sequence 37922, A	c1404	94.5	5.7	1032	20	US-10-363-345A-22309	Sequence 22309, A
1332	98.5	5.9	3381	24	US-11-097-143-35951	Sequence 35951, A	1405	94.5	5.7	1032	20	US-10-363-345A-22310	Sequence 22310, A
1333	98.5	5.9	3799	17	US-10-369-493-26821	Sequence 26821, A	c1406	94.5	5.7	1032	21	US-10-363-483A-22309	Sequence 22309, A
1334	98.5	5.9	5381	24	US-11-097-143-35950	Sequence 35950, A	1407	94.5	5.7	1032	21	US-10-363-483A-22310	Sequence 22310, A
1335	98.5	5.9	267156	11	US-09-968-007A-427	Sequence 427, App	1408	94.5	5.7	1484	20	US-10-425-115-24588	Sequence 24588, A
1336	98.5	5.9	267156	21	US-10-843-641A-6897	Sequence 6897, Ap	1409	94.5	5.7	1608	14	US-10-218-743-20	Sequence 20, Appl
1337	98.5	5.9	684973	9	US-09-263-959-1	Sequence 1, Appli	c1410	94.5	5.7	1608	14	US-10-218-743-22	Sequence 22, Appl
1338	98	5.9	6353	24	US-11-097-143-8000	Sequence 8000, Ap	1411	94.5	5.7	1665	14	US-10-218-743-17	Sequence 17, Appl
1339	98	5.9	8429	24	US-11-097-143-7999	Sequence 7999, Ap	c1412	94.5	5.7	1665	14	US-10-218-743-19	Sequence 19, Appl
c1340	97.5	5.9	585	20	US-10-363-345A-38453	Sequence 38453, A	c1413	94.5	5.7	1751	19	US-10-437-963-9763	Sequence 9763, Ap
1341	97.5	5.9	585	20	US-10-363-345A-38454	Sequence 38454, A	1414	94.5	5.7	1752	14	US-10-218-743-14	Sequence 14, Appl
c1342	97.5	5.9	585	21	US-10-363-483A-38453	Sequence 38453, A	c1415	94.5	5.7	1752	14	US-10-218-743-16	Sequence 16, Appl

1416	94.5	5.7	2901	9	US-09-801-368-371	Sequence 371, App	1489	93	5.6	5931	24	US-11-097-143-35048	Sequence 35048, A
1417	94.5	5.7	3401	19	US-10-451-467A-51	Sequence 51, Appl	cl1490	93	5.6	7931	24	US-11-097-143-35047	Sequence 35047, A
1418	94.5	5.7	4209	18	US-10-188-832-63	Sequence 63, Appl	cl1491	92.5	5.6	647	20	US-10-363-345A-739	Sequence 739, App
1419	94	5.7	819	18	US-10-425-114-4720	Sequence 4720, Ap	1492	92.5	5.6	647	20	US-10-363-345A-740	Sequence 740, App
1420	94	5.7	819	18	US-10-425-114-4725	Sequence 4725, Ap	cl1493	92.5	5.6	647	21	US-10-363-483A-739	Sequence 739, App
1421	94	5.7	1019	19	US-10-437-963-1250	Sequence 1250, Ap	1494	92.5	5.6	647	21	US-10-363-483A-740	Sequence 740, App
cl1422	94	5.7	1199	20	US-10-363-345A-33551	Sequence 33551, A	1495	92.5	5.6	757	20	US-10-425-115-13921	Sequence 13921, A
1423	94	5.7	1199	20	US-10-363-345A-33552	Sequence 33552, A	cl1496	92.5	5.6	778	18	US-10-424-599-74482	Sequence 74482, A
cl1424	94	5.7	1199	21	US-10-363-483A-33551	Sequence 33551, A	cl1497	92.5	5.6	907	19	US-10-767-795-843	Sequence 843, App
1425	94	5.7	1199	21	US-10-363-483A-33552	Sequence 33552, A	1498	92.5	5.6	918	20	US-10-425-115-36844	Sequence 36844, A
1426	94	5.7	1482	19	US-10-437-963-36908	Sequence 36908, A	1499	92.5	5.6	1099	15	US-10-188-012-28	Sequence 28, Appl
1427	94	5.7	1494	19	US-10-767-701-11834	Sequence 11834, A	1500	92.5	5.6	1099	21	US-10-663-497-28	Sequence 28, Appl
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1429	94	5.7	1946	24	US-11-097-143-15890	Sequence 15890, A							
cl1430	94	5.7	3946	14	US-10-270-333-76	Sequence 76, Appl							
cl1431	94	5.7	3946	24	US-11-097-143-15889	Sequence 15889, A							
cl1432	94	5.7	4404	19	US-10-437-963-92371	Sequence 92371, A							
cl1433	94	5.7	6047	15	US-10-311-455-1432	Sequence 1432, Ap							
1434	94	5.7	6313	24	US-11-097-143-32032	Sequence 32032, A							
cl1435	93.5	5.6	739	20	US-10-363-345A-38979	Sequence 38979, A							
1436	93.5	5.6	739	20	US-10-363-345A-38980	Sequence 38980, A							
cl1437	93.5	5.6	739	21	US-10-363-483A-38979	Sequence 38979, A							
1438	93.5	5.6	739	21	US-10-363-483A-38980	Sequence 38980, A							
1439	93.5	5.6	1017	21	US-10-391-939A-1	Sequence 1, Appli							
1440	93.5	5.6	1017	21	US-10-391-939A-27	Sequence 27, Appl							
1441	93.5	5.6	1080	15	US-10-188-012-18	Sequence 18, Appl							
1442	93.5	5.6	1080	15	US-10-188-012-20	Sequence 20, Appl							
1443	93.5	5.6	1080	21	US-10-663-497-18	Sequence 18, Appl							
1444	93.5	5.6	1080	21	US-10-663-497-20	Sequence 20, Appl							
1445	93.5	5.6	1082	22	US-10-450-763-1501	Sequence 1501, Ap							
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1447	93.5	5.6	1185	20	US-10-363-345A-38982	Sequence 38982, A							
cl1448	93.5	5.6	1185	21	US-10-363-483A-38981	Sequence 38981, A							
1449	93.5	5.6	1185	21	US-10-363-483A-38982	Sequence 38982, A							
cl1450	93.5	5.6	1190	20	US-10-363-345A-31167	Sequence 31167, A							
1451	93.5	5.6	1190	20	US-10-363-345A-31168	Sequence 31168, A							
cl1452	93.5	5.6	1190	21	US-10-363-483A-31167	Sequence 31167, A							
1453	93.5	5.6	1190	21	US-10-363-483A-31168	Sequence 31168, A							
1454	93.5	5.6	1241	19	US-10-437-963-29771	Sequence 29771, A							
1455	93.5	5.6	1242	22	US-10-450-763-7914	Sequence 7914, Ap							
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cl1457	93.5	5.6	7348	18	US-10-221-714A-58	Sequence 58, Appl							
cl1458	93.5	5.6	7568	22	US-10-450-763-16627	Sequence 16627, A							
cl1459	93.5	5.6	9161	17	US-10-133-937-37	Sequence 37, Appl							
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cl1462	93.5	5.6	9220	20	US-10-357-930-24403	Sequence 24403, A							
cl1463	93.5	5.6	9220	20	US-10-357-930-25254	Sequence 25254, A							
cl1464	93.5	5.6	9416	19	US-10-755-889-614	Sequence 614, App							
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1470	93	5.6	631	21	US-10-487-901-853	Sequence 853, App							
1471	93	5.6	971	21	US-10-487-901-4021	Sequence 4021, Ap							
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1486	93	5.6	2472	20	US-10-425-115-37319	Sequence 37319, A							
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106	93	5.6	2032	3	US-09-241-581B-5	Sequence 5, Appli	179	88	5.3	1470	3	US-09-292-225-40	Sequence 40, Appl
107	93	5.6	2032	3	US-08-265-428-5	Sequence 5, Appli	c 180	88	5.3	1470	3	US-09-292-225-42	Sequence 42, Appl
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110	92.5	5.6	2096	4	US-09-799-451-592	Sequence 592, App	183	88	5.3	1621	3	US-09-292-225-34	Sequence 34, Appl
111	92.5	5.6	4104	4	US-09-614-221A-146	Sequence 146, App	c 184	88	5.3	1621	3	US-09-292-225-36	Sequence 36, Appl
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113	92	5.6	606	4	US-09-270-767-16050	Sequence 16050, A	c 186	88	5.3	2035	3	US-09-894-698-1	Sequence 1, Appli
114	92	5.6	9960	3	US-08-822-586-46	Sequence 46, Appl	187	88	5.3	2035	3	US-09-894-698-3	Sequence 3, Appli
115	92	5.6	15268	4	US-09-902-540-1142	Sequence 1142, Ap	188	88	5.3	2055	4	US-09-248-796A-6094	Sequence 6094, Ap
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118	91	5.5	1474	4	US-09-270-767-12852	Sequence 12852, A	191	87.5	5.3	1896	3	US-09-620-412C-324	Sequence 324, App
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c 120	91	5.5	2028	4	US-09-107-532A-1973	Sequence 1973, Ap	193	87.5	5.3	2322	4	US-09-476-242-19	Sequence 19, Appl
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c 122	91	5.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli	195	87.5	5.3	2541	4	US-09-476-242-12	Sequence 12, Appl
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128	90.5	5.5	4104	4	US-09-614-221A-44	Sequence 44, Appl	201	87.5	5.3	5275	3	US-08-484-719B-1	Sequence 1, Appli
c 129	90.5	5.5	4167	4	US-09-252-991A-3666	Sequence 3666, Ap	202	87.5	5.3	5275	3	US-08-484-159-1	Sequence 1, Appli
130	90	5.4	1060	4	US-09-050-739-13	Sequence 13, Appl	203	87	5.3	790	4	US-09-771-357-97	Sequence 97, Appl
131	90	5.4	1638	4	US-09-248-796A-10381	Sequence 10381, A	204	87	5.3	790	4	US-10-059-579A-97	Sequence 97, Appl
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133	90	5.4	3168	3	US-09-165-239A-3	Sequence 3, Appli	206	87	5.3	867	4	US-09-216-393B-342	Sequence 342, App
c 134	90	5.4	23673	3	US-09-773-816-1	Sequence 1, Appli	207	87	5.3	1397	4	US-09-216-393B-343	Sequence 343, App
135	90	5.4	77100	4	US-09-949-016-16418	Sequence 16418, A	c 208	87	5.3	1397	4	US-09-216-393B-345	Sequence 345, App
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c 142	90	5.4	234288	4	US-09-949-016-17272	Sequence 17272, A	215	87	5.3	12687	1	US-08-676-169-1	Sequence 647, App
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151	89.5	5.4	2535	4	US-09-476-242-13	Sequence 13, Appl	224	86.5	5.2	1387	4	US-09-475-515-34	Sequence 34, Appl
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155	89	5.4	2422	4	US-09-949-016-3654	Sequence 3654, Ap	c 228	86.5	5.2	1785	3	US-09-669-974-6	Sequence 6, Appli
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c 157	89	5.4	4647	4	US-09-252-991A-5730	Sequence 5730, Ap	230	86.5	5.2	1836	4	US-09-475-515-41	Sequence 41, Appl
c 158	89	5.4	4808	4	US-09-774-528-19	Sequence 19, Appl	231	86.5	5.2	1836	4	US-09-475-515-44	Sequence 44, Appl
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c 160	89	5.4	116966	4	US-09-949-016-17557	Sequence 17557, A	233	86.5	5.2	1929	4	US-09-252-991A-10474	Sequence 10474, A
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162	88.5	5.3	1356	4	US-09-252-991A-630	Sequence 630, App	235	86.5	5.2	1944	4	US-09-475-515-38	Sequence 38, Appl
163	88.5	5.3	2473	2	US-08-540-804-3	Sequence 3, Appli	236	86.5	5.2	1944	4	US-09-475-515-40	Sequence 40, Appl
164	88.5	5.3	2473	2	US-08-218-265-3	Sequence 3, Appli	237	86.5	5.2	1944	4	US-09-475-515-43	Sequence 43, Appl
165	88.5	5.3	2473	3	US-08-521-872-3	Sequence 3, Appli	238	86.5	5.2	1944	4	US-09-475-515-46	Sequence 46, Appl
166	88.5	5.3	2473	3	US-08-590-399-3	Sequence 3, Appli	239	86.5	5.2	2025	4	US-09-475-515-36	Sequence 36, Appl
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c 168	88.5	5.3	3150	4	US-09-252-991A-727	Sequence 727, App	241	86.5	5.2	2025	4	US-09-475-515-42	Sequence 42, Appl
c 169	88.5	5.3	3263	4	US-09-949-016-1018	Sequence 1018, Ap	242	86.5	5.2	2025	4	US-09-475-515-45	Sequence 45, Appl
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c 171	88.5	5.3	29103	4	US-09-902-540-1236	Sequence 1236, App	244	86.5	5.2	2298	4	US-09-476-242-24	Sequence 24, Appl
172	88	5.3	786	4	US-09-248-796A-176	Sequence 176, App	245	86.5	5.2	2298	4	US-09-476-242-3	Sequence 3, Appli
c 173	88	5.3	1123	3	US-09-894-698-9	Sequence 9, Appli	246	86.5	5.2	2310	4	US-09-476-242-8	Sequence 8, Appli
174	88	5.3	1123	3	US-09-894-698-11	Sequence 11, Appl	247	86.5	5.2	2316	4	US-09-476-242-4	Sequence 4, Appli
c 175	88	5.3	1383	3	US-09-894-698-6	Sequence 6, Appli	248	86.5	5.2	2316	4	US-09-476-242-8	Sequence 8, Appli
176	88	5.3	1383	3	US-09-894-698-8	Sequence 8, Appli	249	86.5	5.2	2322	4	US-09-476-242-5	Sequence 5, Appli
c 177	88	5.3	1449	3	US-09-894-698-4	Sequence 4, Appli	250	86.5	5.2	2322	4	US-09-476-242-18	Sequence 18, Appl

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253	86.5	5.2	2334	4	US-09-476-242-7	Sequence 7, Appli	C 326	85	5.1	1797	3	US-09-669-974-4	Sequence 4, Appli
254	86.5	5.2	2352	4	US-09-476-242-26	Sequence 26, Appl	C 327	85	5.1	1797	4	US-09-797-862-4	Sequence 4, Appli
255	86.5	5.2	2358	4	US-09-475-515-50	Sequence 50, Appl	328	85	5.1	6013	4	US-09-774-528-109	Sequence 109, App
256	86.5	5.2	2358	4	US-09-476-242-25	Sequence 25, Appl	C 329	85	5.1	7194	4	US-09-601-326-76	Sequence 76, Appl
257	86.5	5.2	2466	4	US-09-475-515-49	Sequence 49, Appl	C 330	85	5.1	7661	4	US-09-902-540-912	Sequence 912, Appl
258	86.5	5.2	2517	4	US-09-476-242-16	Sequence 16, Appl	331	85	5.1	12588	2	US-08-387-942C-1	Sequence 1, Appli
259	86.5	5.2	2517	4	US-09-476-242-17	Sequence 17, Appl	C 332	85	5.1	12685	4	US-09-479-467A-3	Sequence 3, Appli
260	86.5	5.2	2523	4	US-09-476-242-15	Sequence 15, Appl	333	85	5.1	15378	3	US-08-785-420-1	Sequence 1, Appli
261	86.5	5.2	2529	4	US-09-476-242-14	Sequence 14, Appl	C 334	85	5.1	15420	4	US-09-601-326-54	Sequence 54, Appl
262	86.5	5.2	2541	4	US-09-476-242-9	Sequence 9, Appli	C 335	85	5.1	23417	4	US-09-902-540-1207	Sequence 1207, Ap
263	86.5	5.2	2541	4	US-09-476-242-10	Sequence 10, Appl	336	85	5.1	28804	2	US-08-592-874-1	Sequence 1, Appli
264	86.5	5.2	2541	4	US-09-476-242-11	Sequence 11, Appl	337	85	5.1	28804	3	US-09-096-942-2	Sequence 2, Appli
265	86.5	5.2	2547	4	US-09-475-515-48	Sequence 48, Appl	338	85	5.1	28804	3	US-09-096-867-2	Sequence 2, Appli
266	86.5	5.2	2640	4	US-09-962-357-1	Sequence 1, Appli	339	85	5.1	43507	4	US-09-949-016-13297	Sequence 13297, A
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C 268	86.5	5.2	3136	4	US-09-949-016-2659	Sequence 2659, Ap	341	85	5.1	50453	4	US-09-949-016-16642	Sequence 16642, A
269	86.5	5.2	4608	4	US-09-475-515-76	Sequence 76, Appl	342	85	5.1	51242	4	US-09-949-016-12486	Sequence 12486, A
270	86.5	5.2	4689	4	US-09-475-515-74	Sequence 74, Appl	C 343	84.5	5.1	601	4	US-09-949-016-61087	Sequence 61087, A
271	86.5	5.2	7541	4	US-09-637-048C-4	Sequence 4, Appli	344	84.5	5.1	1016	4	US-09-220-132-17	Sequence 17, Appl
272	86.5	5.2	7541	4	US-10-435-835-4	Sequence 4, Appli	345	84.5	5.1	1017	4	US-09-949-016-4435	Sequence 4435, Ap
273	86.5	5.2	9700	4	US-09-698-295-9	Sequence 9, Appli	346	84.5	5.1	2158	4	US-09-949-016-3018	Sequence 3018, Ap
274	86.5	5.2	9865	4	US-09-698-295-2	Sequence 2, Appli	347	84.5	5.1	2158	4	US-09-949-016-3026	Sequence 3026, Ap
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C 276	86.5	5.2	57859	4	US-09-949-016-12334	Sequence 12334, A	C 349	84.5	5.1	3033	4	US-09-457-571-1	Sequence 1, Appli
C 277	86.5	5.2	57859	4	US-09-949-016-14657	Sequence 14657, A	350	84.5	5.1	3243	4	US-09-543-681A-1875	Sequence 1875, Ap
C 278	86.5	5.2	57859	4	US-09-949-016-14658	Sequence 14658, A	351	84.5	5.1	3486	4	US-09-614-221A-292	Sequence 292, App
C 279	86	5.2	564	4	US-09-583-110-2585	Sequence 2585, Ap	352	84.5	5.1	5697	3	US-08-814-052-11	Sequence 11, Appl
280	86	5.2	813	4	US-09-248-796A-372	Sequence 372, App	353	84.5	5.1	5697	3	US-08-812-829-11	Sequence 11, Appl
281	86	5.2	813	4	US-09-949-016-2247	Sequence 2247, Ap	354	84.5	5.1	6002	4	US-09-949-016-13696	Sequence 13696, A
C 282	86	5.2	1150	4	US-09-771-357-96	Sequence 96, Appl	355	84.5	5.1	6452	3	US-08-836-325-9	Sequence 9, Appli
C 283	86	5.2	1150	4	US-10-059-579A-96	Sequence 96, Appl	356	84.5	5.1	6452	4	US-09-457-571-9	Sequence 9, Appli
C 284	86	5.2	1797	3	US-09-377-155-12	Sequence 12, Appl	C 357	84.5	5.1	10521	4	US-09-949-016-13516	Sequence 13516, A
C 285	86	5.2	1797	3	US-09-669-974-12	Sequence 12, Appl	358	84.5	5.1	51723	4	US-09-949-016-12152	Sequence 12152, A
C 286	86	5.2	1797	4	US-09-797-862-12	Sequence 12, Appl	359	84.5	5.1	51723	4	US-09-949-016-16991	Sequence 16991, A
287	86	5.2	3385	3	US-08-666-221B-9	Sequence 9, Appli	360	84.5	5.1	276237	4	US-09-949-016-17504	Sequence 17504, A
288	86	5.2	5774	4	US-09-949-016-13989	Sequence 13989, A	C 361	84.5	5.1	421491	4	US-09-949-016-12805	Sequence 12805, A
C 289	86	5.2	16720	4	US-09-902-540-1168	Sequence 1168, Ap	C 362	84.5	5.1	421494	4	US-09-949-016-14060	Sequence 14060, A
C 290	86	5.2	33529	3	US-09-144-085-3	Sequence 3, Appli	363	84	5.1	993	4	US-09-252-991A-10494	Sequence 10494, A
291	86	5.2	34094	4	US-09-292-034-1	Sequence 1, Appli	364	84	5.1	1125	2	US-08-997-080-153	Sequence 153, App
292	86	5.2	53500	4	US-09-266-965-76	Sequence 76, Appl	365	84	5.1	1125	2	US-08-997-362-153	Sequence 153, App
C 293	86	5.2	142783	4	US-09-949-016-15127	Sequence 15127, A	366	84	5.1	1125	3	US-09-095-855-153	Sequence 153, App
294	86	5.2	176006	4	US-09-949-016-16804	Sequence 16804, A	367	84	5.1	1125	3	US-09-324-542-153	Sequence 153, App
295	86	5.2	253375	4	US-09-949-016-12849	Sequence 12849, A	368	84	5.1	1125	3	US-09-205-426-153	Sequence 153, App
296	86	5.2	254405	4	US-09-949-016-14381	Sequence 14381, A	C 369	84	5.1	2007	3	US-09-052-089A-7	Sequence 7, Appli
297	85.5	5.2	985	3	US-09-160-246-9	Sequence 9, Appli	C 370	84	5.1	2007	4	US-09-949-016-793	Sequence 793, App
298	85.5	5.2	985	3	US-09-160-246-13	Sequence 13, Appl	380	84	5.1	2403	1	US-08-471-033-30	Sequence 30, Appl
299	85.5	5.2	1173	4	US-09-826-509-426	Sequence 426, App	381	84	5.1	2403	2	US-08-471-044-30	Sequence 30, Appl
300	85.5	5.2	1320	3	US-09-221-654-1	Sequence 1, Appli	382	84	5.1	2403	2	US-08-463-483A-30	Sequence 30, Appl
301	85.5	5.2	1320	3	US-08-989-358A-1	Sequence 1, Appli	383	84	5.1	2403	2	US-08-471-046A-30	Sequence 30, Appl
C 302	85.5	5.2	1359	4	US-09-010-147B-21	Sequence 21, Appl	384	84	5.1	2403	2	US-08-470-566B-30	Sequence 30, Appl
303	85.5	5.2	1401	4	US-09-252-991A-10908	Sequence 10908, A	385	84	5.1	2403	2	US-08-838-219B-7	Sequence 7, Appli
304	85.5	5.2	1440	4	US-09-252-991A-11041	Sequence 11041, A	386	84	5.1	2403	2	US-08-469-334-30	Sequence 30, Appl
305	85.5	5.2	1593	3	US-08-993-359-23	Sequence 23, Appl	387	84	5.1	2403	3	US-09-300-529-30	Sequence 30, Appl
306	85.5	5.2	1593	4	US-09-482-558A-23	Sequence 23, Appl	388	84	5.1	2403	3	US-09-233-336A-7	Sequence 7, Appli
307	85.5	5.2	1690	2	US-08-461-812-3	Sequence 3, Appli	389	84	5.1	2403	3	US-09-233-752A-7	Sequence 7, Appli
308	85.5	5.2	1690	4	US-09-371-705-3	Sequence 3, Appli	390	84	5.1	2403	3	US-09-402-036-7	Sequence 7, Appli
309	85.5	5.2	2346	4	US-09-949-016-1088	Sequence 1088, Ap	391	84	5.1	2403	3	US-09-904-226-7	Sequence 7, Appli
310	85.5	5.2	2635	4	US-09-016-434-1258	Sequence 1258, Ap	392	84	5.1	2471	4	US-09-806-536A-16	Sequence 16, Appl
311	85.5	5.2	4227	4	US-09-902-540-8919	Sequence 8919, Ap	393	84	5.1	2635	4	US-09-620-312D-1070	Sequence 1070, Ap
C 312	85.5	5.2	5043	4	US-09-902-540-574	Sequence 574, App	394	84	5.1	3250	1	US-07-718-575-9	Sequence 9, Appli
C 313	85.5	5.2	6060	4	US-08-956-171E-534	Sequence 534, App	395	84	5.1	3250	1	US-08-481-206-9	Sequence 9, Appli
C 314	85.5	5.2	6060	4	US-08-781-986A-534	Sequence 534, App	396	84	5.1	3250	2	US-08-486-269A-9	Sequence 9, Appli
C 315	85.5	5.2	9367	4	US-09-902-540-951	Sequence 951, App	C 397	84	5.1	4386	3	US-09-300-008B-1	Sequence 1, Appli
C 316	85.5	5.2	16011	4	US-09-600-319-3	Sequence 3, Appli	398	84	5.1	5163	3	US-08-700-651-1	Sequence 1, Appli
C 317	85.5	5.2	30350	4	US-10-118-328-3	Sequence 3, Appli	399	84	5.1	5163	3	US-08-928-361B-4	Sequence 4, Appli
318	85	5.1	804	4	US-09-902-540-5636	Sequence 5636, Ap	400	84	5.1	5163	4	US-09-588-995A-4	Sequence 4, Appli
319	85	5.1	957	4	US-09-902-540-2935	Sequence 2935, Ap	401	84	5.1	5318	3	US-08-700-651-2	Sequence 2, Appli
320	85	5.1	1176	2	US-08-387-942C-17	Sequence 17, Appl	402	84	5.1	5318	3	US-08-928-361B-3	Sequence 3, Appli
321	85	5.1	1251	4	US-09-614-912-81	Sequence 81, Appl	403	84	5.1	5318	4	US-09-588-995A-3	Sequence 3, Appli
322	85	5.1	1371	4	US-09-350-756-3	Sequence 3, Appli	404	84	5.1	5511	3	US-08-928-361B-2	Sequence 2, Appli
323	85	5.1	1636	4	US-09-614-912-69	Sequence 69, Appl	405	84	5.1	5511	4	US-09-588-995A-2	Sequence 2, Appli

406	84	5.1	5679	3	US-08-814-052-9	Sequence 9, Appli	479	83	5.0	6885	4	US-09-854-856-49	Sequence 49, Appl
407	84	5.1	5679	3	US-08-812-829-9	Sequence 9, Appli	480	83	5.0	6969	4	US-09-854-856-33	Sequence 33, Appl
408	84	5.1	7334	3	US-08-928-361B-1	Sequence 1, Appli	481	83	5.0	7065	4	US-09-854-856-17	Sequence 17, Appl
409	84	5.1	7334	4	US-08-988-995A-1	Sequence 1, Appli	482	83	5.0	7149	4	US-09-854-856-1	Sequence 1, Appli
410	84	5.1	13926	3	US-08-961-527-5	Sequence 5, Appli	c 483	83	5.0	32207	2	US-08-770-379-20	Sequence 20, Appl
411	84	5.1	20870	4	US-09-949-016-16017	Sequence 16017, A	c 484	83	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
412	84	5.1	21511	4	US-09-902-540-1201	Sequence 1201, Ap	c 485	83	5.0	32207	3	US-09-230-371A-20	Sequence 20, Appl
413	84	5.1	99960	4	US-09-762-311-2	Sequence 2, Appli	c 486	83	5.0	40897	4	US-09-949-016-13910	Sequence 13910, A
c 414	83.5	5.0	429	4	US-09-252-991A-11731	Sequence 11731, A	c 487	83	5.0	40897	4	US-09-949-016-13911	Sequence 13911, A
c 415	83.5	5.0	840	4	US-09-902-540-56	Sequence 56, Appl	c 488	83	5.0	40897	4	US-09-949-016-13912	Sequence 13912, A
416	83.5	5.0	939	4	US-09-248-796A-6040	Sequence 6040, Ap	c 489	83	5.0	40897	4	US-09-949-016-13913	Sequence 13913, A
417	83.5	5.0	1107	2	US-08-991-300-1	Sequence 1, Appli	c 490	83	5.0	40897	4	US-09-949-016-14409	Sequence 14409, A
418	83.5	5.0	1344	4	US-09-252-991A-11510	Sequence 11510, A	c 491	83	5.0	40897	4	US-09-949-016-14410	Sequence 14410, A
419	83.5	5.0	1459	3	US-09-377-557-13	Sequence 13, Appl	c 492	83	5.0	40897	4	US-09-949-016-14411	Sequence 14411, A
c 420	83.5	5.0	1620	4	US-09-252-991A-499	Sequence 499, App	c 493	83	5.0	40897	4	US-09-949-016-14412	Sequence 14412, A
c 421	83.5	5.0	1995	4	US-09-252-991A-11521	Sequence 11521, A	c 494	83	5.0	72704	4	US-09-902-540-1273	Sequence 1273, Ap
422	83.5	5.0	2136	4	US-09-252-991A-11628	Sequence 11628, A	c 495	83	5.0	194889	4	US-09-949-016-15654	Sequence 15654, A
423	83.5	5.0	2353	4	US-09-369-247-12	Sequence 12, Appl	c 496	83	5.0	767677	4	US-09-949-016-12147	Sequence 12147, A
424	83.5	5.0	2945	4	US-09-714-767A-3	Sequence 3, Appli	c 497	83	5.0	767677	4	US-09-949-016-17361	Sequence 17361, A
425	83.5	5.0	2951	1	US-08-413-118-104	Sequence 104, App	c 498	83	5.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
426	83.5	5.0	2951	3	US-08-473-446-104	Sequence 104, App	c 499	83	5.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
427	83.5	5.0	3000	1	US-08-220-151-1	Sequence 1, Appli	500	82.5	5.0	660	3	US-09-134-001C-2814	Sequence 2814, Ap
428	83.5	5.0	3000	1	US-08-413-118-1	Sequence 1, Appli	501	82.5	5.0	669	3	US-09-221-017B-288	Sequence 288, App
429	83.5	5.0	3000	3	US-08-473-446-1	Sequence 1, Appli	502	82.5	5.0	1119	3	US-07-757-022B-63	Sequence 63, Appl
c 430	83.5	5.0	3177	4	US-09-252-991A-521	Sequence 521, App	503	82.5	5.0	1269	3	US-07-757-022B-67	Sequence 67, Appl
c 431	83.5	5.0	3211	2	US-08-574-959A-8	Sequence 8, Appli	504	82.5	5.0	1272	3	US-07-757-022B-65	Sequence 65, Appl
c 432	83.5	5.0	3211	3	US-09-357-014-8	Sequence 8, Appli	505	82.5	5.0	1392	3	US-07-757-022B-53	Sequence 53, Appl
c 433	83.5	5.0	3901	2	US-08-574-959A-6	Sequence 6, Appli	c 506	82.5	5.0	1647	4	US-09-540-236-469	Sequence 469, App
c 434	83.5	5.0	3901	3	US-09-357-014-6	Sequence 6, Appli	507	82.5	5.0	1776	4	US-09-270-767-1058	Sequence 1058, Ap
435	83.5	5.0	7478	4	US-09-618-425-10	Sequence 10, Appl	508	82.5	5.0	1776	4	US-09-270-767-16340	Sequence 16340, A
436	83.5	5.0	7498	2	US-08-816-693A-1	Sequence 1, Appli	c 509	82.5	5.0	1842	4	US-09-016-434-1236	Sequence 1236, Ap
437	83.5	5.0	7498	3	US-08-885-291-1	Sequence 1, Appli	510	82.5	5.0	2298	4	US-09-252-991A-13540	Sequence 13540, A
438	83.5	5.0	7498	3	US-09-496-672-1	Sequence 1, Appli	511	82.5	5.0	2373	4	US-09-949-016-1146	Sequence 1146, Ap
c 439	83.5	5.0	13926	3	US-08-961-527-5	Sequence 5, Appli	512	82.5	5.0	2373	4	US-09-949-016-2298	Sequence 2298, Ap
440	83.5	5.0	26659	4	US-09-902-540-1237	Sequence 1237, Ap	513	82.5	5.0	2373	4	US-09-949-016-2299	Sequence 2299, Ap
441	83.5	5.0	65848	4	US-09-949-016-13285	Sequence 13285, A	c 514	82.5	5.0	2412	4	US-09-252-991A-13908	Sequence 13908, A
442	83	5.0	601	4	US-09-949-016-66454	Sequence 66454, A	515	82.5	5.0	6022	4	US-08-956-171E-92	Sequence 92, Appl
443	83	5.0	615	4	US-09-248-796A-7881	Sequence 7881, Ap	516	82.5	5.0	6022	4	US-08-781-986A-92	Sequence 92, Appl
444	83	5.0	630	4	US-09-270-767-1924	Sequence 1924, Ap	517	82.5	5.0	6373	4	US-09-949-016-12830	Sequence 12830, A
445	83	5.0	630	4	US-09-270-767-17206	Sequence 17206, A	518	82.5	5.0	6373	4	US-09-949-016-12888	Sequence 12888, A
446	83	5.0	966	4	US-09-252-991A-11896	Sequence 11896, A	519	82.5	5.0	6374	4	US-09-949-016-14040	Sequence 14040, A
447	83	5.0	1056	4	US-09-248-796A-9572	Sequence 9572, Ap	520	82.5	5.0	6374	4	US-09-949-016-14041	Sequence 14041, A
448	83	5.0	1084	4	US-09-949-016-2175	Sequence 2175, Ap	521	82.5	5.0	9461	3	US-09-221-017B-513	Sequence 513, App
c 449	83	5.0	1084	4	US-09-949-016-2176	Sequence 2176, Ap	522	82.5	5.0	23847	4	US-09-902-540-1177	Sequence 1177, Ap
c 450	83	5.0	1225	4	US-09-976-594-416	Sequence 416, App	c 523	82.5	5.0	24333	4	US-09-639-207-9	Sequence 9, Appli
451	83	5.0	1350	3	US-09-149-476-248	Sequence 248, App	524	82.5	5.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
c 452	83	5.0	1779	3	US-09-377-155-16	Sequence 16, Appl	c 525	82.5	5.0	58909	4	US-09-596-002-30	Sequence 30, Appl
c 453	83	5.0	1779	3	US-09-669-974-16	Sequence 16, Appl	c 526	82.5	5.0	194937	4	US-09-949-016-17032	Sequence 17032, A
c 454	83	5.0	1779	4	US-09-797-862-16	Sequence 16, Appl	c 527	82.5	5.0	194937	4	US-09-949-016-17033	Sequence 17033, A
455	83	5.0	2241	2	US-08-838-219B-20	Sequence 20, Appl	528	82	4.9	423	1	US-08-470-179-160	Sequence 160, App
456	83	5.0	2241	3	US-09-233-336A-20	Sequence 20, Appl	c 529	82	4.9	855	4	US-09-252-991A-10673	Sequence 10673, A
457	83	5.0	2241	3	US-09-233-752A-20	Sequence 20, Appl	530	82	4.9	875	4	US-09-443-067-27	Sequence 27, Appl
458	83	5.0	2241	3	US-09-402-036-20	Sequence 20, Appl	531	82	4.9	1208	4	US-09-602-787A-409	Sequence 409, App
459	83	5.0	2241	3	US-09-904-226-20	Sequence 20, Appl	532	82	4.9	1280	4	US-09-602-787A-407	Sequence 407, App
460	83	5.0	2370	2	US-08-838-219B-19	Sequence 19, Appl	533	82	4.9	1371	4	US-09-252-991A-9440	Sequence 9440, Ap
461	83	5.0	2370	3	US-09-233-336A-19	Sequence 19, Appl	c 534	82	4.9	1383	4	US-09-489-039A-3928	Sequence 3928, Ap
462	83	5.0	2370	3	US-09-233-752A-19	Sequence 19, Appl	535	82	4.9	1521	2	US-09-004-502-2	Sequence 2, Appli
463	83	5.0	2370	3	US-09-402-036-19	Sequence 19, Appl	536	82	4.9	1521	3	US-09-360-125-2	Sequence 2, Appli
464	83	5.0	2370	3	US-09-904-226-19	Sequence 19, Appl	537	82	4.9	1527	4	US-09-248-796A-4088	Sequence 4088, Ap
465	83	5.0	2905	4	US-09-949-016-410	Sequence 410, App	538	82	4.9	1575	4	US-09-248-796A-4898	Sequence 4898, Ap
466	83	5.0	2906	4	US-09-949-016-5249	Sequence 5249, Ap	539	82	4.9	1590	4	US-09-248-796A-6083	Sequence 6083, Ap
467	83	5.0	3252	4	US-09-614-221A-303	Sequence 303, App	540	82	4.9	1617	4	US-09-248-796A-6739	Sequence 6739, Ap
468	83	5.0	3489	2	US-08-728-323A-1	Sequence 1, Appli	541	82	4.9	1662	1	US-08-651-572-1	Sequence 1, Appli
469	83	5.0	3489	3	US-09-298-568-1	Sequence 1, Appli	542	82	4.9	1662	3	US-09-066-544-1	Sequence 1, Appli
470	83	5.0	3489	4	US-09-410-399-1	Sequence 1, Appli	543	82	4.9	1662	3	US-08-951-086-1	Sequence 1, Appli
471	83	5.0	3489	4	US-09-894-273-1	Sequence 1, Appli	544	82	4.9	1662	3	US-09-430-669-1	Sequence 1, Appli
c 472	83	5.0	3924	1	US-08-395-246C-1	Sequence 1, Appli	545	82	4.9	1867	4	US-09-949-016-4889	Sequence 4889, Ap
c 473	83	5.0	4063	4	US-09-902-540-595	Sequence 595, App	546	82	4.9	1867	4	US-09-949-016-4890	Sequence 4890, Ap
474	83	5.0	4545	3	US-09-221-017B-1011	Sequence 1011, Ap	c 547	82	4.9	2016	4	US-09-949-016-5734	Sequence 5734, Ap
475	83	5.0	6474	4	US-09-854-856-51	Sequence 51, Appl	c 548	82	4.9	2065	2	US-08-968-751-1	Sequence 1, Appli
476	83	5.0	6558	4	US-09-854-856-35	Sequence 35, Appl	549	82	4.9	3081	4	US-09-248-796A-2025	Sequence 2025, Ap
477	83	5.0	6654	4	US-09-854-856-19	Sequence 19, Appl	550	82	4.9	4014	4	US-09-949-016-4648	Sequence 4648, Ap
478	83	5.0	6738	4	US-09-854-856-3	Sequence 3, Appli	551	82	4.9	4014	4	US-09-949-016-4649	Sequence 4649, Ap

C 552	82	4.9	5449	4	US-09-949-016-2138	Sequence 2138, Ap	625	81	4.9	7680	4	US-09-953-318-3	Sequence 3, Appli
553	82	4.9	15163	4	US-09-949-016-13246	Sequence 13246, A	626	81	4.9	7718	4	US-09-976-594-244	Sequence 244, App
554	82	4.9	40586	4	US-09-949-016-16965	Sequence 16965, A	C 627	81	4.9	14367	4	US-09-902-540-1113	Sequence 1113, Ap
C 555	82	4.9	44821	4	US-09-949-016-13764	Sequence 13764, A	628	81	4.9	18853	4	US-09-820-005-3	Sequence 3, Appli
556	81.5	4.9	767	4	US-09-270-767-2226	Sequence 2226, Ap	629	81	4.9	18853	4	US-10-109-856-3	Sequence 3, Appli
557	81.5	4.9	767	4	US-09-270-767-17508	Sequence 17508, A	630	81	4.9	80161	3	US-09-036-987A-1	Sequence 1, Appli
C 558	81.5	4.9	879	5	PCT-US96-03916-16	Sequence 16, Appl	631	81	4.9	80161	3	US-09-370-700-1	Sequence 1, Appli
559	81.5	4.9	1069	4	US-09-949-016-2654	Sequence 2654, Ap	632	81	4.9	80161	4	US-09-603-207-1	Sequence 1, Appli
560	81.5	4.9	1069	4	US-09-949-016-2655	Sequence 2655, Ap	C 633	81	4.9	100848	4	US-09-596-002-39	Sequence 39, Appl
561	81.5	4.9	1421	3	US-09-188-930-70	Sequence 70, Appl	634	81	4.9	110585	4	US-09-949-016-13427	Sequence 13427, A
562	81.5	4.9	1421	4	US-09-312-283C-70	Sequence 70, Appl	635	81	4.9	119211	4	US-09-596-002-40	Sequence 40, Appl
563	81.5	4.9	1569	4	US-09-248-796A-18	Sequence 18, Appl	C 636	81	4.9	271134	4	US-09-949-016-12705	Sequence 12705, A
564	81.5	4.9	1677	4	US-09-252-991A-9544	Sequence 9544, Ap	C 637	81	4.9	305491	4	US-09-949-016-17550	Sequence 17550, A
565	81.5	4.9	1758	2	US-08-630-822A-69	Sequence 69, Appl	638	80.5	4.9	771	4	US-09-902-540-5814	Sequence 5814, Ap
566	81.5	4.9	1758	2	US-09-005-069-69	Sequence 69, Appl	639	80.5	4.9	837	3	US-08-339-214-23	Sequence 23, Appl
567	81.5	4.9	1758	3	US-09-171-156A-29	Sequence 29, Appl	640	80.5	4.9	927	3	US-08-339-214-36	Sequence 36, Appl
568	81.5	4.9	1758	4	US-09-004-730A-29	Sequence 29, Appl	641	80.5	4.9	927	3	US-08-339-214-103	Sequence 103, App
569	81.5	4.9	1758	4	US-08-981-799A-29	Sequence 29, Appl	642	80.5	4.9	940	3	US-09-479-524-2	Sequence 2, Appli
570	81.5	4.9	1788	4	US-09-614-912-65	Sequence 65, Appl	C 643	80.5	4.9	940	3	US-09-479-524-8	Sequence 8, Appli
571	81.5	4.9	1795	4	US-09-197-970B-6	Sequence 6, Appli	C 644	80.5	4.9	1071	4	US-09-902-540-4828	Sequence 4828, Ap
572	81.5	4.9	2309	3	US-09-091-725-9	Sequence 9, Appli	645	80.5	4.9	1099	4	US-09-949-016-1829	Sequence 1829, Ap
C 573	81.5	4.9	2586	4	US-10-101-464A-883	Sequence 883, App	C 646	80.5	4.9	1119	4	US-09-252-991A-9448	Sequence 9448, Ap
574	81.5	4.9	2886	4	US-09-248-796A-5312	Sequence 5312, Ap	647	80.5	4.9	1140	3	US-09-462-270-1	Sequence 1, Appli
575	81.5	4.9	2943	1	US-08-042-747A-7	Sequence 7, Appli	648	80.5	4.9	1227	3	US-09-074-912-3	Sequence 3, Appli
576	81.5	4.9	4338	1	US-08-015-986A-1	Sequence 1, Appli	649	80.5	4.9	1227	3	US-09-290-136-3	Sequence 3, Appli
577	81.5	4.9	4338	2	US-08-446-363-1	Sequence 1, Appli	C 650	80.5	4.9	1239	4	US-09-252-991A-9383	Sequence 9383, Ap
C 578	81.5	4.9	4760	3	US-09-221-017B-875	Sequence 875, App	C 651	80.5	4.9	1293	4	US-09-902-540-5999	Sequence 5999, Ap
579	81.5	4.9	6301	4	US-09-902-540-842	Sequence 842, App	C 652	80.5	4.9	1356	4	US-09-328-352-4027	Sequence 4027, Ap
580	81.5	4.9	8697	3	US-08-961-527-123	Sequence 123, App	653	80.5	4.9	1417	4	US-09-949-016-4521	Sequence 4521, Ap
581	81.5	4.9	13473	5	PCT-US96-03916-1	Sequence 1, Appli	654	80.5	4.9	1421	3	US-09-188-930-254	Sequence 254, App
582	81.5	4.9	18912	5	PCT-US96-03916-59	Sequence 59, Appl	655	80.5	4.9	1421	4	US-09-312-283C-254	Sequence 254, App
583	81.5	4.9	20250	4	US-09-902-540-1213	Sequence 1213, Ap	656	80.5	4.9	1476	4	US-09-976-594-147	Sequence 147, App
584	81.5	4.9	29598	3	US-09-341-587-6	Sequence 6, Appli	C 657	80.5	4.9	1505	4	US-09-620-312D-544	Sequence 544, App
585	81.5	4.9	33748	4	US-09-949-016-14283	Sequence 14283, A	658	80.5	4.9	1537	4	US-09-902-540-222	Sequence 222, App
586	81	4.9	621	1	US-08-028-463-7	Sequence 7, Appli	659	80.5	4.9	1707	3	US-08-339-214-31	Sequence 31, Appl
587	81	4.9	621	1	US-08-461-836-7	Sequence 7, Appli	C 660	80.5	4.9	1716	3	US-09-040-681A-3	Sequence 3, Appli
C 588	81	4.9	801	4	US-09-489-039A-1028	Sequence 1028, Ap	C 661	80.5	4.9	1716	3	US-09-497-897-3	Sequence 3, Appli
589	81	4.9	1023	4	US-09-492-709A-102	Sequence 102, App	662	80.5	4.9	1783	4	US-09-949-016-1954	Sequence 1954, Ap
590	81	4.9	1291	2	US-08-887-365-35	Sequence 35, Appl	672	80.5	4.9	1875	3	US-09-877-730-23	Sequence 23, Appl
591	81	4.9	1389	4	US-09-602-787A-77	Sequence 77, Appl	673	80.5	4.9	2139	3	US-09-877-730-21	Sequence 21, Appl
592	81	4.9	1425	4	US-09-578-063-2	Sequence 2, Appli	674	80.5	4.9	2382	3	US-09-877-730-27	Sequence 27, Appl
593	81	4.9	1555	3	US-08-669-408B-9	Sequence 9, Appli	C 675	80.5	4.9	2458	3	US-09-071-101-5	Sequence 5, Appli
594	81	4.9	1596	4	US-09-248-796A-1457	Sequence 1457, Ap	C 676	80.5	4.9	2458	3	US-09-369-618-6	Sequence 6, Appli
595	81	4.9	1656	4	US-09-578-063-1	Sequence 1, Appli	C 677	80.5	4.9	2458	3	US-09-369-617-6	Sequence 6, Appli
596	81	4.9	1850	4	US-09-848-726-1	Sequence 1, Appli	C 678	80.5	4.9	2976	3	US-09-877-730-11	Sequence 11, Appl
597	81	4.9	1875	3	US-09-039-609-1	Sequence 1, Appli	679	80.5	4.9	3190	4	US-09-949-016-5181	Sequence 5181, Ap
C 598	81	4.9	2001	4	US-09-248-796A-4560	Sequence 4560, Ap	680	80.5	4.9	3210	3	US-09-877-730-1	Sequence 1, Appli
C 599	81	4.9	2040	3	US-08-604-789B-1	Sequence 1, Appli	681	80.5	4.9	3219	3	US-09-877-730-17	Sequence 17, Appl
C 600	81	4.9	2040	3	US-08-604-789B-12	Sequence 12, Appl	682	80.5	4.9	3453	3	US-09-877-730-7	Sequence 7, Appli
C 601	81	4.9	2040	3	US-09-312-721A-1	Sequence 1, Appli	683	80.5	4.9	3604	4	US-09-799-451-287	Sequence 287, App
C 602	81	4.9	2040	3	US-09-312-721A-12	Sequence 12, Appl	684	80.5	4.9	3622	4	US-09-949-016-2172	Sequence 2172, Ap
C 603	81	4.9	2040	4	US-09-733-300-1	Sequence 1, Appli	685	80.5	4.9	3627	2	US-08-232-087A-1	Sequence 1, Appli
C 604	81	4.9	2040	4	US-09-733-300-12	Sequence 12, Appl	686	80.5	4.9	3630	4	US-09-023-655-1028	Sequence 1028, Ap
C 605	81	4.9	2071	4	US-09-949-016-1517	Sequence 1517, Ap	687	80.5	4.9	3630	4	US-09-949-016-177	Sequence 177, App
606	81	4.9	2313	1	US-08-232-538-5	Sequence 5, Appli	688	80.5	4.9	3874	3	US-09-877-730-31	Sequence 31, Appl
607	81	4.9	2313	3	US-09-427-353-1	Sequence 1, Appli	689	80.5	4.9	5220	4	US-09-677-046A-1	Sequence 1, Appli
608	81	4.9	2465	5	PCT-US92-08090-1	Sequence 1, Appli	C 690	80.5	4.9	5682	4	US-10-164-595-1	Sequence 1, Appli
609	81	4.9	2523	3	US-09-051-363-1	Sequence 1, Appli	691	80.5	4.9	6114	4	US-09-914-272A-4	Sequence 4, Appli
C 610	81	4.9	2553	4	US-09-949-016-488	Sequence 488, App	692	80.5	4.9	6114	4	US-10-638-333-4	Sequence 4, Appli
611	81	4.9	2582	4	US-09-270-767-12851	Sequence 12851, A	693	80.5	4.9	6359	4	US-09-475-252-1	Sequence 1, Appli
612	81	4.9	2651	2	US-08-786-164-5	Sequence 5, Appli	694	80.5	4.9	7000	4	US-09-902-540-833	Sequence 833, App
613	81	4.9	2651	4	US-09-953-318-19	Sequence 19, Appl	C 695	80.5	4.9	7948	4	US-09-949-016-14929	Sequence 14929, A
614	81	4.9	2652	4	US-09-248-796A-4828	Sequence 4828, Ap	C 696	80.5	4.9	7960	4	US-09-949-016-14930	Sequence 14930, A
615	81	4.9	2674	4	US-10-066-130-19	Sequence 19, Appl	697	80.5	4.9	9542	3	US-08-968-685A-9	Sequence 9, Appli
616	81	4.9	2771	4	US-10-066-130-18	Sequence 18, Appl	C 698	80.5	4.9	12180	4	US-09-949-016-12527	Sequence 12527, A
C 617	81	4.9	2911	4	US-09-799-451-888	Sequence 888, App	C 699	80.5	4.9	12180	4	US-09-949-016-14323	Sequence 14323, A
618	81	4.9	3498	4	US-09-520-781-3	Sequence 3, Appli	C 700	80.5	4.9	16924	4	US-09-949-016-13720	Sequence 13720, A
619	81	4.9	4200	1	US-07-841-654B-1	Sequence 1, Appli	C 701	80.5	4.9	21164	4	US-09-949-016-16457	Sequence 16457, A
620	81	4.9	4200	1	US-07-946-234A-1	Sequence 1, Appli	C 702	80.5	4.9	40408	4	US-09-949-016-16331	Sequence 16331, A
621	81	4.9	4200	1	US-08-123-161A-1	Sequence 1, Appli	703	80	4.8	156	1	US-08-225-477B-7	Sequence 7, Appli
622	81	4.9	4200	1	US-08-483-278-1	Sequence 1, Appli	704	80	4.8	156	5	PCT-US95-04353-7	Sequence 7, Appli
623	81	4.9	4200	5	PCT-US93-01560-1	Sequence 1, Appli	705	80	4.8	288	4	US-09-252-991A-11933	Sequence 11933, A
624	81	4.9	5860	4	US-10-066-130-17	Sequence 17, Appl	706	80	4.8	597	4	US-09-902-540-8148	Sequence 8148, Ap

707	80	4.8	615	4	US-09-902-540-6862	Sequence 6862, Ap	780	79.5	4.8	3048	1	US-08-332-643-41	Sequence 41, Appl
c 708	80	4.8	618	4	US-09-902-540-58	Sequence 58, Appl	781	79.5	4.8	3048	1	US-08-332-638-47	Sequence 47, Appl
c 709	80	4.8	744	4	US-09-252-991A-15538	Sequence 15538, A	782	79.5	4.8	3492	4	US-09-023-655-1219	Sequence 1219, Ap
710	80	4.8	756	4	US-09-248-796A-9113	Sequence 9113, Ap	783	79.5	4.8	3677	4	US-09-949-016-1969	Sequence 1969, Ap
711	80	4.8	774	4	US-09-902-540-7907	Sequence 7907, Ap	784	79.5	4.8	3683	3	US-09-844-634-3	Sequence 3, Appli
c 712	80	4.8	807	4	US-09-252-991A-15427	Sequence 15427, A	785	79.5	4.8	3683	4	US-09-968-455-1	Sequence 1, Appli
713	80	4.8	975	3	US-09-365-150-4	Sequence 4, Appli	786	79.5	4.8	3683	4	US-09-949-016-148	Sequence 148, App
714	80	4.8	1119	4	US-09-248-796A-5793	Sequence 5793, Ap	787	79.5	4.8	3976	4	US-09-799-451-131	Sequence 131, App
715	80	4.8	1216	4	US-09-270-767-10155	Sequence 10155, A	788	79.5	4.8	4171	4	US-09-667-422-3	Sequence 3, Appli
716	80	4.8	1270	4	US-09-270-767-12871	Sequence 12871, A	789	79.5	4.8	5491	4	US-09-262-537-5	Sequence 5, Appli
717	80	4.8	1275	4	US-09-252-991A-15254	Sequence 15254, A	790	79.5	4.8	5597	4	US-09-262-537-1	Sequence 1, Appli
718	80	4.8	1315	4	US-09-902-540-215	Sequence 215, App	791	79.5	4.8	5598	4	US-09-262-537-33	Sequence 33, Appl
719	80	4.8	1359	4	US-09-252-991A-15302	Sequence 15302, A	792	79.5	4.8	5617	4	US-09-262-537-3	Sequence 3, Appli
720	80	4.8	1449	4	US-09-902-540-4922	Sequence 4922, Ap	c 793	79.5	4.8	28473	3	US-08-961-527-83	Sequence 83, Appl
721	80	4.8	1615	4	US-09-949-016-4275	Sequence 4275, Ap	c 794	79.5	4.8	31300	4	US-09-949-016-16967	Sequence 16967, A
722	80	4.8	2093	1	US-08-287-001A-1	Sequence 1, Appli	c 795	79.5	4.8	38239	4	US-09-949-016-12348	Sequence 12348, A
723	80	4.8	2093	5	PCT-US94-09941-1	Sequence 1, Appli	c 796	79.5	4.8	38252	4	US-09-949-016-13570	Sequence 13570, A
724	80	4.8	2472	4	US-09-248-796A-2596	Sequence 2596, Ap	797	79.5	4.8	121427	4	US-09-949-016-11950	Sequence 11950, A
c 725	80	4.8	2538	4	US-09-248-796A-3859	Sequence 3859, Ap	798	79.5	4.8	121433	4	US-09-949-016-13230	Sequence 13230, A
c 726	80	4.8	2839	5	PCT-US94-07297-38	Sequence 38, Appl	c 799	79.5	4.8	157866	4	US-09-949-016-12982	Sequence 12982, A
727	80	4.8	2893	4	US-09-902-540-9663	Sequence 9663, Ap	c 800	79.5	4.8	157866	4	US-09-949-016-12983	Sequence 12983, A
728	80	4.8	4359	4	US-08-943-144-3	Sequence 3, Appli	c 801	79.5	4.8	157866	4	US-09-949-016-12984	Sequence 12984, A
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730	80	4.8	5720	4	US-08-939-106-1	Sequence 1, Appli	c 803	79.5	4.8	1230230	4	US-09-438-185A-1	Sequence 1, Appli
731	80	4.8	5720	4	US-09-442-102-1	Sequence 1, Appli	804	79.5	4.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
732	80	4.8	6269	4	US-09-902-540-836	Sequence 836, App	c 805	79.5	4.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 733	80	4.8	7994	4	US-09-902-540-797	Sequence 797, App	c 806	79.5	4.8	1664976	4	US-09-692-570-1	Sequence 1, Appli
734	80	4.8	14555	4	US-09-902-540-1096	Sequence 1096, Ap	c 807	79.5	4.8	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 735	80	4.8	16265	4	US-09-902-540-1126	Sequence 1126, Ap	817	79	4.8	465	4	US-09-377-502-58	Sequence 58, Appl
c 736	80	4.8	28783	4	US-09-902-540-1242	Sequence 1242, Ap	818	79	4.8	615	4	US-09-134-000C-149	Sequence 149, App
c 737	80	4.8	35519	3	US-08-923-137-2	Sequence 2, Appli	819	79	4.8	714	4	US-09-252-991A-8966	Sequence 8966, Ap
c 738	80	4.8	36800	4	US-08-311-731A-139	Sequence 139, App	c 820	79	4.8	837	4	US-09-252-991A-9123	Sequence 9123, Ap
739	80	4.8	42325	4	US-08-311-731A-131	Sequence 131, App	821	79	4.8	900	4	US-09-248-796A-2142	Sequence 2142, Ap
c 740	80	4.8	247781	4	US-09-949-016-14193	Sequence 14193, A	c 822	79	4.8	975	4	US-09-498-520A-1	Sequence 1, Appli
c 741	80	4.8	264206	4	US-09-949-016-12731	Sequence 12731, A	c 823	79	4.8	975	4	US-09-583-110-1252	Sequence 1252, Ap
c 742	80	4.8	264304	4	US-09-949-016-13249	Sequence 13249, A	c 824	79	4.8	975	4	US-09-968-129-1	Sequence 1, Appli
c 743	80	4.8	536165	4	US-09-214-808-1	Sequence 1, Appli	c 825	79	4.8	996	4	US-09-107-433-2480	Sequence 2480, Ap
744	79.5	4.8	462	4	US-09-252-991A-1309	Sequence 1309, Ap	826	79	4.8	1005	4	US-09-107-532A-2682	Sequence 2682, Ap
745	79.5	4.8	462	4	US-09-270-767-8870	Sequence 8870, Ap	827	79	4.8	1063	4	US-09-949-016-5303	Sequence 5303, Ap
746	79.5	4.8	462	4	US-09-270-767-24152	Sequence 24152, A	c 828	79	4.8	1383	4	US-09-813-453B-40	Sequence 40, Appl
c 747	79.5	4.8	601	4	US-09-949-016-22247	Sequence 22247, A	c 829	79	4.8	1446	4	US-09-543-681A-554	Sequence 554, App
c 748	79.5	4.8	601	4	US-09-949-016-51354	Sequence 51354, A	830	79	4.8	1510	1	US-08-361-920-26	Sequence 26, Appl
749	79.5	4.8	612	4	US-09-270-767-3415	Sequence 3415, Ap	831	79	4.8	1510	1	US-08-479-939-26	Sequence 26, Appl
750	79.5	4.8	612	4	US-09-270-767-18697	Sequence 18697, A	832	79	4.8	1510	1	US-08-483-432-26	Sequence 26, Appl
751	79.5	4.8	768	4	US-09-248-796A-7148	Sequence 7148, Ap	c 833	79	4.8	1675	4	US-09-774-528-343	Sequence 343, App
752	79.5	4.8	909	4	US-09-252-991A-2103	Sequence 2103, Ap	834	79	4.8	1686	4	US-09-252-991A-7673	Sequence 7673, Ap
753	79.5	4.8	959	4	US-09-902-540-102	Sequence 102, App	835	79	4.8	1722	4	US-09-902-540-9668	Sequence 9668, Ap
754	79.5	4.8	975	4	US-09-489-039A-1422	Sequence 1422, Ap	836	79	4.8	1762	4	US-09-489-847-50	Sequence 50, Appl
755	79.5	4.8	1002	4	US-09-252-991A-2014	Sequence 2014, Ap	846	79	4.8	1917	4	US-09-248-796A-4636	Sequence 4636, Ap
756	79.5	4.8	1125	4	US-09-248-796A-3180	Sequence 3180, Ap	847	79	4.8	2091	3	US-08-899-437-22	Sequence 22, Appl
757	79.5	4.8	1194	4	US-09-248-796A-7496	Sequence 7496, Ap	848	79	4.8	2091	3	US-09-126-121-22	Sequence 22, Appl
c 758	79.5	4.8	1505	1	US-07-915-246-1	Sequence 1, Appli	849	79	4.8	2196	4	US-10-069-540A-1	Sequence 1, Appli
759	79.5	4.8	1641	1	US-08-385-229-1	Sequence 1, Appli	851	79	4.8	2313	3	US-08-738-168B-14	Sequence 14, Appl
760	79.5	4.8	1641	2	US-08-650-000-1	Sequence 1, Appli	850	79	4.8	2352	1	US-08-232-538-17	Sequence 17, Appl
761	79.5	4.8	1641	4	US-08-406-824A-1	Sequence 1, Appli	852	79	4.8	2352	2	US-08-786-164-17	Sequence 17, Appl
762	79.5	4.8	1641	4	US-09-758-124-1	Sequence 1, Appli	c 853	79	4.8	2379	4	US-09-252-991A-9205	Sequence 9205, Ap
763	79.5	4.8	1641	6	5395760-1	Patent No. 5395760	854	79	4.8	2481	4	US-09-270-767-14710	Sequence 14710, A
764	79.5	4.8	1641	6	5395760-1	Patent No. 5395760	855	79	4.8	2502	3	US-08-899-437-5	Sequence 5, Appli
765	79.5	4.8	1680	4	US-09-543-681A-3069	Sequence 3069, Ap	856	79	4.8	2502	3	US-09-126-121-5	Sequence 5, Appli
766	79.5	4.8	1803	4	US-09-270-767-13926	Sequence 13926, A	857	79	4.8	2689	4	US-09-902-540-2831	Sequence 2831, Ap
767	79.5	4.8	1965	2	US-08-809-763-5	Sequence 5, Appli	858	79	4.8	3767	4	US-09-823-038A-44	Sequence 44, Appl
768	79.5	4.8	1965	3	US-08-956-253-5	Sequence 5, Appli	c 859	79	4.8	3813	4	US-09-902-540-7085	Sequence 7085, Ap
769	79.5	4.8	2070	4	US-09-252-991A-16098	Sequence 16098, A	860	79	4.8	3815	4	US-09-902-540-634	Sequence 634, App
770	79.5	4.8	2212	4	US-09-270-767-14682	Sequence 14682, A	861	79	4.8	3919	1	US-08-301-722A-1	Sequence 1, Appli
771	79.5	4.8	2224	3	US-08-477-347-2	Sequence 2, Appli	862	79	4.8	3926	4	US-09-949-016-1224	Sequence 1224, Ap
772	79.5	4.8	2224	3	US-08-476-862-1	Sequence 1, Appli	863	79	4.8	3946	4	US-09-949-016-146	Sequence 146, App
773	79.5	4.8	2224	4	US-09-800-909-1	Sequence 1, Appli	864	79	4.8	3960	4	US-09-902-540-8918	Sequence 8918, Ap
774	79.5	4.8	2224	4	US-09-800-908-2	Sequence 2, Appli	c 865	79	4.8	4226	4	US-09-620-312D-480	Sequence 480, App
775	79.5	4.8	2388	4	US-09-270-767-12079	Sequence 12079, A	866	79	4.8	5183	1	US-08-459-568-3	Sequence 3, Appli
776	79.5	4.8	2454	4	US-09-614-221A-393	Sequence 393, App	c 867	79	4.8	5183	2	US-08-399-411-3	Sequence 3, Appli
777	79.5	4.8	2905	4	US-09-902-540-473	Sequence 473, App	c 868	79	4.8	5516	4	US-09-949-016-868	Sequence 868, App
778	79.5	4.8	3003	1	US-08-434-730-15	Sequence 15, Appl	c 869	79	4.8	5868	3	US-08-516-859A-3	Sequence 3, Appli
779	79.5	4.8	3048	1	US-08-188-228-47	Sequence 47, Appl	c 870	79	4.8	5868	3	US-09-586-472-3	Sequence 3, Appli

C 871	79	4.8	5868	3	US-09-528-706-3	Sequence 3, Appli	C 944	78	4.7	1630	4	US-09-949-016-3674	Sequence 3674, Ap
C 872	79	4.8	6002	3	US-09-345-882-4	Sequence 4, Appli	945	78	4.7	1632	1	US-08-324-243-34	Sequence 34, Appl
C 873	79	4.8	6008	4	US-09-949-016-5058	Sequence 5058, Ap	946	78	4.7	1632	1	US-08-532-390-34	Sequence 34, Appl
C 874	79	4.8	6173	4	US-09-949-016-5511	Sequence 5511, Ap	947	78	4.7	1632	3	US-08-717-294-34	Sequence 34, Appl
C 875	79	4.8	6173	4	US-09-949-016-5512	Sequence 5512, Ap	948	78	4.7	1632	5	PCT-US95-11511-34	Sequence 34, Appl
C 876	79	4.8	9367	4	US-09-902-540-951	Sequence 951, App	949	78	4.7	1677	3	US-09-545-814-13	Sequence 13, Appl
C 877	79	4.8	9578	4	US-09-949-016-17106	Sequence 17106, A	C 950	78	4.7	1677	3	US-09-545-814-15	Sequence 15, Appl
C 878	79	4.8	11907	3	US-08-061-376-4	Sequence 4, Appli	951	78	4.7	1749	3	US-09-545-814-4	Sequence 4, Appli
C 879	79	4.8	14464	4	US-09-902-540-1135	Sequence 1135, Ap	C 952	78	4.7	1749	3	US-09-545-814-6	Sequence 6, Appli
C 880	79	4.8	14555	4	US-09-902-540-1096	Sequence 1096, Ap	953	78	4.7	1758	4	US-09-902-540-9019	Sequence 9019, Ap
C 881	79	4.8	19702	3	US-08-961-527-7	Sequence 7, Appli	C 954	78	4.7	1809	4	US-09-252-991A-13958	Sequence 13958, A
C 882	79	4.8	23257	4	US-09-949-016-12894	Sequence 12894, A	955	78	4.7	1892	3	US-09-232-160-8	Sequence 8, Appli
C 883	79	4.8	23260	4	US-09-949-016-14300	Sequence 14300, A	956	78	4.7	1919	3	US-09-545-814-31	Sequence 31, Appl
C 884	79	4.8	36519	3	US-08-923-137-2	Sequence 2, Appli	C 957	78	4.7	1919	3	US-09-545-814-33	Sequence 33, Appl
C 885	79	4.8	42672	4	US-09-949-016-17253	Sequence 17253, A	C 958	78	4.7	2157	4	US-09-252-991A-15294	Sequence 15294, A
C 886	79	4.8	42672	4	US-09-949-016-17254	Sequence 17254, A	C 959	78	4.7	2280	4	US-09-248-796A-5157	Sequence 5157, Ap
C 887	79	4.8	49225	4	US-09-902-540-1269	Sequence 1269, Ap	960	78	4.7	2361	4	US-09-252-991A-15546	Sequence 15546, A
C 888	79	4.8	78125	4	US-09-949-016-16006	Sequence 16006, A	961	78	4.7	2421	4	US-09-565-501A-103	Sequence 103, App
C 889	79	4.8	154746	4	US-09-827-688-8	Sequence 8, Appli	962	78	4.7	2421	4	US-09-639-206A-103	Sequence 103, App
C 890	79	4.8	246240	2	US-08-724-394A-20	Sequence 20, Appl	963	78	4.7	2421	4	US-09-874-923-103	Sequence 103, App
C 891	79	4.8	246240	2	US-08-724-394A-21	Sequence 21, Appl	964	78	4.7	2481	1	US-08-324-243-35	Sequence 35, Appl
C 892	79	4.8	246240	2	US-08-724-394A-22	Sequence 22, Appl	965	78	4.7	2481	1	US-08-532-390-35	Sequence 35, Appl
C 893	78.5	4.7	532	4	US-09-270-767-1305	Sequence 1305, Ap	966	78	4.7	2481	3	US-08-717-294-35	Sequence 35, Appl
C 894	78.5	4.7	532	4	US-09-270-767-16587	Sequence 16587, A	967	78	4.7	2481	5	PCT-US95-11511-35	Sequence 35, Appl
C 895	78.5	4.7	966	4	US-09-248-796A-9577	Sequence 9577, Ap	968	78	4.7	2571	4	US-09-552-950-4	Sequence 4, Appli
C 896	78.5	4.7	1083	4	US-09-489-039A-2212	Sequence 2212, Ap	969	78	4.7	2571	4	US-09-936-572-4	Sequence 4, Appli
C 897	78.5	4.7	1440	4	US-09-270-767-12289	Sequence 12289, A	970	78	4.7	2610	3	US-09-545-814-1	Sequence 1, Appli
C 898	78.5	4.7	1482	4	US-09-252-991A-9689	Sequence 9689, Ap	C 971	78	4.7	2610	3	US-09-545-814-3	Sequence 3, Appli
C 899	78.5	4.7	1596	4	US-09-270-767-1002	Sequence 1002, Ap	972	78	4.7	2804	1	US-08-446-794A-3	Sequence 3, Appli
C 900	78.5	4.7	1596	4	US-09-270-767-16284	Sequence 16284, A	973	78	4.7	3793	4	US-09-902-540-587	Sequence 587, App
C 901	78.5	4.7	1614	4	US-09-252-991A-9607	Sequence 9607, Ap	C 974	78	4.7	3945	4	US-09-602-777A-359	Sequence 359, App
C 902	78.5	4.7	1623	4	US-09-252-991A-9650	Sequence 9650, Ap	975	78	4.7	3996	4	US-09-949-016-2026	Sequence 2026, Ap
C 903	78.5	4.7	1692	4	US-09-252-991A-978	Sequence 978, App	976	78	4.7	4152	3	US-08-826-134-5	Sequence 5, Appli
C 904	78.5	4.7	1764	4	US-09-857-669-5	Sequence 5, Appli	977	78	4.7	4792	3	US-09-221-017B-107	Sequence 107, App
C 905	78.5	4.7	1770	4	US-09-902-540-7164	Sequence 7164, Ap	978	78	4.7	5280	4	US-09-949-016-5586	Sequence 5586, Ap
C 906	78.5	4.7	1779	4	US-09-302-626B-5	Sequence 5, Appli	979	78	4.7	5293	4	US-09-949-016-524	Sequence 524, App
C 907	78.5	4.7	1788	1	US-08-225-989-1	Sequence 1, Appli	980	78	4.7	5294	3	US-08-826-134-1	Sequence 1, Appli
C 908	78.5	4.7	1788	1	US-08-570-923-1	Sequence 1, Appli	981	78	4.7	5516	4	US-09-949-016-13954	Sequence 13954, A
C 909	78.5	4.7	1788	1	US-08-580-014-1	Sequence 1, Appli	C 982	78	4.7	5541	1	US-08-920-812-20	Sequence 20, Appl
C 910	78.5	4.7	1788	3	US-09-079-785-1	Sequence 1, Appli	C 983	78	4.7	5541	1	US-08-920-827-20	Sequence 20, Appl
C 911	78.5	4.7	1788	4	US-09-921-667-5	Sequence 5, Appli	C 984	78	4.7	5541	1	US-08-921-177-20	Sequence 20, Appl
C 912	78.5	4.7	1788	4	US-09-628-126-1	Sequence 1, Appli	C 985	78	4.7	5541	1	US-08-362-577C-20	Sequence 20, Appl
C 913	78.5	4.7	1800	3	US-09-377-155-14	Sequence 14, Appl	C 986	78	4.7	5541	2	US-08-920-828-20	Sequence 20, Appl
C 914	78.5	4.7	1800	3	US-09-669-974-14	Sequence 14, Appl	C 987	78	4.7	5631	4	US-09-949-016-15416	Sequence 15416, A
C 915	78.5	4.7	1800	4	US-09-797-862-14	Sequence 14, Appl	C 988	78	4.7	5751	4	US-09-023-655-1415	Sequence 1415, Ap
C 916	78.5	4.7	2341	4	US-09-520-781-9	Sequence 9, Appli	989	78	4.7	6008	4	US-09-949-016-5058	Sequence 5058, Ap
C 917	78.5	4.7	2450	4	US-09-620-312D-336	Sequence 336, App	C 990	78	4.7	6312	1	US-08-531-601-3	Sequence 3, Appli
C 918	78.5	4.7	2467	4	US-09-799-451-628	Sequence 628, App	C 991	78	4.7	6312	2	US-08-859-032-3	Sequence 3, Appli
C 919	78.5	4.7	2950	4	US-09-710-279-3349	Sequence 3349, Ap	C 992	78	4.7	7198	3	US-08-994-035C-4	Sequence 4, Appli
C 920	78.5	4.7	3233	4	US-09-949-016-2531	Sequence 2531, Ap	C 993	78	4.7	7198	3	US-09-395-861-4	Sequence 4, Appli
C 921	78.5	4.7	3352	4	US-10-101-464A-868	Sequence 868, App	994	78	4.7	7376	4	US-09-949-016-4052	Sequence 4052, Ap
C 922	78.5	4.7	3424	3	US-09-336-643A-9	Sequence 9, Appli	C 995	78	4.7	10085	4	US-09-902-540-964	Sequence 964, App
C 923	78.5	4.7	3760	4	US-09-710-279-4029	Sequence 4029, Ap	C 996	78	4.7	23738	4	US-09-902-540-1203	Sequence 1203, Ap
C 924	78.5	4.7	3941	4	US-09-902-540-660	Sequence 660, App	C 997	78	4.7	35081	2	US-08-752-760A-1	Sequence 1, Appli
C 925	78.5	4.7	6891	4	US-09-902-540-886	Sequence 886, App	C 998	78	4.7	43360	3	US-09-453-702B-206	Sequence 206, App
C 926	78.5	4.7	30922	4	US-09-949-016-16700	Sequence 16700, A	C 999	78	4.7	45325	3	US-09-453-702B-261	Sequence 261, App
C 927	78.5	4.7	30922	4	US-09-949-016-16700	Sequence 16700, A	1000	78	4.7	50937	3	US-09-428-517-1	Sequence 1, Appli
C 928	78.5	4.7	70770	4	US-09-949-016-16938	Sequence 16938, A	C1001	78	4.7	57139	4	US-09-949-016-11771	Sequence 11771, A
C 929	78.5	4.7	81819	4	US-09-949-016-16661	Sequence 16661, A	C1002	78	4.7	57150	4	US-09-949-016-16233	Sequence 16233, A
C 930	78.5	4.7	81819	4	US-09-949-016-16662	Sequence 16662, A	1003	78	4.7	84761	4	US-09-949-016-11919	Sequence 11919, A
C 931	78	4.7	510	4	US-09-252-991A-9469	Sequence 9469, Ap	1004	78	4.7	84763	4	US-09-949-016-13914	Sequence 13914, A
C 932	78	4.7	772	4	US-09-367-572-3	Sequence 3, Appli	C1005	78	4.7	84875	4	US-09-949-016-17334	Sequence 17334, A
C 933	78	4.7	1140	4	US-09-489-039A-4643	Sequence 4643, Ap	C1006	78	4.7	84875	4	US-09-949-016-17335	Sequence 17335, A
C 934	78	4.7	1197	4	US-09-248-796A-875	Sequence 875, App	C1007	78	4.7	84875	4	US-09-949-016-17336	Sequence 17336, A
C 935	78	4.7	1245	4	US-09-489-039A-5399	Sequence 5399, Ap	C1008	78	4.7	84875	4	US-09-949-016-17337	Sequence 17337, A
C 936	78	4.7	1340	4	US-09-949-016-1700	Sequence 1700, Ap	C1009	78	4.7	85152	4	US-09-949-016-12665	Sequence 12665, A
C 937	78	4.7	1419	3	US-09-625-188-5	Sequence 5, Appli	C1010	78	4.7	85152	4	US-09-949-016-12666	Sequence 12666, A
C 938	78	4.7	1478	3	US-09-545-814-28	Sequence 28, Appl	C1011	78	4.7	85152	4	US-09-949-016-12667	Sequence 12667, A
C 939	78	4.7	1478	3	US-09-545-814-30	Sequence 30, Appl	C1012	78	4.7	85152	4	US-09-949-016-12668	Sequence 12668, A
C 940	78	4.7	1485	4	US-09-248-796A-2443	Sequence 2443, Ap	C1013	78	4.7	152481	4	US-09-949-016-12521	Sequence 12521, A
C 941	78	4.7	1549	2	US-08-865-597A-1	Sequence 1, Appli	C1014	78	4.7	152798	4	US-09-949-016-12775	Sequence 12775, A
C 942	78	4.7	1596	1	US-08-531-601-2	Sequence 2, Appli	C1015	78	4.7	152822	4	US-09-949-016-17518	Sequence 17518, A
C 943	78	4.7	1596	2	US-08-859-032-2	Sequence 2, Appli	C1016	78	4.7	152822	4	US-09-949-016-17519	Sequence 17519, A

1017	78	4.7	536165	4	US-09-214-808-1	Sequence 1, Appli	1090	77	4.6	1069	3	US-09-372-422A-7	Sequence 7, Appli
1018	77.5	4.7	429	4	US-09-107-532A-2661	Sequence 2661, Ap	c1091	77	4.6	1092	4	US-09-252-991A-14341	Sequence 14341, A
c1019	77.5	4.7	522	4	US-09-621-976-2854	Sequence 2854, Ap	1092	77	4.6	1167	4	US-09-252-991A-14278	Sequence 14278, A
1020	77.5	4.7	601	4	US-09-949-016-45651	Sequence 45651, A	c1093	77	4.6	1206	4	US-09-252-991A-13220	Sequence 13220, A
1021	77.5	4.7	813	4	US-09-134-000C-148	Sequence 148, App	1094	77	4.6	1350	4	US-09-252-991A-11976	Sequence 11976, A
1022	77.5	4.7	1023	4	US-09-248-796A-10497	Sequence 10497, A	c1095	77	4.6	1368	4	US-09-543-681A-2871	Sequence 2871, Ap
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1024	77.5	4.7	1288	4	US-09-602-787A-417	Sequence 417, App	1097	77	4.6	1472	4	US-09-270-767-18947	Sequence 18947, A
1025	77.5	4.7	1584	1	US-07-667-276A-1	Sequence 1, Appli	1098	77	4.6	1719	4	US-09-252-991A-12741	Sequence 12741, A
1026	77.5	4.7	1857	3	US-09-377-557-9	Sequence 9, Appli	1099	77	4.6	1749	4	US-09-489-039A-4884	Sequence 4884, Ap
1027	77.5	4.7	1865	3	US-09-370-253-5	Sequence 5, Appli	c1100	77	4.6	1779	4	US-09-248-796A-3286	Sequence 3286, Ap
1028	77.5	4.7	1874	4	US-09-270-767-11069	Sequence 11069, A	c1101	77	4.6	1875	4	US-09-252-991A-8812	Sequence 8812, Ap
1029	77.5	4.7	2325	2	US-08-714-677-3	Sequence 3, Appli	1102	77	4.6	1920	4	US-09-248-796A-6480	Sequence 6480, Ap
1030	77.5	4.7	2325	2	US-08-393-540-3	Sequence 3, Appli	1103	77	4.6	1923	4	US-09-302-626B-19	Sequence 19, Appl
1031	77.5	4.7	2325	2	US-08-714-537-3	Sequence 3, Appli	c1104	77	4.6	1998	4	US-09-949-016-444	Sequence 44, App
1032	77.5	4.7	2371	2	US-08-343-443B-1	Sequence 1, Appli	1105	77	4.6	2172	4	US-09-893-737-99	Sequence 99, Appl
1033	77.5	4.7	2511	4	US-09-252-991A-9132	Sequence 9132, Ap	1106	77	4.6	2220	2	US-08-932-376A-3	Sequence 3, Appli
1034	77.5	4.7	2513	4	US-09-620-312D-337	Sequence 337, App	1107	77	4.6	2430	4	US-09-252-991A-12709	Sequence 12709, A
1035	77.5	4.7	3073	2	US-08-714-677-11	Sequence 11, Appl	c1108	77	4.6	2439	4	US-09-023-655-1455	Sequence 1455, Ap
1036	77.5	4.7	3073	2	US-08-393-540-11	Sequence 11, Appl	c1109	77	4.6	2458	3	US-08-611-587-6	Sequence 6, Appli
1037	77.5	4.7	3073	2	US-08-714-537-11	Sequence 11, Appl	1110	77	4.6	2463	4	US-09-252-991A-8582	Sequence 8582, Ap
1038	77.5	4.7	3789	4	US-09-107-433-2464	Sequence 2464, Ap	1111	77	4.6	2517	4	US-09-252-991A-9238	Sequence 9238, Ap
1039	77.5	4.7	3990	4	US-09-799-451-538	Sequence 538, App	1112	77	4.6	2538	3	US-08-899-437-1	Sequence 1, Appli
1040	77.5	4.7	4673	1	US-07-638-431-1	Sequence 1, Appli	1113	77	4.6	2538	3	US-09-126-121-1	Sequence 1, Appli
1041	77.5	4.7	4673	5	PCT-US92-00018-1	Sequence 1, Appli	c1114	77	4.6	2607	4	US-09-252-991A-13249	Sequence 13249, A
1042	77.5	4.7	5099	1	US-08-487-890A-4	Sequence 4, Appli	1115	77	4.6	2744	3	US-09-071-101-1	Sequence 1, Appli
1043	77.5	4.7	5099	2	US-08-478-435-4	Sequence 4, Appli	1116	77	4.6	2744	3	US-09-369-618-1	Sequence 1, Appli
1044	77.5	4.7	5099	2	US-08-337-483-4	Sequence 4, Appli	1117	77	4.6	2744	3	US-09-369-617-1	Sequence 1, Appli
1045	77.5	4.7	5099	2	US-08-478-373-4	Sequence 4, Appli	c1118	77	4.6	2748	4	US-09-252-991A-8662	Sequence 8662, Ap
1046	77.5	4.7	5099	3	US-08-474-671-4	Sequence 4, Appli	1119	77	4.6	3292	3	US-09-068-140A-12	Sequence 12, Appl
1047	77.5	4.7	5099	3	US-08-483-577A-4	Sequence 4, Appli	1120	77	4.6	3423	4	US-09-614-221A-91	Sequence 91, Appl
1048	77.5	4.7	5099	3	US-08-897-438-4	Sequence 4, Appli	1121	77	4.6	3464	4	US-09-949-016-1167	Sequence 1167, Ap
1049	77.5	4.7	5099	3	US-08-637-654-4	Sequence 4, Appli	1122	77	4.6	3872	4	US-09-949-016-1709	Sequence 1709, Ap
1050	77.5	4.7	5099	3	US-08-649-518-4	Sequence 4, Appli	1123	77	4.6	3955	3	US-09-214-278-4	Sequence 4, Appli
1051	77.5	4.7	7785	2	US-08-276-967-1	Sequence 1, Appli	1124	77	4.6	3955	4	US-09-855-722-4	Sequence 4, Appli
c1052	77.5	4.7	8132	3	US-08-766-528-3	Sequence 3, Appli	1125	77	4.6	4108	3	US-08-981-729-8	Sequence 8, Appli
c1053	77.5	4.7	8132	4	US-09-661-858-3	Sequence 3, Appli	1126	77	4.6	4108	3	US-08-981-446B-1	Sequence 1, Appli
1054	77.5	4.7	8442	3	US-09-272-032-6	Sequence 6, Appli	1127	77	4.6	4108	4	US-09-613-811-8	Sequence 8, Appli
c1055	77.5	4.7	9171	2	US-08-629-001A-2	Sequence 2, Appli	1128	77	4.6	6476	3	US-09-127-670-5	Sequence 5, Appli
c1056	77.5	4.7	9171	3	US-08-642-274D-2	Sequence 2, Appli	1129	77	4.6	6627	4	US-09-345-236B-94	Sequence 94, Appl
c1058	77.5	4.7	9171	3	US-08-952-014C-2	Sequence 2, Appli	1130	77	4.6	6627	4	US-09-345-236B-100	Sequence 100, App
c1059	77.5	4.7	9196	4	US-08-984-090-1	Sequence 1, Appli	c1131	77	4.6	6627	4	US-09-345-236B-106	Sequence 106, App
c1060	77.5	4.7	9385	2	US-08-874-266-1	Sequence 1, Appli	c1132	77	4.6	6627	4	US-09-345-236B-113	Sequence 113, App
c1061	77.5	4.7	9385	3	US-09-360-416-1	Sequence 1, Appli	1134	77	4.6	7212	4	US-09-345-236B-117	Sequence 117, App
c1062	77.5	4.7	9389	4	US-09-949-016-4409	Sequence 4409, Ap	c1135	77	4.6	7212	4	US-09-345-236B-126	Sequence 126, App
c1063	77.5	4.7	9870	1	US-08-508-836A-9	Sequence 9, Appli	c1136	77	4.6	7212	4	US-09-345-236B-130	Sequence 130, App
1064	77.5	4.7	9992	4	US-09-902-540-952	Sequence 952, App	1137	77	4.6	7559	2	US-08-250-848-2	Sequence 2, Appli
1065	77.5	4.7	11706	4	US-09-902-540-1038	Sequence 1038, Ap	c1138	77	4.6	14349	4	US-09-949-016-15434	Sequence 15434, A
c1066	77.5	4.7	12619	4	US-09-616-289-49	Sequence 49, Appl	c1139	77	4.6	16225	4	US-09-949-016-15152	Sequence 15152, A
c1067	77.5	4.7	13987	2	US-08-804-227C-13	Sequence 13, Appl	c1140	77	4.6	16225	4	US-09-949-016-15160	Sequence 15160, A
1068	77.5	4.7	14255	1	US-08-320-559-1	Sequence 1, Appli	c1141	77	4.6	16225	4	US-09-949-016-15196	Sequence 15196, A
1069	77.5	4.7	14255	1	US-08-327-392-1	Sequence 1, Appli	1142	77	4.6	19269	4	US-09-902-540-1175	Sequence 1175, Ap
1070	77.5	4.7	14255	1	US-08-306-691B-55	Sequence 55, Appl	1143	77	4.6	22906	4	US-09-949-016-16471	Sequence 16471, A
1071	77.5	4.7	14255	3	US-08-545-860D-1	Sequence 1, Appli	1144	77	4.6	28809	4	US-09-949-016-12825	Sequence 12825, A
1072	77.5	4.7	14255	5	PCT-US94-04496-1	Sequence 1, Appli	c1145	77	4.6	36611	4	US-09-949-016-17287	Sequence 17287, A
1073	77.5	4.7	17723	4	US-09-949-016-15832	Sequence 15832, A	1146	77	4.6	52314	4	US-09-949-016-14622	Sequence 14622, A
c1074	77.5	4.7	43280	2	US-08-804-227C-1	Sequence 1, Appli	1147	77	4.6	91831	4	US-09-949-016-13694	Sequence 13694, A
1075	77.5	4.7	58133	4	US-09-949-016-16464	Sequence 16464, A	1148	77	4.6	99916	4	US-09-816-095-3	Sequence 3, Appli
c1076	77.5	4.7	67620	4	US-09-949-016-16939	Sequence 16939, A	c1149	77	4.6	134987	4	US-09-949-016-15348	Sequence 15348, A
1077	77.5	4.7	112112	4	US-09-949-016-15639	Sequence 15639, A	c1150	77	4.6	134987	4	US-09-949-016-15349	Sequence 15349, A
c1078	77.5	4.7	137949	4	US-09-949-016-12196	Sequence 12196, A	c1151	77	4.6	134987	4	US-09-949-016-15350	Sequence 15350, A
c1079	77.5	4.7	137956	4	US-09-949-016-17260	Sequence 17260, A	c1152	77	4.6	134987	4	US-09-949-016-15507	Sequence 15507, A
1080	77.5	4.7	141115	4	US-09-949-016-17490	Sequence 17490, A	c1153	77	4.6	134987	4	US-09-949-016-15508	Sequence 15508, A
1081	77.5	4.7	142783	4	US-09-949-016-15127	Sequence 15127, A	c1154	77	4.6	134987	4	US-09-949-016-15509	Sequence 15509, A
c1082	77.5	4.7	150394	4	US-09-949-016-13042	Sequence 13042, A	c1155	77	4.6	156942	4	US-09-949-016-12227	Sequence 12227, A
1083	77	4.6	346	4	US-09-377-502-53	Sequence 53, Appl	c1156	77	4.6	156950	4	US-09-949-016-15946	Sequence 15946, A
1084	77	4.6	535	4	US-09-621-976-48	Sequence 48, Appl	c1157	77	4.6	340380	4	US-09-949-016-14179	Sequence 14179, A
c1085	77	4.6	542	4	US-09-167-206-23	Sequence 23, Appl	1158	76.5	4.6	405	4	US-09-248-796A-13214	Sequence 13214, A
c1086	77	4.6	543	4	US-09-489-039A-5453	Sequence 5453, Ap	1159	76.5	4.6	601	4	US-09-949-016-175056	Sequence 175056,
c1087	77	4.6	601	4	US-09-949-016-86892	Sequence 86892, A	1160	76.5	4.6	909	4	US-09-248-796A-166	Sequence 166, App
1088	77	4.6	882	3	US-09-068-140A-1	Sequence 1, Appli	c1161	76.5	4.6	951	4	US-09-107-532A-1270	Sequence 1270, Ap
1089	77	4.6	939	4	US-09-252-991A-9154	Sequence 9154, Ap	c1162	76.5	4.6	957	4	US-09-902-540-3584	Sequence 3584, Ap

1163	76.5	4.6	975	4	US-09-252-991A-7594	Sequence 7594, Ap	cl1236	76.5	4.6	9775	3	US-09-647-540A-5	Sequence 5, Appli
1164	76.5	4.6	1029	4	US-09-252-991A-3332	Sequence 3332, Ap	1237	76.5	4.6	9775	3	US-09-647-540A-7	Sequence 7, Appli
cl1165	76.5	4.6	1047	4	US-09-252-991A-3235	Sequence 3235, Ap	cl1238	76.5	4.6	9775	4	US-10-119-600-1	Sequence 1, Appli
1166	76.5	4.6	1065	4	US-09-340-798A-31	Sequence 31, Appl	cl1239	76.5	4.6	9775	4	US-10-119-600-3	Sequence 3, Appli
1167	76.5	4.6	1122	4	US-09-902-540-7103	Sequence 7103, Ap	cl1240	76.5	4.6	9775	4	US-10-119-600-5	Sequence 5, Appli
1168	76.5	4.6	1141	4	US-09-270-767-12501	Sequence 12501, A	1241	76.5	4.6	9775	4	US-10-119-600-7	Sequence 7, Appli
1169	76.5	4.6	1329	4	US-09-252-991A-15277	Sequence 15277, A	cl1242	76.5	4.6	9775	4	US-10-119-651-1	Sequence 1, Appli
cl1170	76.5	4.6	1340	4	US-09-513-999C-14928	Sequence 14928, A	cl1243	76.5	4.6	9775	4	US-10-119-651-3	Sequence 3, Appli
1171	76.5	4.6	1356	4	US-09-248-796A-2116	Sequence 2116, Ap	cl1244	76.5	4.6	9775	4	US-10-119-651-5	Sequence 5, Appli
cl1172	76.5	4.6	1386	4	US-09-270-767-15263	Sequence 15263, A	1245	76.5	4.6	9775	4	US-10-119-651-7	Sequence 7, Appli
1173	76.5	4.6	1398	4	US-09-252-991A-8277	Sequence 8277, Ap	1246	76.5	4.6	10106	4	US-09-949-016-17187	Sequence 17187, A
1174	76.5	4.6	1551	4	US-09-252-991A-15327	Sequence 15327, A	cl1247	76.5	4.6	10318	4	US-09-902-540-973	Sequence 973, App
cl1175	76.5	4.6	1578	4	US-09-107-532A-2089	Sequence 2089, Ap	1248	76.5	4.6	11003	4	US-09-949-016-13166	Sequence 13166, A
1176	76.5	4.6	1608	4	US-09-252-991A-8157	Sequence 8157, Ap	cl1249	76.5	4.6	14298	4	US-09-949-016-16639	Sequence 16639, A
1177	76.5	4.6	1620	3	US-08-814-052-12	Sequence 12, Appl	1250	76.5	4.6	15363	3	US-08-961-527-139	Sequence 139, App
1178	76.5	4.6	1620	3	US-08-814-052-13	Sequence 13, Appl	cl1251	76.5	4.6	16387	4	US-09-902-540-1156	Sequence 1156, Ap
1179	76.5	4.6	1697	4	US-09-799-451-509	Sequence 509, App	1252	76.5	4.6	17605	4	US-09-949-016-13599	Sequence 13599, A
1180	76.5	4.6	1725	4	US-09-943-075A-7	Sequence 7, Appli	1253	76.5	4.6	18475	3	US-08-961-527-38	Sequence 38, Appl
cl1181	76.5	4.6	1734	4	US-09-252-991A-7986	Sequence 7986, Ap	1254	76.5	4.6	25231	4	US-09-949-016-12041	Sequence 12041, A
cl1182	76.5	4.6	1770	3	US-09-377-155-18	Sequence 18, Appl	1255	76.5	4.6	27933	4	US-09-949-016-12369	Sequence 12369, A
cl1183	76.5	4.6	1770	3	US-09-669-974-18	Sequence 18, Appl	cl1256	76.5	4.6	32379	4	US-09-949-016-15217	Sequence 15217, A
cl1184	76.5	4.6	1770	4	US-09-797-862-18	Sequence 18, Appl	cl1257	76.5	4.6	32379	4	US-09-949-016-15218	Sequence 15218, A
cl1185	76.5	4.6	1771	4	US-09-949-016-4307	Sequence 4307, Ap	cl1258	76.5	4.6	32379	4	US-09-949-016-15219	Sequence 15219, A
cl1186	76.5	4.6	1927	4	US-09-949-016-3372	Sequence 3372, Ap	cl1259	76.5	4.6	32379	4	US-09-949-016-15220	Sequence 15220, A
1187	76.5	4.6	1941	4	US-09-603-208A-55	Sequence 55, Appl	cl1260	76.5	4.6	32379	4	US-09-949-016-15221	Sequence 15221, A
cl1188	76.5	4.6	2001	1	US-08-674-168-24	Sequence 24, Appl	cl1261	76.5	4.6	32379	4	US-09-949-016-15222	Sequence 15222, A
cl1189	76.5	4.6	2001	3	US-08-985-908-10	Sequence 10, Appl	cl1262	76.5	4.6	32379	4	US-09-949-016-15223	Sequence 15223, A
cl1190	76.5	4.6	2001	3	US-08-852-730-23	Sequence 23, Appl	cl1263	76.5	4.6	32379	4	US-09-949-016-15224	Sequence 15224, A
1191	76.5	4.6	2213	3	US-09-383-586-27	Sequence 27, Appl	cl1264	76.5	4.6	32379	4	US-09-949-016-15225	Sequence 15225, A
1192	76.5	4.6	2213	4	US-09-823-038A-27	Sequence 27, Appl	cl1265	76.5	4.6	32379	4	US-09-949-016-15226	Sequence 15226, A
1193	76.5	4.6	2219	3	US-08-510-646B-17	Sequence 17, Appl	cl1266	76.5	4.6	36620	4	US-09-952-060-31	Sequence 31, Appl
cl1194	76.5	4.6	2406	4	US-09-902-540-8703	Sequence 8703, Ap	cl1267	76.5	4.6	37474	4	US-09-952-060-26	Sequence 26, Appl
1195	76.5	4.6	2496	1	US-08-073-384C-2	Sequence 2, Appli	cl1268	76.5	4.6	38519	4	US-09-952-060-29	Sequence 29, Appl
1196	76.5	4.6	2496	1	US-08-254-359A-2	Sequence 2, Appli	cl1269	76.5	4.6	61158	4	US-09-949-016-15041	Sequence 15041, A
1197	76.5	4.6	2496	1	US-08-483-043-2	Sequence 2, Appli	cl1270	76.5	4.6	64377	4	US-09-949-016-15212	Sequence 15212, A
1198	76.5	4.6	2496	1	US-08-481-238-2	Sequence 2, Appli	cl1271	76.5	4.6	64377	4	US-09-949-016-15213	Sequence 15213, A
1199	76.5	4.6	2496	2	US-08-471-066B-2	Sequence 2, Appli	cl1272	76.5	4.6	64377	4	US-09-949-016-15214	Sequence 15214, A
1200	76.5	4.6	2496	2	US-08-484-956-2	Sequence 2, Appli	cl1273	76.5	4.6	64377	4	US-09-949-016-15215	Sequence 15215, A
1201	76.5	4.6	2496	2	US-08-757-653-2	Sequence 2, Appli	cl1274	76.5	4.6	64377	4	US-09-949-016-15216	Sequence 15216, A
1202	76.5	4.6	2496	2	US-08-599-491-2	Sequence 2, Appli	cl1275	76.5	4.6	75431	4	US-09-949-016-15122	Sequence 15122, A
1203	76.5	4.6	2496	2	US-08-756-386-2	Sequence 2, Appli	cl1276	76.5	4.6	100463	4	US-09-949-016-12511	Sequence 12511, A
1204	76.5	4.6	2496	2	US-08-823-516-2	Sequence 2, Appli	cl1277	76.5	4.6	100468	4	US-09-949-016-13725	Sequence 13725, A
1205	76.5	4.6	2496	3	US-08-682-853A-2	Sequence 2, Appli	cl1278	76.5	4.6	112874	4	US-09-949-016-13180	Sequence 13180, A
1206	76.5	4.6	2496	3	US-08-759-038-2	Sequence 2, Appli	1279	76.5	4.6	767677	4	US-09-949-016-12147	Sequence 12147, A
1207	76.5	4.6	2496	3	US-08-758-314-2	Sequence 2, Appli	1280	76.5	4.6	767677	4	US-09-949-016-17361	Sequence 17361, A
1208	76.5	4.6	2496	3	US-09-350-309-2	Sequence 2, Appli	1281	76	4.6	601	4	US-09-949-016-138697	Sequence 138697,
1209	76.5	4.6	2496	3	US-08-520-946-2	Sequence 2, Appli	cl1282	76	4.6	750	4	US-09-107-433-906	Sequence 906, App
1210	76.5	4.6	2496	4	US-09-684-938-2	Sequence 2, Appli	1283	76	4.6	966	4	US-09-248-796A-6043	Sequence 6043, Ap
1211	76.5	4.6	2496	4	US-09-308-825A-2	Sequence 2, Appli	1284	76	4.6	1013	4	US-08-930-830B-1	Sequence 1, Appli
1212	76.5	4.6	2496	4	US-09-758-282B-2	Sequence 2, Appli	1285	76	4.6	1038	4	US-09-543-681A-1978	Sequence 1978, Ap
1213	76.5	4.6	2496	4	US-09-758-282B-2	Sequence 2, Appli	cl1286	76	4.6	1074	4	US-09-489-039A-6272	Sequence 6272, Ap
1214	76.5	4.6	2496	4	US-09-655-378A-2	Sequence 2, Appli	cl1287	76	4.6	1086	4	US-09-540-236-244	Sequence 244, App
1215	76.5	4.6	2496	4	US-09-940-244-2	Sequence 2, Appli	1288	76	4.6	1119	4	US-09-602-777A-27	Sequence 27, Appl
1216	76.5	4.6	2496	4	US-09-333-145-2	Sequence 2, Appli	1289	76	4.6	1122	4	US-09-902-540-4288	Sequence 4288, Ap
1217	76.5	4.6	2496	4	US-09-577-304A-2	Sequence 2, Appli	1290	76	4.6	1143	3	US-09-134-001C-1721	Sequence 1721, Ap
1218	76.5	4.6	2706	4	US-09-248-796A-644	Sequence 644, App	1291	76	4.6	1161	4	US-09-328-352-596	Sequence 596, App
1219	76.5	4.6	2735	4	US-09-620-312D-842	Sequence 842, App	1292	76	4.6	1173	4	US-09-902-540-2437	Sequence 2437, Ap
cl1220	76.5	4.6	2850	2	US-08-224-482-7	Sequence 7, Appli	cl1293	76	4.6	1185	4	US-09-252-991A-11261	Sequence 11261, A
1221	76.5	4.6	3162	4	US-09-543-681A-1809	Sequence 1809, Ap	1294	76	4.6	1211	2	US-08-997-080-40	Sequence 40, Appl
1222	76.5	4.6	3185	4	US-09-710-279-3758	Sequence 3758, Ap	1295	76	4.6	1211	2	US-08-997-362-40	Sequence 40, Appl
1223	76.5	4.6	3792	3	US-08-860-886-1	Sequence 1, Appli	1296	76	4.6	1211	3	US-08-873-970-40	Sequence 40, Appl
cl1224	76.5	4.6	3818	4	US-09-949-016-5445	Sequence 5445, Ap	1297	76	4.6	1211	3	US-09-095-855-40	Sequence 40, Appl
1225	76.5	4.6	3889	3	US-09-484-970B-39	Sequence 39, Appl	1298	76	4.6	1211	3	US-08-705-347A-40	Sequence 40, Appl
1226	76.5	4.6	4289	4	US-09-949-016-627	Sequence 627, App	1299	76	4.6	1211	3	US-09-324-542-40	Sequence 40, Appl
1227	76.5	4.6	4403	2	US-08-284-941-1	Sequence 1, Appli	1300	76	4.6	1211	3	US-09-205-426-40	Sequence 40, Appl
1228	76.5	4.6	4403	2	US-08-447-642-1	Sequence 1, Appli	1301	76	4.6	1211	3	US-09-200-643-40	Sequence 40, Appl
1229	76.5	4.6	4403	3	US-09-236-503-1	Sequence 1, Appli	1302	76	4.6	1295	1	US-08-433-854-3	Sequence 3, Appli
1230	76.5	4.6	4403	4	US-09-949-016-369	Sequence 369, App	1303	76	4.6	1295	1	US-08-174-745A-3	Sequence 3, Appli
1231	76.5	4.6	4403	5	PCT-US93-02147A-1	Sequence 1, Appli	1304	76	4.6	1295	2	US-08-195-947-3	Sequence 3, Appli
cl1232	76.5	4.6	5063	4	US-09-949-016-1375	Sequence 1375, Ap	1305	76	4.6	1295	2	US-08-433-885-3	Sequence 3, Appli
1233	76.5	4.6	7052	4	US-09-526-193A-22	Sequence 22, Appl	1306	76	4.6	1295	2	US-08-433-908B-3	Sequence 3, Appli
1234	76.5	4.6	7109	4	US-09-902-540-922	Sequence 922, App	1307	76	4.6	1295	3	US-08-410-614-3	Sequence 3, Appli
cl1235	76.5	4.6	9775	3	US-09-647-540A-1	Sequence 1, Appli	1308	76	4.6	1307	4	US-09-774-639-49	Sequence 49, Appl

1309	76	4.6	1308	4	US-09-801-861-4	Sequence 4, Appli	Sequence 4, Appli	1391	76	4.6	4183	4	US-09-895-547-1	Sequence 1, Appli
1310	76	4.6	1308	4	US-10-224-562-4	Sequence 4, Appli	Sequence 4, Appli	1392	76	4.6	4464	2	US-08-400-159-7	Sequence 7, Appli
1311	76	4.6	1311	4	US-09-252-991A-1607	Sequence 1607, Ap	Sequence 1607, Ap	1393	76	4.6	4483	3	US-08-611-729A-7	Sequence 7, Appli
1312	76	4.6	1320	4	US-09-949-016-1481	Sequence 1481, Ap	Sequence 1481, Ap	1394	76	4.6	4483	4	US-09-195-524-7	Sequence 7, Appli
1313	76	4.6	1347	4	US-09-252-991A-10926	Sequence 10926, A	Sequence 10926, A	1395	76	4.6	4597	4	US-09-949-016-5173	Sequence 5173, Ap
1314	76	4.6	1365	4	US-09-252-991A-11429	Sequence 11429, A	Sequence 11429, A	1396	76	4.6	4792	3	US-08-781-891-205	Sequence 205, App
1315	76	4.6	1395	4	US-09-252-991A-10988	Sequence 10988, A	Sequence 10988, A	1397	76	4.6	4792	4	US-09-618-166-205	Sequence 205, App
1316	76	4.6	1413	4	US-09-252-991A-11269	Sequence 11269, A	Sequence 11269, A	1398	76	4.6	5724	4	US-09-976-594-768	Sequence 768, App
1317	76	4.6	1467	4	US-09-620-312D-662	Sequence 662, App	Sequence 662, App	1399	76	4.6	6122	1	US-08-403-545-1	Sequence 1, Appli
1318	76	4.6	1502	4	US-09-620-312D-362	Sequence 362, App	Sequence 362, App	1400	76	4.6	6122	3	US-08-404-381-1	Sequence 1, Appli
1319	76	4.6	1554	4	US-09-902-540-8489	Sequence 8489, Ap	Sequence 8489, Ap	1401	76	4.6	7147	3	US-08-961-527-23	Sequence 23, Appl
1320	76	4.6	1629	4	US-09-489-039A-4586	Sequence 4586, Ap	Sequence 4586, Ap	1402	76	4.6	7390	4	US-09-566-921-95	Sequence 95, Appl
1321	76	4.6	1659	4	US-09-252-991A-6121	Sequence 6121, Ap	Sequence 6121, Ap	1403	76	4.6	7529	4	US-09-902-540-893	Sequence 893, App
1322	76	4.6	1669	4	US-09-902-540-3010	Sequence 3010, Ap	Sequence 3010, Ap	1404	76	4.6	8517	3	US-08-827-208-1	Sequence 1, Appli
1323	76	4.6	1755	4	US-09-252-991A-11461	Sequence 11461, A	Sequence 11461, A	1405	76	4.6	8517	3	US-09-500-358-1	Sequence 1, Appli
1324	76	4.6	1776	3	US-09-377-155-10	Sequence 10, Appl	Sequence 10, Appl	1406	76	4.6	8517	3	US-09-498-809-1	Sequence 1, Appli
1325	76	4.6	1776	3	US-09-377-155-20	Sequence 20, Appl	Sequence 20, Appl	1407	76	4.6	11707	3	US-09-136-574A-1	Sequence 1, Appli
1326	76	4.6	1776	3	US-09-669-974-10	Sequence 10, Appl	Sequence 10, Appl	1408	76	4.6	14352	4	US-09-902-540-1070	Sequence 1070, Ap
1327	76	4.6	1776	3	US-09-669-974-20	Sequence 20, Appl	Sequence 20, Appl	1409	76	4.6	14899	4	US-09-902-540-1107	Sequence 1107, Ap
1328	76	4.6	1776	4	US-09-797-862-10	Sequence 10, Appl	Sequence 10, Appl	1410	76	4.6	16738	4	US-09-949-016-12168	Sequence 12168, A
1329	76	4.6	1776	4	US-09-797-862-20	Sequence 20, Appl	Sequence 20, Appl	1411	76	4.6	16738	4	US-09-949-016-14678	Sequence 14678, A
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1331	76	4.6	1776	4	US-09-700-293-3	Sequence 3, Appli	Sequence 3, Appli	1413	76	4.6	28030	4	US-09-949-016-16948	Sequence 16948, A
1332	76	4.6	1818	4	US-09-148-545-87	Sequence 87, Appl	Sequence 87, Appl	1414	76	4.6	33478	4	US-09-949-016-13615	Sequence 13615, A
1333	76	4.6	1822	4	US-09-397-243D-1	Sequence 1, Appli	Sequence 1, Appli	1415	76	4.6	36412	4	US-08-311-731A-132	Sequence 132, App
1334	76	4.6	1857	4	US-09-023-655-902	Sequence 902, App	Sequence 902, App	1416	76	4.6	41965	4	US-09-949-016-13067	Sequence 13067, A
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1336	76	4.6	1878	4	US-09-252-991A-6434	Sequence 6434, Ap	Sequence 6434, Ap	1418	76	4.6	43555	4	US-09-949-016-13993	Sequence 13993, A
1337	76	4.6	1925	4	US-09-148-545-86	Sequence 86, Appl	Sequence 86, Appl	1419	76	4.6	43795	3	US-08-742-185-101	Sequence 101, App
1338	76	4.6	1926	4	US-09-148-545-21	Sequence 21, Appl	Sequence 21, Appl	1420	76	4.6	43986	4	US-09-949-016-17155	Sequence 17155, A
1339	76	4.6	1941	4	US-09-248-796A-2598	Sequence 2598, Ap	Sequence 2598, Ap	1421	76	4.6	62909	4	US-09-596-002-32	Sequence 32, Appl
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1341	76	4.6	2091	4	US-09-107-532A-1551	Sequence 1551, Ap	Sequence 1551, Ap	1423	76	4.6	71989	3	US-09-443-501A-2	Sequence 2, Appli
1342	76	4.6	2203	4	US-09-801-861-1	Sequence 1, Appli	Sequence 1, Appli	1424	76	4.6	197496	4	US-09-877-177A-10	Sequence 10, Appl
1343	76	4.6	2203	4	US-10-224-562-1	Sequence 1, Appli	Sequence 1, Appli	1425	75.5	4.6	594	4	US-09-252-991A-7647	Sequence 7647, Ap
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1349	76	4.6	2955	4	US-09-248-796A-1987	Sequence 1987, Ap	Sequence 1987, Ap	1431	75.5	4.6	815	3	US-09-383-586-9	Sequence 9, Appli
1359	76	4.6	3045	4	US-09-596-248D-24	Sequence 24, Appl	Sequence 24, Appl	1432	75.5	4.6	815	4	US-09-823-038A-9	Sequence 9, Appli
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1471	75.5	4.6	2205	1	US-08-035-392-3	Sequence 3, Appli
1472	75.5	4.6	2205	1	US-08-504-511A-3	Sequence 3, Appli
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1474	75.5	4.6	2340	4	US-09-475-515-67	Sequence 67, Appl
1475	75.5	4.6	2385	4	US-09-475-515-68	Sequence 68, Appl
1476	75.5	4.6	2412	1	US-08-437-027-18	Sequence 18, Appl
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1497	75.5	4.6	2502	4	US-09-333-145-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

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Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

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RESULT 2
US-09-949-016-1894
; Sequence 1894, Application US/09949016
; Patent No. 6812339


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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1894
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1894
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Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              4          Gaps:      0
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RESULT 3
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; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.:	2.56e-183	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
DB	160	ATGGCCAGGTGCTTCAGCTGGTGTGTTCTCTCACTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
DB	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCAGGTGTCATGCAGAAATATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
DB	280	ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTTCACAGAAGCTAAGGAGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
DB	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerpGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
DB	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
DB	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
DB	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
DB	580	CCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
DB	640	GAATTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACATACTGCC	699
QY	181	ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200

DB	700	CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
DB	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
DB	820	GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
DB	880	CTAGTGCTTGCTCTCCTCTTCTTTTGGTGTGCAGCTGGTCTTTGGATTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
DB	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
DB	1000	AAAGTAGTAAAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAGAAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
DB	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAGAAAACTACCGTGGATGCGTGGAAAGCT	1119
QY	321	GluVal 322	
DB	1120	GAAGTT 1125	

RESULT 4
; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594

;
;
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
;
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
;
; SEQ ID NO 200
;
; LENGTH: 2372
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 2,56e-183 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrPThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCCATCTCGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTGGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGAAAAAATGGGGTGGTGTCTCTGATTTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGTGCAGCTGGTCTTTGGATTTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAAACCCAGAAGAGTCCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 5
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

;
;
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.:	2.56e-183	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0
QY	1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20		
Db	160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCCTG 219		
QY	21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40		
Db	220 GTCCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279		
QY	41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60		
Db	280 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339		
QY	61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80		
Db	340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGCAAGTGAACAGCCTTGAAAGCT 399		
QY	81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgile 100		
Db	400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTTAGGATT 459		
QY	101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120		
Db	460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG 519		
QY	121 SerArgGlnPheAlaIatyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140		
Db	520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579		

QY	141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160		
Db	580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAAC TGCAACACAAACA 639		
QY	161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180		
Db	640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGATCCCCTTACTCTACAATACCTGCC 699		
QY	181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200		
Db	700 CCTACTACTCTCTCTGCCAGCTTCCACTTCTATCCACGGAGAAAAAATTGATT 759		
QY	201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220		
Db	760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819		
QY	221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240		
Db	820 GAAATAAAGCAGCATTCAAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879		
QY	241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260		
Db	880 CTAGTGCTTGCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939		
QY	261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280		
Db	940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 999		
QY	281 LysValValLysGluGluSerLysLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300		
Db	1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059		
QY	301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320		
Db	1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCGAAGCT 1119		
QY	321 GluVal 322		
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RESULT 6

; Sequence 200, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700

; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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DB: 4 Gaps: 0

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTTCCTCTCACTTCCATCTGGACCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTCCATCCAGGTGTCAATGCAGAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTCCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGACGCTATGGCTGGTGGGTTGGAGATGGATTCTGTGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCCTGATTGTGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCACCGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCACCAAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 7
; Sequence 200, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

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; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:      2,56e-183      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     100.00%      Indels:       0
DB:              4              Gaps:         0

QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
      160 ATGCCCAGGTGCTTCAGCCTGGTGTTCCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTCTGATTTGGAAAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCACTATCGATACTTGGACTAACTCGTGCATT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      700 CCTACTACTACTCTCTCTCTCTTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrGluProPheVal 220
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      760 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      820 GAAATATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTCGAGGTTGGAGGTGTCGCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      880 CTAGTGCTTGCTCTCTCTCTTCTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAA 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC 999
QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1000 AAAGTAGTAAGGAGGAGGAGGCAATGATAGCAACCCCTAATAGGGAATCAAAGAAAAACT 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1060 GATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGGAAGCT 1119
QY      321 GluVal 322
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Db      1120 GAAGTT 1125

RESULT 8
; Sequence 200, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```



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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:          2,56e-183      Length:      2372
Score:             1657.00        Matches:     322
Percent Similarity: 100.00%       Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:       100.00%        Indels:      0
DB:                4              Gaps:        0

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
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      160  ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGCTCCTG 219
      |||
QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
      220  GTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
      |||
QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
      280  ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339
      |||
QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
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      340  TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
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QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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      400  AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTCATCTCTAGGATT 459
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QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||
      460  AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG 519
      |||
QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||
      520  AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
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QY      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
      580  CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACAACA 639
      |||
QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||
      640  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
      |||
QY      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
      700  CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
      |||
QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||
      760  TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
      |||
QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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      820  GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG 879
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QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||
      880  CTAGTGCTTGCTCTCTCTTCTTCTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939
      |||
QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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      940  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
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QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||
      1000  AAAGTAGTAAAGGAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059
      |||
QY      301  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
      |||
      1060  GATAAAAAACCCAGAAAGAGTCCCAAGAGTCCAAGGACCAAAACTACCGTGCATGCCTGGAAGCT 1119
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QY      321  GluVal 322
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      1120  GAAGTT 1125

RESULT 9
; Sequence 200, Application US/09909064
; Patent No. 681849
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:      2.56e-183      Length:      2372
Score:          1657.00      Matches:     322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:              4      Gaps:         0

Qy      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
      |||
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTTCACTTCCATCTGGACCACGAGCTCCTG 219

Qy      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279
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Qy      41  IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db      280 ATCACCCCTTGTGAGCAAAAAGGCGAACCAACGACGCTGAATTCACAGAAGCTAAGAGGCC 339

Qy      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

Qy      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTTAGGATT 459

Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 519

Qy      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGTACTTGGACTAACTCGTGCATT 579

Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACTCATCTGTACTTGAACACACAAACA 639

Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db      640 GAAATTTATTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCCCTTACTCTACAACTACCTGCC 699

Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
Db      700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCCACTTCTATTCACGGAGAAAAAATTGATT 759

Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||
Db      760 TGTGTACACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db      820 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCCGGCTCTG 879

Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||
Db      880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGTCAGCTGGTCTTGGATTTTGTATGTCAAA 939

Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999

Qy      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db      1000 AAAGTAGTAAAGGAGGAGAGGCAATGATACCAACCCCTAATGAGGAATCAAAGAAAACT 1059

Qy      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCCAAGCAAAACTACCCGTGCGATGCCCTGGAAGCT 1119

Qy      321 GluVal 322
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Db      1120 GAAGTT 1125

RESULT 10
; Sequence 200, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```

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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

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Pred. No.:      2,56e-183      Length:      2372
Score:          1657.00      Matches:     322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               4          Gaps:          0

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||||||
Db      280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAATTCACAGAAGCTTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||||||
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGACCTTGAAAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
      |||||||
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||||||
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCystYrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||||||
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAATCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||||||
Db      580 CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||||||
Db      640 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||||||
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||||||
Db      760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||||||
Db      820 GAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||||||
Db      880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||||||
Db      940 AGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||||
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db      1060 GATAAAACCCAGAGAGAGTCCCAAGAGTCCAAGCAAAACTACCCGTGCGATGCCTGGAAGCT 1119

QY      321 GluVal 322
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Db      1120 GAAGTT 1125

RESULT 11
; Sequence 200, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
```



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; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2313 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1056
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1056
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..153
;
; US-08-892-880-1

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Alignment Scores:		
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Best Local Similarity:	99.69%	1
Query Match:	99.64%	0
DB:	2	0
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	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

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Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	151	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	210
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	211	ATCACCCCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	270
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80

Db	271	TGTAGGCTGTTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT	330
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	331	AGCTTTGCAACTTGCAGCTATGGCTGGGTGGCGATGGATTTCGTGGTCATCTCTAGGATT	390
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	391	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGTGGAAGGTTCAGTG	450
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	451	AGCCGACAGTTTGACGCTATTGTTACAACATCATCTGATACTTGGACTAACTCGTGCATT	510
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	511	CCAGAAATATATCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA	570
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	571	GAATTTATTGTCTAGTGACAGTACCTACTCGTGGCATCCCCCTTACTCTACATACCTGCC	630
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	631	CCTACTACTCTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	690
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	691	TGTGTACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAAACCATTTGTT	750
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	751	GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	810
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	811	CTAGTGTCTCTCTCTCTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGTCTATGTCAAA	870
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	871	AGGTATGTGAAGCCCTTCCCTTTTACAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	930
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	931	AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT	990
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	991	GATAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT	1050
QY	321	GluVal 322	
Db	1051	GAAGTT 1056	
RESULT 13			
US-09-724-864-28			
; Sequence 28, Application US/09724864			
; Patent No. 6380362			
; GENERAL INFORMATION:			
; APPLICANT: Watson, James D			
; APPLICANT: Murison, James G.			
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed			
; TITLE OF INVENTION: by the polynucleotides and methods for their use.			
; FILE REFERENCE: 11000.1050U1			
; CURRENT APPLICATION NUMBER: US/09/724,864			
; CURRENT FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678			
; PRIOR FILING DATE: 1999-12-23			
; NUMBER OF SEQ ID NOS: 72			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 28			
; LENGTH: 1896			

Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	279	TGTAGGTTGCTNGGACTAAGTTTGGCCGCAAGGCCAGTTG---AACAGCTGAAAGT-	334
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGly-----	91
Db	335	AGCTTTGAAAT-TGCAGTTTGGCTTGGTTGGGATGGTTCGNGNCATTTAGGTTAGCCCAA	393
Qy	92	-----AspGlyPheValValIleSerArgIleSerPro	102
Db	394	CCCANTTTGGAAANTGGGTGGNNCNATTTGNAGTCCCTTAGCCCN	438

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Job time : 281.474 secs

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Run on: October 8, 2005, 16:25:15 ; Search time 672.622 Seconds
(without alignments)
2833.919 Million cell updates/sec

Title: US-10-063-670-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLTISIWTRLL.....NPESKSPSKTTVRCLEAEV 322
Scoring table: BLOSUM62
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAF93818	standard;	CDNA;	1755	BP.	
DE	Human	CDNA	encoding	a	membrane or secretory protein	clone PSEC0135.
PN	EP1067182-A2.					
PD	10-JAN-2001.					
PA	(HELI-) HELIX	RES	INST.			
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 2						
ID	ADE71449	standard;	CDNA;	2027	BP.	
DE	Human	CDNA	encoding	PDEBC	#2.	
PN	US2003124543-A1.					
PD	03-JUL-2003.					
PA	(STUA/) STUART	S	G.			
PA	(STRE/) STREETER	D	G.			
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 3						
ID	AAZ98172	standard;	CDNA;	2029	BP.	
DE	Human	signal peptide	containing	protein	HSPP-64	CDNA SEQ ID NO:198.
PN	WO200000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE	PHARM	INC.			
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 4						
ID	ADE71445	standard;	CDNA;	2029	BP.	
DE	Human	CDNA	encoding	PDEBC	Incyte 3044710CB1.	
PN	US2003124543-A1.					
PD	03-JUL-2003.					
PA	(STUA/) STUART	S	G.			
PA	(STRE/) STREETER	D	G.			
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 5						
ID	ADR41319	standard;	CDNA;	2369	BP.	
DE	Human	CD-like molecule	HEMFC27	CDNA,	SEQ ID NO:118.	
PN	WO200226930-A2.					
PD	04-APR-2002.					
PA	(HUMA-) HUMAN	GENOME	SCI	INC.		

Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 6				
ID	AAZ52250	standard;	DNA; 2372	BP.
DE	Protein	PRO263	CDNA	clone DNA34431-1171.
PN	WO9914328-A2.			
PD	25-MAR-1999.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 7				
ID	ADC78520	standard;	CDNA; 2372	BP.
DE	Human	PRO263	CDNA.	
PN	WO200015796-A2.			
PD	23-MAR-2000.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 8				
ID	AAF72408	standard;	CDNA; 2372	BP.
DE	Human	PRO263	CDNA.	
PN	WO200104311-A1.			
PD	18-JAN-2001.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 9				
ID	AAF92060	standard;	CDNA; 2372	BP.
DE	Human	PRO263	CDNA.	
PN	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 10				
ID	ABS74380	standard;	CDNA; 2372	BP.
DE	Human	CDNA	encoding	secreted/transmembrane protein
PN	US2002119130-A1.			PRO263.
PD	29-AUG-2002.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 11				
ID	ABL88087	standard;	CDNA; 2372	BP.
DE	Human	PRO263	CDNA	sequence SEQ ID NO:31.
PN	WO200200690-A2.			
PD	03-JAN-2002.			
PA	(GETH) GENENTECH	INC.		
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 12				
ID	ABL95576	standard;	CDNA; 2372	BP.
DE	Human	angiogenesis	related	CDNA
PN	WO200208284-A2.			PRO263
PD	31-JAN-2002.			SEQ ID NO: 31.
PA	(GETH) GENENTECH	INC.		
PA	(BAKE/) BAKER	K	P.	
PA	(FERR/) FERRARA	N.		
PA	(GERB/) GERBER	H.		
PA	(GERR/) GERRITSEN	M	E.	
PA	(GODD/) GODDARD	A.		
PA	(GODO/) GODOWSKI	P	J.	
PA	(GURN/) GURNEY	A	L.	
PA	(HILL/) HILLAN	K	J.	
PA	(MARS/) MARSTERS	S	A.	
PA	(PANJ/) PAN	J.		
PA	(PAON/) PAONI	N	F.	
PA	(STEP/) STEPHAN	J	F.	
PA	(WATA/) WATANABE	C	K.	
PA	(WILL/) WILLIAMS	P	M.	
PA	(WOOD/) WOOD	W	I.	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	

RESULT 13
ID ACA60164 standard; cDNA; 2372 BP.
DE Human cDNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ACD07564 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA91166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACD81543 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA60365 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA58812 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22

ID ACA91252 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ACD20169 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACH66246 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ACD02300 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ACA89291 standard; cDNA; 2372 BP.

DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ACA68928 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ACA54972 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 34
ID ACA98450 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 35
ID ACA63375 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 36
ID ACD19807 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 37
ID ADB29405 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 38
ID ADB17062 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 39
ID ACH03578 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 40
ID ADA18261 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.

PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 41
ID ACD66954 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 42
ID ADA19867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 43
ID ADB17250 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 44
ID ACD83115 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 45
ID ADA16236 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 46
ID ADA20039 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 47
ID ACD82092 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 48
ID ADA42381 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 49
ID ACD23293 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064367-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 50
ID ADA00336 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 51
ID ADA16660 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 52
ID ADA13089 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 53
ID ADA41957 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 54
ID ADA17304 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 55
ID ADA42807 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 56
ID ACD23655 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 57
ID ADB05578 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 58
ID ADB7726 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077654-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 59
ID ADB74862 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 60
ID ADB68257 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 61
ID ADB68064 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 62
ID ADB90881 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 63
ID ADC28508 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 64
ID ADC39708 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ADC40222 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 66
ID ADC19046 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 67
ID ADC34346 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ADC29401 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ADC28932 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ADC40817 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ADC19474 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ADC06961 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ADC17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
RESULT 77
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADD36009 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADE34833 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 86
ID ADG01010 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ADG08563 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADF95184 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADH24037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADH34063 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADH29896 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ADH23867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ADG85271 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ADH24547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95

ID ADH37403 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ADH01992 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ADH37573 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ADG85611 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ADH24207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ADH38501 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 101
ID ADG83622 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 102
ID ADH29430 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 103
ID ADH27546 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 104
ID ADH37743 standard; cDNA; 2372 BP.

DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 105
ID ADH37920 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 106
ID ADH57340 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 107
ID ADH59316 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 108
ID ADH53482 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 109
ID ADH53652 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 110
ID ADH51988 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 111
ID ADH49843 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 112
ID ADI25353 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 113
ID ADH90146 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.

PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 114
ID ADI25523 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 115
ID ADH97697 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 116
ID ADI38095 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 117
ID ADI03545 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 118
ID ADI11902 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 119
ID ADH89976 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 120
ID ADH98377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 121
ID ADI11052 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 122
ID ADI11562 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181684-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 128
ID ADI05025 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ADI03375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADI04770 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADH78224 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181668-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADI19568 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADH90316 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADI03035 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADH77884 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADH97867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADI01252 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADI01947 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADI03205 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADI11392 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ADI02294 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADI11732 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ADI05369 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ADH79441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 145
ID ADI19398 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 146
ID ADI05199 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 147
ID ADH79611 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 148
ID ADI01437 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 149
ID ADI01607 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
RESULT 150
ID ADI01777 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 151
ID ADH79781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 152
ID ADI04599 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 153
ID ADI02735 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 154
ID ADH78054 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 155
ID ADI25693 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 156
ID ADI25863 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 157
ID ADK5375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 158
ID ADH98717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 159
ID ADH79958 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADJ26363 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADL93689 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADC52143 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADE79278 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADE79702 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADE41281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168

ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADH06405 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADG58826 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180855-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ADH27716 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ADH25057 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ADH33689 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ADG92296 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ADH02332 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ADH07939 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 183
ID ADG69336 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 184
ID ADH39157 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ADG92723 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027146-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ADG83897 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ADG85441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ADH06235 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADH30231 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADH24377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADG69506 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADH07769 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADG85781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ADH39327 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ADH333519 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ADH33859 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ADH01069 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ADG69676 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ADH02162 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 200
ID ADG69166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 201
ID ADG85951 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ADH24887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 203
ID ADH39504 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

Query Match: 100.00% Indels: 0
RESULT 204
ID ADH02502 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 205
ID ADG68996 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADH07599 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ADG86121 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ADH24717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ADH25765 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADH38331 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADH20512 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADH57170 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 213
ID ADH43464 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADH07367 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADH52158 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADH59912 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADH49524 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADH06940 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADH90486 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADI11222 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181683-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADI18682 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADH98887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADI02117 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADH90656 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI37665 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADH97461 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI65829 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH60572 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 229
ID ADJ99629 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ADL08822 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ADJ98531 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ADJ98701 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ADH78860 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ADJ99094 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ADJ99264 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADJ98882 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADH79030 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 238

ID ADK00890 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 239
ID ADK14411 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 240
ID ADM25163 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 241
ID ADM29913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 242
ID ADK82809 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 243
ID ADM80860 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 244
ID ADO06235 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 245
ID ADR11087 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 246
ID ADR17996 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cdNA, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.

PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 247
ID ADT03672 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 248
ID ADS74635 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane cDNA #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 249
ID ADQ25003 standard; DNA; 2667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ABA09223 standard; cDNA; 2324 BP.
DE Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.
PN WO200157188-A2.
PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 99.82% Indels: 0
RESULT 251
ID AAV22687 standard; DNA; 2313 BP.
DE DNA encoding a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.64% Indels: 0
RESULT 252
ID ABL90698 standard; cDNA; 2369 BP.
DE Human polynucleotide SEQ ID NO 1260.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.64% Indels: 0
RESULT 253
ID ADP65684 standard; DNA; 2313 BP.
DE Human extracellular link domain containing 1 (XLKD1) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 98.85% Indels: 0
RESULT 254
ID ADM67137 standard; DNA; 2313 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 273.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 98.85% Indels: 0
RESULT 255
ID ADN05865 standard; cDNA; 2313 BP.
DE Antipsoriatic cDNA sequence #1164.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 98.85% Indels: 0
RESULT 256
ID ADQ21088 standard; DNA; 2313 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 98.85% Indels: 0
RESULT 257
ID AAC59803 standard; DNA; 2967 BP.
DE Human secreted protein encoding DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Best Local Similarity: 61.69% Mismatches: 0
Query Match: 93.36% Indels: 200
RESULT 258
ID ADD04999 standard; cDNA; 1680 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 93.79% Mismatches: 0
Query Match: 92.40% Indels: 20
RESULT 259
ID ACA10111 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.

Best Local Similarity: 92.24% Mismatches: 0
Query Match: 91.22% Indels: 25
RESULT 260
ID ADO08254 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Best Local Similarity: 92.24% Mismatches: 0
Query Match: 91.22% Indels: 25
RESULT 261
ID AAD10132 standard; cDNA; 1896 BP.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 66.57% Indels: 4
RESULT 262
ID ABL35066 standard; cDNA; 1896 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 595.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 66.57% Indels: 4
RESULT 263
ID ADM67136 standard; DNA; 1516 BP.
DE Murine adipocyte specific DNA SeqID 272.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Best Local Similarity: 69.09% Mismatches: 64
Query Match: 66.08% Indels: 4
RESULT 264
ID ABT09892 standard; cDNA; 596 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 26.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 97.88% Mismatches: 4
Query Match: 54.38% Indels: 3
RESULT 265
ID AAF94017 standard; DNA; 716 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 451.

PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 94.77% Mismatches: 6
Query Match: 48.46% Indels: 3
RESULT 266
ID ACH20895 standard; cDNA; 411 BP.
DE Human adult liver cDNA #507.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 40.62% Indels: 0
RESULT 267
ID ADE71446 standard; cDNA; 559 BP.
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 69.57% Mismatches: 40
Query Match: 35.94% Indels: 7
RESULT 268
ID AAX41156 standard; cDNA; 451 BP.
DE Human secreted protein 5' EST SEQ ID NO:100.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.73% Indels: 0
RESULT 269
ID ACH22904 standard; cDNA; 486 BP.
DE Human adult ovary cDNA #1284.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.55% Indels: 0
RESULT 270
ID ADE71447 standard; cDNA; 279 BP.
DE Rat cDNA encoding PDEBC variant Incyte 701647942H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 87.64% Mismatches: 10
Query Match: 23.30% Indels: 0
RESULT 271
ID ABA54110 standard; DNA; 469 BP.
DE Human foetal liver single exon nucleic acid probe #2415.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 272
ID AAI33763 standard; DNA; 469 BP.
DE Probe #2449 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 273
ID ABA23859 standard; DNA; 469 BP.

DE Probe #2325 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 274
ID AAK27829 standard; DNA; 469 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2386.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 275
ID ABS27409 standard; DNA; 469 BP.
DE Human liver single exon probe, SEQ ID No 2399.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 276
ID ABS02280 standard; DNA; 469 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2271.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 277
ID AAX41003 standard; cDNA; 363 BP.
DE Human secreted protein 5' EST SEQ ID NO: 215.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 91.30% Mismatches: 5
Query Match: 17.20% Indels: 1
RESULT 278
ID AAI33382 standard; DNA; 457 BP.
DE Probe #2068 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 16.99% Indels: 7
RESULT 279
ID ABS01959 standard; DNA; 457 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1950.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 16.99% Indels: 7
RESULT 280
ID AAX51631 standard; cDNA; 373 BP.
DE Human secreted protein 5' EST SEQ ID NO:210.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 16.72% Indels: 0
RESULT 281
ID AAQ06236 standard; DNA; 1537 BP.
DE B7 adhesion receptor cDNA clone.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Best Local Similarity: 28.01% Mismatches: 109
Query Match: 14.15% Indels: 111
RESULT 282
ID ABN86523 standard; cDNA; 1089 BP.
DE Nucleotide sequence of hamster CD44 cDNA.

PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 26.30% Mismatches: 147
Query Match: 14.09% Indels: 63
RESULT 283
ID ABN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 23.92% Mismatches: 158
Query Match: 13.94% Indels: 66
RESULT 284
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.92% Mismatches: 158
Query Match: 13.94% Indels: 66
RESULT 285
ID ABN86522 standard; cDNA; 1177 BP.
DE Nucleotide sequence of mouse CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 24.93% Mismatches: 148
Query Match: 13.85% Indels: 63
RESULT 286
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
RESULT 287
ID AB235325 standard; cDNA; 1992 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 436.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Best Local Similarity: 26.28% Mismatches: 134
Query Match: 13.46% Indels: 67
RESULT 288
ID ABA66678 standard; DNA; 141 BP.
DE Human foetal liver single exon nucleic acid probe #14983.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 289
ID AAI46891 standard; DNA; 141 BP.
DE Probe #15577 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 290
ID ABA33740 standard; DNA; 141 BP.
DE Probe #12206 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 291

ID AAK40837 standard; DNA; 141 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15394.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 292
ID ABS40414 standard; DNA; 141 BP.
DE Human liver single exon probe, SEQ ID No 15404.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 293
ID ABS14788 standard; DNA; 141 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14779.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 97.87% Mismatches: 0
Query Match: 13.40% Indels: 1
RESULT 294
ID AAQ21185 standard; DNA; 1354 BP.
DE Clone CD44.5 coding for haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 295
ID AAT14724 standard; cDNA; 1354 BP.
DE Human haematopoietic CD44 cDNA clone CD44.5.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 296
ID AAV63461 standard; cDNA; 1354 BP.
DE Human CD44 antigen cDNA.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 297
ID AAV81218 standard; cDNA; 1354 BP.
DE Human CD44 antigen cDNA.
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 298
ID AAA50597 standard; cDNA; 1354 BP.
DE Human haematopoietic CD44.5 cDNA.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 299
ID AAS03191 standard; cDNA; 1354 BP.
DE Human haematopoietic antigen CD44 cDNA sequence.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 300
ID ADO49372 standard; cDNA; 1354 BP.

DE Human CD44 cDNA #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Best Local Similarity: 26.79% Mismatches: 125
Query Match: 12.98% Indels: 78
RESULT 301
ID AAA52811 standard; cDNA; 1794 BP.
DE Human CD44 cDNA.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.85% Indels: 78
RESULT 302
ID ABV94385 standard; cDNA; 1794 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:376.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.85% Indels: 78
RESULT 303
ID ABK84043 standard; cDNA; 1794 BP.
DE Human cDNA differentially expressed in granulocytic cells #614.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.85% Indels: 78
RESULT 304
ID ADQ38557 standard; DNA; 4335 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 220.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.85% Indels: 78
RESULT 305
ID ADD90591 standard; cDNA; 1083 BP.
DE Human CD44std glycoprotein encoding cDNA SEQ ID NO:1.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 306
ID AAD48131 standard; DNA; 1807 BP.
DE Human CD44 antigen encoding DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 307
ID ADH18929 standard; cDNA; 1874 BP.
DE Human cell adhesion and extracellular matrix CADECM-25 cDNA - SEQ 56.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.41% Mismatches: 116
Query Match: 12.79% Indels: 78
RESULT 308

ID ADJ56374 standard; cDNA; 1981 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 180.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 309
ID ADE25668 standard; cDNA; 4365 BP.
DE Human cDNA differentially expressed in foam cells #72.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 310
ID ADP10572 standard; DNA; 4633 BP.
DE Reference mRNA sequences for marker probe #249.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 311
ID ADL61887 standard; DNA; 5165 BP.
DE Human ovarian cancer DNA marker #20099.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.79% Indels: 78
RESULT 312
ID ABN86521 standard; cDNA; 1297 BP.
DE Nucleotide sequence of human CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.67% Indels: 78
RESULT 313
ID ADI31550 standard; cDNA; 1297 BP.
DE Human cDNA #876.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 26.79% Mismatches: 126
Query Match: 12.67% Indels: 78
RESULT 314
ID ADQ38556 standard; DNA; 5452 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 219.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 29.29% Mismatches: 96
Query Match: 12.64% Indels: 17
RESULT 315
ID ADP65670 standard; DNA; 3091 BP.
DE Human mRNA for transmembrane glycoprotein (CD44 gene) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 23.22% Mismatches: 110
Query Match: 12.40% Indels: 96
RESULT 316
ID ADP65097 standard; DNA; 3091 BP.
DE Human CD44 antigen (homing function and Indian blood group DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 23.22% Mismatches: 110

Query Match: 12.40% Indels: 96
RESULT 317
ID ADR67138 standard; DNA; 3091 BP.
DE Human bladder cancer associated nucleotide sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Best Local Similarity: 23.22% Mismatches: 110
Query Match: 12.40% Indels: 96
RESULT 318
ID ADQ38561 standard; DNA; 4633 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 224.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.21% Mismatches: 123
Query Match: 12.40% Indels: 100
RESULT 319
ID ADQ38554 standard; DNA; 4723 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 217.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 23.74% Mismatches: 120
Query Match: 12.37% Indels: 134
RESULT 320
ID ACN39193 standard; cDNA; 3083 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325446, SEQ ID NO:3187.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 23.22% Mismatches: 110
Query Match: 12.34% Indels: 96
RESULT 321
ID AAA91130 standard; DNA; 1483 BP.
DE CD44Hextra/tmFAScyto coding sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Best Local Similarity: 25.38% Mismatches: 130
Query Match: 12.25% Indels: 78
RESULT 322
ID ADQ38563 standard; DNA; 3091 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 226.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.25% Mismatches: 129
Query Match: 12.25% Indels: 92
RESULT 323
ID ADQ38562 standard; DNA; 5468 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 225.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.78% Mismatches: 130
Query Match: 12.25% Indels: 84
RESULT 324
ID ADQ38555 standard; DNA; 5674 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 218.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.25% Mismatches: 129
Query Match: 12.25% Indels: 92
RESULT 325
ID ADQ38558 standard; DNA; 5739 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 221.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.25% Mismatches: 129
Query Match: 12.25% Indels: 92
RESULT 326
ID AAA91129 standard; DNA; 1468 BP.
DE CD44HextraFAStm/cyto coding sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Best Local Similarity: 24.70% Mismatches: 130
Query Match: 12.22% Indels: 77
RESULT 327
ID ABN86520 standard; cDNA; 1737 BP.
DE Nucleotide sequence of human CD44R cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 22.19% Mismatches: 138
Query Match: 12.04% Indels: 105
RESULT 328
ID ADK61304 standard; DNA; 1737 BP.
DE Ovarian cancer-related DNA #459 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Best Local Similarity: 22.19% Mismatches: 138
Query Match: 12.04% Indels: 105
RESULT 329
ID ABZ70446 standard; cDNA; 1824 BP.
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 22.92% Mismatches: 136
Query Match: 12.04% Indels: 78
RESULT 330
ID AAA91011 standard; DNA; 2100 BP.
DE Human CD44 splice variant (RA-CD44) coding sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Best Local Similarity: 22.92% Mismatches: 136
Query Match: 12.04% Indels: 78
RESULT 331
ID ADD90593 standard; cDNA; 2100 BP.
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:3.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 22.92% Mismatches: 136
Query Match: 12.04% Indels: 78
RESULT 332
ID AAS03192 standard; cDNA; 2307 BP.
DE Human epithelial antigen CD44 cDNA sequence.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 333
ID AAQ21186 standard; DNA; 2308 BP.
DE Clone CD44 coding for epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 334
ID AAT14725 standard; cDNA; 2308 BP.

DE Human epithelial CD44 cDNA.
PN US5506126-A.
PD 09-APR-1996.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 335
ID AAV63462 standard; cDNA; 2308 BP.
DE Human CD44 antigen cDNA.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 336
ID AAV81219 standard; cDNA; 2308 BP.
DE Human CD44 antigen cDNA.
PN US5849898-A.
PD 15-DEC-1998.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 337
ID AAA50598 standard; cDNA; 2308 BP.
DE Human epithelial CD44 cDNA.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEO) GEN HOSPITAL CORP.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 338
ID ADO49374 standard; cDNA; 2308 BP.
DE Human CD44 cDNA #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Best Local Similarity: 23.57% Mismatches: 100
Query Match: 12.04% Indels: 75
RESULT 339
ID ABX77520 standard; cDNA; 4674 BP.
DE Differentially expressed breast cancer associated cDNA #15.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Best Local Similarity: 22.19% Mismatches: 138
Query Match: 12.04% Indels: 105
RESULT 340
ID ADJ56375 standard; cDNA; 4674 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 181.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHEIT J M.
Best Local Similarity: 22.19% Mismatches: 138
Query Match: 12.04% Indels: 105
RESULT 341
ID ADM86790 standard; cDNA; 4674 BP.
DE Human cDNA #51 differentially expressed in lung cancer.
PN US2003175704-A1.
PD 18-SEP-2003.
PA (LASE/) LASEK A K W.
PA (SHYJ/) SHYJAN A W.

PA (TURN/) TURNER C M. Mismatches: 138
Best Local Similarity: 22.19% Indels: 105
Query Match: 12.04%
RESULT 342
ID ADI61729 standard; cDNA; 4675 BP.
DE Human cDNA upregulated in Alzheimer's disease, INCYTE 234630.26.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 22.19% Mismatches: 138
Query Match: 12.04% Indels: 105
RESULT 343
ID ADQ38553 standard; DNA; 5053 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 216.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 25.96% Mismatches: 109
Query Match: 11.95% Indels: 63
RESULT 344
ID ADD90595 standard; cDNA; 2097 BP.
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:5.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Best Local Similarity: 23.32% Mismatches: 128
Query Match: 11.89% Indels: 69
RESULT 345
ID ACN42246 standard; cDNA; 2342 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1121.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.96% Mismatches: 109
Query Match: 11.89% Indels: 63
RESULT 346
ID ABX76192 standard; DNA; 2387 BP.
DE Lung cancer-associated polynucleotide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 23.32% Mismatches: 128
Query Match: 11.89% Indels: 69
RESULT 347
ID ADL61117 standard; DNA; 2387 BP.
DE Human protein tyrosine kinase biomarker CD44 antigen DNA.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 23.32% Mismatches: 128
Query Match: 11.89% Indels: 69
RESULT 348
ID ABX63495 standard; cDNA; 2905 BP.
DE Human cDNA #495 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Best Local Similarity: 23.32% Mismatches: 128
Query Match: 11.89% Indels: 69
RESULT 349
ID ADA10891 standard; cDNA; 3474 BP.
DE Human cDNA differentially expressed in colon cancer #7.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Best Local Similarity: 23.32% Mismatches: 128
Query Match: 11.89% Indels: 69
RESULT 350
ID ADQ38560 standard; DNA; 4874 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 223.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 11.89% Indels: 14
RESULT 351
ID ADI60527 standard; DNA; 1190 BP.
DE Secreted polypeptide encoding gene #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 30.86% Mismatches: 84
Query Match: 11.83% Indels: 14
RESULT 352
ID ACC43051 standard; DNA; 339 BP.
DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.28% Mismatches: 53
Query Match: 11.56% Indels: 1
RESULT 353
ID ACC43049 standard; DNA; 336 BP.
DE Nucleotide sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 11.47% Indels: 2
RESULT 354
ID ACC43052 standard; DNA; 336 BP.
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 11.35% Indels: 2
RESULT 355
ID ACC43053 standard; DNA; 336 BP.
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 11.23% Indels: 2
RESULT 356
ID ACC43054 standard; DNA; 336 BP.
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 11.10% Indels: 2
RESULT 357
ID ACC43050 standard; DNA; 336 BP.
DE Nucleotide sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Best Local Similarity: 36.04% Mismatches: 51
Query Match: 11.10% Indels: 2
RESULT 358
ID ADQ38560 standard; DNA; 4874 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 223.
PN WO2004058052-A2.

ID AAS81254 standard; cDNA; 2764 BP.
DE DNA encoding novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 26.03% Mismatches: 119
Query Match: 10.89% Indels: 74
RESULT 359
ID AAS81258 standard; cDNA; 2273 BP.
DE DNA encoding novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 21.83% Mismatches: 129
Query Match: 10.80% Indels: 88
RESULT 360
ID AAI46523 standard; DNA; 106 BP.
DE Probe #15209 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.26% Indels: 0
RESULT 361
ID ABS14478 standard; DNA; 106 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14469.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.26% Indels: 0
RESULT 362
ID ACH49200 standard; cDNA; 399 BP.
DE Human leukocyte cDNA #794.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 37.36% Mismatches: 41
Query Match: 10.05% Indels: 1
RESULT 363
ID ADE71448 standard; cDNA; 820 BP.
DE Dog cDNA encoding PDEBC variant Incyte 704113673J1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 78.79% Mismatches: 11
Query Match: 9.96% Indels: 5
RESULT 364
ID ABZ34973 standard; cDNA; 549 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 85.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 9.54% Indels: 8
RESULT 365
ID ABZ91738 standard; DNA; 549 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 9.54% Indels: 8
RESULT 366
ID ADK61306 standard; DNA; 549 BP.
DE Ovarian cancer-related DNA #461 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 9.54% Indels: 8
RESULT 367
ID ABD27968 standard; DNA; 549 BP.
DE AA282906 DNA fragment.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 34.92% Mismatches: 61
Query Match: 9.54% Indels: 8
RESULT 368
ID ADB62456 standard; cDNA; 2863 BP.
DE Human cDNA encoding clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 21.26% Mismatches: 98
Query Match: 9.11% Indels: 102
RESULT 369
ID ACH48521 standard; cDNA; 425 BP.
DE Human leukocyte cDNA #115.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 36.59% Mismatches: 36
Query Match: 8.96% Indels: 1
RESULT 370
ID ABX74436 standard; cDNA; 781 BP.
DE Human cDNA sequence #8 up-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 8.78% Indels: 13
RESULT 371
ID ADL13961 standard; DNA; 834 BP.
DE Osteoarthritis-associated polymorphic nucleotide #493.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 8.78% Indels: 13
RESULT 372
ID ABX63446 standard; cDNA; 1144 BP.
DE Human cDNA #446 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 8.78% Indels: 13
RESULT 373
ID ADE25720 standard; cDNA; 1144 BP.
DE Human cDNA differentially expressed in foam cells #124.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.22% Mismatches: 62
Query Match: 8.78% Indels: 13
RESULT 374
ID ADL13963 standard; DNA; 1414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #495.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 22.79% Mismatches: 123
Query Match: 8.78% Indels: 59

RESULT 375									
ID	ABX76382 standard; DNA; 1422 BP.								
DE	Lung cancer-associated polynucleotide #246.								
PN	WO200286443-A2.								
PD	31-OCT-2002.								
PA	(EOSB-) EOS BIOTECHNOLOGY INC.								
Best Local Similarity:	22.79%	Mismatches:	123						
Query Match:	8.78%	Indels:	59						
RESULT 376									
ID	ACC72678 standard; cDNA; 1422 BP.								
DE	Human cancer related protein encoding cDNA SEQ ID NO:17.								
PN	WO2003025138-A2.								
PD	27-MAR-2003.								
PA	(EOSB-) EOS BIOTECHNOLOGY INC.								
Best Local Similarity:	22.79%	Mismatches:	123						
Query Match:	8.78%	Indels:	59						
RESULT 377									
ID	ADN38973 standard; cDNA; 1422 BP.								
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:291.								
PN	WO2003042661-A2.								
PD	22-MAY-2003.								
PA	(EOSB-) EOS BIOTECHNOLOGY INC.								
Best Local Similarity:	22.79%	Mismatches:	123						
Query Match:	8.78%	Indels:	59						
RESULT 378									
ID	ADN39702 standard; cDNA; 1430 BP.								
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C74.								
PN	WO2003042661-A2.								
PD	22-MAY-2003.								
PA	(EOSB-) EOS BIOTECHNOLOGY INC.								
Best Local Similarity:	30.22%	Mismatches:	62						
Query Match:	8.78%	Indels:	13						
RESULT 379									
ID	ADQ21505 standard; DNA; 1440 BP.								
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 4325.								
PN	WO2004048938-A2.								
PD	10-JUN-2004.								
PA	(PROT-) PROTEIN DESIGN LABS INC.								
Best Local Similarity:	22.79%	Mismatches:	123						
Query Match:	8.78%	Indels:	59						
RESULT 380									
ID	ADQ25341 standard; DNA; 1461 BP.								
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 8161.								
PN	WO2004048938-A2.								
PD	10-JUN-2004.								
PA	(PROT-) PROTEIN DESIGN LABS INC.								
Best Local Similarity:	30.22%	Mismatches:	62						
Query Match:	8.78%	Indels:	13						
RESULT 381									
ID	ABX63445 standard; cDNA; 1728 BP.								
DE	Human cDNA #445 differentially expressed in activated vascular tissue.								
PN	US2002137081-A1.								
PD	26-SEP-2002.								
PA	(BAND/) BANDMAN O.								
Best Local Similarity:	30.22%	Mismatches:	62						
Query Match:	8.78%	Indels:	13						
RESULT 382									
ID	ADK67833 standard; cDNA; 7840 BP.								
DE	Human BRCC300 gene coding sequence.								
PN	WO2004012755-A1.								
PD	12-FEB-2004.								
PA	(WIST-) WISTAR INST.								
Best Local Similarity:	21.71%	Mismatches:	107						
Query Match:	8.78%	Indels:	66						
RESULT 383									
ID	ABV95472 standard; cDNA; 351 BP.								
DE	Human pancreatic cancer expressed cDNA SEQ ID NO 880.								
PN	WO200260317-A2.								
PD	08-AUG-2002.								
PA	(CORI-) CORIXA CORP.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 384									
ID	ADM80849 standard; cDNA; 813 BP.								
DE	Human CADECM-36 encoding cDNA SEQ ID NO:78.								
PN	WO2004015396-A2.								
PD	19-FEB-2004.								
PA	(INCY-) INCYTE CORP.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 385									
ID	AAQ27190 standard; cDNA; 1414 BP.								
DE	Tumour necrosis factor-induced glycoprotein TSG-6 gene.								
PN	WO9212175-A1.								
PD	23-JUL-1992.								
PA	(UYNY) UNIV NEW YORK STATE.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 386									
ID	AAV71778 standard; cDNA; 1414 BP.								
DE	Tumour necrosis factor stimulated gene 6 (TSG-6) protein encoding cDNA.								
PN	US5846763-A.								
PD	08-DEC-1998.								
PA	(UYNY) UNIV NEW YORK STATE.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 387									
ID	AAD06019 standard; cDNA; 1414 BP.								
DE	Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) cDNA.								
PN	US6210905-B1.								
PD	03-APR-2001.								
PA	(UYNY) UNIV NEW YORK STATE.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 388									
ID	ABS54635 standard; cDNA; 1414 BP.								
DE	Human cDNA encoding tumour necrosis factor stimulated gene 6, TSG-6.								
PN	US2002090708-A1.								
PD	11-JUL-2002.								
PA	(UYNY) UNIV NEW YORK STATE.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.75%	Indels:	2						
RESULT 389									
ID	ADS85080 standard; DNA; 1605 BP.								
DE	Mouse atopic dermatitis-related gene sequence SeqID82.								
PN	WO2004031386-A1.								
PD	15-APR-2004.								
PA	(GENO-) GENOX RES INC.								
PA	(UYJU-) UNIV JUNTENDO.								
Best Local Similarity:	32.95%	Mismatches:	41						
Query Match:	8.69%	Indels:	2						
RESULT 390									
ID	AAD48132 standard; DNA; 3366 BP.								
DE	Rat CD44i DNA.								
PN	WO200276510-A1.								
PD	03-OCT-2002.								
PA	(AGYT-) AGY THERAPEUTICS INC.								
Best Local Similarity:	26.69%	Mismatches:	93						
Query Match:	8.69%	Indels:	63						
RESULT 391									
ID	ACH30555 standard; cDNA; 396 BP.								
DE	Human testis cDNA #941.								
PN	US2003073623-A1.								
PD	17-APR-2003.								
PA	(DRMA/) DRMANAC R T.								
PA	(LABA/) LABAT I.								
PA	(STAC/) STACHE-CRAIN B.								
PA	(DICK/) DICKSON M C.								
PA	(JONE/) JONES L W.								
Best Local Similarity:	31.58%	Mismatches:	58						
Query Match:	8.66%	Indels:	13						
RESULT 392									
ID	ABT08487 standard; cDNA; 8444 BP.								
DE	Human novel protein NOVla coding sequence SEQ ID NO: 1.								
PN	WO200259315-A2.								
PD	01-AUG-2002.								

PA (CURA-) CURAGEN CORP. Mismatches: 151
Best Local Similarity: 21.59% Indels: 38
Query Match: 8.60%
RESULT 393
ID ADO09835 standard; cDNA; 8444 BP.
DE Human NOV1a cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Best Local Similarity: 21.59% Mismatches: 151
Query Match: 8.60% Indels: 38
RESULT 394
ID AAF87120 standard; DNA; 3625 BP.
DE NOV9 coding sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.44% Mismatches: 134
Query Match: 8.54% Indels: 59
RESULT 395
ID ADH71325 standard; DNA; 3625 BP.
DE Human gene of the invention NOV9h SEQ ID NO:221.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.44% Mismatches: 134
Query Match: 8.54% Indels: 59
RESULT 396
ID ABT08488 standard; cDNA; 8495 BP.
DE Human novel protein NOV1b coding sequence SEQ ID NO: 3.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.44% Mismatches: 134
Query Match: 8.54% Indels: 59
RESULT 397
ID ADH71331 standard; DNA; 8495 BP.
DE Human gene of the invention NOV9k SEQ ID NO:227.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 24.44% Mismatches: 134
Query Match: 8.54% Indels: 59
RESULT 398
ID ADO09837 standard; cDNA; 8495 BP.
DE Human NOV1b cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.

PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Best Local Similarity: 24.44% Mismatches: 134
Query Match: 8.54% Indels: 59
RESULT 399
ID AAH23114 standard; DNA; 1411 BP.
DE Osteoarthritis tissue-derived nucleic acid sequence #44.
PN WO200153531-A2.
PD 26-JUL-2001.
PA (PHAA) PHARMACIA CORP.
Best Local Similarity: 31.62% Mismatches: 62
Query Match: 8.36% Indels: 13
RESULT 400
ID ADO09967 standard; cDNA; 3256 BP.
DE Human NOV1c cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 401
ID ABT08489 standard; cDNA; 3260 BP.
DE Human novel protein NOV1c coding sequence SEQ ID NO: 210.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 402
ID ADH71311 standard; DNA; 3260 BP.

DE Human gene of the invention NOV9a SEQ ID NO:207.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 403
ID ADH71355 standard; DNA; 4527 BP.
DE Human gene of the invention NOV9w SEQ ID NO:251.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 404
ID ABA04662 standard; cDNA; 4576 BP.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 405
ID ABX13822 standard; cDNA; 4642 BP.
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 406
ID ABX13823 standard; cDNA; 4962 BP.
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 407
ID ADH71357 standard; DNA; 5416 BP.
DE Human gene of the invention NOV9x SEQ ID NO:253.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 408
ID ADM90626 standard; DNA; 5688 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 19.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 409
ID ADM91044 standard; DNA; 5688 BP.
DE Human DNA encoding a pharmaceutically useful protein SeqID 437.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 410
ID ADH71359 standard; DNA; 7670 BP.
DE Human gene of the invention NOV9y SEQ ID NO:255.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 22.03% Mismatches: 134
Query Match: 8.27% Indels: 90
RESULT 411
ID ABA04648 standard; cDNA; 4706 BP.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 22.42% Mismatches: 138
Query Match: 8.21% Indels: 80
RESULT 412
ID ABX13821 standard; cDNA; 4706 BP.
DE cDNA encoding rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Best Local Similarity: 22.42% Mismatches: 138
Query Match: 8.21% Indels: 80
RESULT 413
ID AAF29464 standard; cDNA; 3153 BP.
DE Murine brevidin cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 8.18% Indels: 30
RESULT 414
ID ACD66770 standard; cDNA; 3153 BP.
DE Secreted polypeptide-related cDNA #76.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 8.18% Indels: 30
RESULT 415
ID ADB90788 standard; cDNA; 3153 BP.
DE Mouse cDNA encoding brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 8.18% Indels: 30
RESULT 416
ID ADF71523 standard; cDNA; 3153 BP.
DE Murine brevidin protein cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97
Query Match: 8.18% Indels: 30
RESULT 417
ID ADQ10339 standard; cDNA; 3153 BP.
DE Human polynucleotide #61.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.88% Mismatches: 97

Query Match: 8.18% Indels: 30
RESULT 418
ID ABS70406 standard; cDNA; 1734 BP.
DE Human bone remodelling gene #63.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.00% Mismatches: 61
Query Match: 8.06% Indels: 14
RESULT 419
ID ADB63670 standard; cDNA; 2160 BP.
DE Human cDNA encoding clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 25.93% Mismatches: 105
Query Match: 8.00% Indels: 49
RESULT 420
ID ACN42826 standard; cDNA; 7678 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.00% Indels: 59
RESULT 421
ID ACN42825 standard; cDNA; 7975 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.00% Indels: 59
RESULT 422
ID ABZ81727 standard; cDNA; 2652 BP.
DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 7.94% Indels: 39
RESULT 423
ID ADK67780 standard; DNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 7.94% Indels: 39
RESULT 424
ID AAF29460 standard; cDNA; 2013 BP.
DE Human TANGO 332 cDNA open reading frame.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 425
ID ACD66767 standard; cDNA; 2013 BP.
DE Secreted polypeptide-related cDNA #51.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.

PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 426
ID ADB90775 standard; cDNA; 2013 BP.
DE Human TANGO 332 open reading frame.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 427
ID ADF71510 standard; cDNA; 2013 BP.
DE Human TANGO 332 CDS.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 428
ID ADQ10328 standard; cDNA; 2013 BP.
DE Human polynucleotide #58.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 429
ID AAF29459 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 430
ID ACD66766 standard; cDNA; 2730 BP.
DE Secreted polypeptide-related cDNA #50.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 431
ID ADB90774 standard; cDNA; 2730 BP.
DE Human cDNA encoding TANGO 332.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 432
ID ADF71509 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 433
ID ADQ10327 standard; cDNA; 2730 BP.

DE Human polynucleotide #57.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 434
ID ACN37482 standard; cDNA; 3275 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 435
ID ADH18923 standard; cDNA; 3293 BP.
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 436
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMCAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 437
ID AAA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 438
ID ABK69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 439
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 440
ID ADA3748 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 441
ID ADA3516 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 442
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.

PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 443
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 444
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 445
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 446
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 447
ID ADB99675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 448
ID ADB86958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 449
ID ADB66113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 450
ID ADB99791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 451
ID ADB99446 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003082731-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 452
ID ADB65997 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 453
ID ADC23395 standard; cDNA; 3476 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 454
ID ADC26088 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 455
ID ADE04915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 456
ID ADE11221 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 457
ID ADD88152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 458
ID ADD95447 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 459
ID ADE06377 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 460
ID ADE38152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119120-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 461
ID ADD88268 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 462
ID ADD90849 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 463
ID ADF99404 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 464
ID ADG06497 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 465
ID ADG05448 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 466
ID ADG82449 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 467
ID ADE51702 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 468
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 469
ID ADE37676 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 488
ID ADE06261 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 489
ID ADD90120 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 490
ID ADE38628 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 491
ID ADE39559 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 492
ID ADD89164 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 493
ID ADD88931 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 494
ID ADE19825 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 495
ID ADE77403 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 496
ID ADE65279 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 497

ID ADE39327 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 498
ID ADE38512 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 499
ID ADG11065 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 500
ID ADG10949 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 501
ID ADH31477 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 502
ID ADH38725 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 503
ID ADH29360 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 504
ID ADH23663 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 505
ID ADH26993 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 506
ID ADH38261 standard; cDNA; 3476 BP.

DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 507
ID ADH26877 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 508
ID ADH38145 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 509
ID ADH38841 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 510
ID ADH23779 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 511
ID ADH40155 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 512
ID ADH40039 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 513
ID ADH31361 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 514
ID ADH29239 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 515
ID ADH49454 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.

PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 516
ID ADH51918 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 517
ID ADH49773 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 518
ID ADH52374 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 519
ID ADH52490 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 520
ID ADH58487 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 521
ID ADH51802 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 522
ID ADH58363 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 523
ID ADI13560 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 524
ID ADK00816 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003186373-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 525
ID ADL08557 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 526
ID ABZ81728 standard; cDNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MAT/) MATTHEWS R T.
Best Local Similarity: 23.32% Mismatches: 101
Query Match: 7.88% Indels: 37
RESULT 527
ID ADK67781 standard; DNA; 2652 BP.
DE Rat glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Best Local Similarity: 23.32% Mismatches: 101
Query Match: 7.88% Indels: 37
RESULT 528
ID ADB59097 standard; DNA; 3077 BP.
DE Toxicity-related gene, SEQ ID 4123.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.32% Mismatches: 101
Query Match: 7.88% Indels: 37
RESULT 529
ID ADP72861 standard; DNA; 3077 BP.
DE Renal toxin progression gene marker #1450.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 23.32% Mismatches: 101
Query Match: 7.88% Indels: 37
RESULT 530
ID ABL90758 standard; cDNA; 3681 BP.
DE Human polynucleotide SEQ ID NO 1320.
PN WO2001903104-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 20.62% Mismatches: 122
Query Match: 7.88% Indels: 97
RESULT 531
ID ADL13490 standard; DNA; 6951 BP.
DE Osteoarthritis-associated polymorphic nucleotide #22.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 7.88% Indels: 59
RESULT 532
ID ADL13489 standard; DNA; 7137 BP.
DE Osteoarthritis-associated polymorphic nucleotide #21.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 7.88% Indels: 59
RESULT 533
ID ADP65694 standard; DNA; 7137 BP.
DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.

PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 7.88% Indels: 59
RESULT 534
ID ADP65777 standard; DNA; 7137 BP.
DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 7.88% Indels: 59
RESULT 535
ID ACN37944 standard; cDNA; 7871 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324323, SEQ ID NO:1163.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.62% Mismatches: 122
Query Match: 7.88% Indels: 97
RESULT 536
ID ACF04000 standard; cDNA; 7879 BP.
DE Human CLEVER-1 encoding cDNA SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Best Local Similarity: 20.73% Mismatches: 133
Query Match: 7.85% Indels: 124
RESULT 537
ID ADQ22919 standard; DNA; 8038 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5739.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 20.73% Mismatches: 133
Query Match: 7.85% Indels: 124
RESULT 538
ID AAA57363 standard; DNA; 1522 BP.
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 20.88% Mismatches: 112
Query Match: 7.82% Indels: 89
RESULT 539
ID AAA57362 standard; DNA; 6761 BP.
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 20.88% Mismatches: 112
Query Match: 7.82% Indels: 89
RESULT 540
ID AAT05627 standard; cDNA; 3259 BP.
DE Bovine brevicin core protein cDNA.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Best Local Similarity: 21.97% Mismatches: 100
Query Match: 7.75% Indels: 97
RESULT 541
ID ACH15082 standard; cDNA; 488 BP.
DE Human adult brain cDNA #2294.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 542
ID ADP07636 standard; DNA; 859 BP.
DE Human secreted protein encoding DNA, seq id 119.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 543
ID AAI58121 standard; cDNA; 1365 BP.
DE Human polynucleotide SEQ ID NO 324.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 544
ID ADL91792 standard; cDNA; 1844 BP.
DE Human PRO271 encoding cDNA SEQ ID NO:13.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 545
ID ADQ23710 standard; DNA; 1925 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6530.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 546
ID AAX52252 standard; DNA; 1984 BP.
DE Protein PRO271 cDNA clone DNA39423-1182.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 547
ID ADC78532 standard; cDNA; 1984 BP.
DE Human PRO271 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 548
ID ADR18008 standard; cDNA; 1984 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A. Mismatches: 39
PA (BOTS/) BOTSTEIN D. Indels: 4
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.

PA (MATH/) MATHER J P. Mismatches: 39
PA (PANJ/) PAN J. Indels: 4
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 549
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 550
ID AAS45938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 551
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 552
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 553
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 554
ID ACA05713 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 555
ID ACA66547 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 556
ID ACD07574 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%

RESULT 557
ID ACF20122 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040063-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 558
ID ACF19508 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040064-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 559
ID ACD21796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 560
ID ACF12961 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036160-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 561
ID ACD25064 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 562
ID ACF00113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 563
ID ACA72170 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 564
ID ACD04694 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 565
ID ACD18155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 566
ID ACD08162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 567
ID ABX71622 standard; cDNA; 1985 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 568
ID ACA88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 569
ID ACA70038 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 570
ID ACD12260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 571
ID ACC74175 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 572
ID ACD15803 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 573
ID ACD25371 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 574
ID ACD17848 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 575
ID ACC88135 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 576
ID ACD21489 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 577
ID ACD18556 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003044916-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 578
ID ACH06954 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane polypeptide PRO271 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 579
ID ABX98166 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN US2003036156-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 580
ID ACD13917 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 581
ID ACD09697 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 582
ID ACC88442 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027266-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 583
ID ACD21182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 584
ID ABX75554 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 585
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 586
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 587
ID ACA57696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN US2003036143-A1.

PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 588
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 589
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 590
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036132-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 591
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 592
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 593
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032137-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 594
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027269-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 595
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027268-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 596
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027274-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 597
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032135-A1.
PD 13-FEB-2003.

Query Match: 7.69% Indels: 4
RESULT 618
ID ACA68203 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 619
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 620
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 621
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 622
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 623
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 624
ID ACF12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 625
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 626
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 627
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 628

ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 629
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 630
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 631
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 632
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 633
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 634
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 635
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 636
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 637
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 638
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.

PN US2003036154-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 639
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 640
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 641
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 642
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 643
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 644
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 645
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 646
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 647
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 648
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 649
ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 650
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 651
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 652
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 653
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 654
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 655
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 656
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 657
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 658
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 659
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 660
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 661
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 662
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 663
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 664
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 665
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 666
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 667
ID ACD46632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4

RESULT 668
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 669
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 670
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 671
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 672
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 673
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 674
ID ACF48763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 675
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 676
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 677
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

RESULT 696
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 697
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 698
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 699
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 700
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 701
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 702
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 703
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 704
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 705
ID ACF76699 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 706
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 707
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 708
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 709
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 710
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 711
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 712
ID ACD22410 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 713
ID ACF15110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 714
ID ACC97205 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 715
ID ADA18273 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 716
ID ACD66964 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 717
ID ACC92235 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 718
ID ACF13882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 719
ID ACF14189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 720
ID ACF09420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 721
ID ACD45711 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 722
ID ACD47860 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 723
ID ACD67591 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 724
ID ACF25399 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 725
ID ACF29083 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 726
ID ACD84861 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 727
ID ACD83940 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 728
ID ACD87931 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 729
ID ACF30618 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 730
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 731
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 732
ID ACH12188 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 733
ID ACD40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032134-A1.

PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 734
ID ACF18052 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 735
ID ACF08499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 736
ID ACF31300 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 737
ID ACF52140 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 738
ID ACD50009 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 739
ID ACF38712 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 740
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 741
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 742
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 743
ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 744
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 745
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 746
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087374-A1.
PD 08-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 747
ID ACH12495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 748
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 749
ID ACD03773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 750
ID ACD10311 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 751
ID ACD11953 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 752
ID ACD83125 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.

PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 753
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 754
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 755
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 756
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 757
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 758
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 759
ID ACF33793 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 760
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 761
ID ACD90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 762
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 763
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 764
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 765
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 766
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PD 08-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 767
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096353-A1.
PD 22-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 768
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 769
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 770
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 771
ID ACF07885 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 772
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 773
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 774
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 775
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 776
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 777
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 778
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 779
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 780
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003082715-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 781
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 782
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 783
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 784
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 785
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 786
ID ACD30630 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 787
ID ACD31551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 788
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 789
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4

RESULT 790
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 791
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 792
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 793
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 794
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 795
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 796
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 797
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 798
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 799
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 800
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 801
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 802
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 803
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 804
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 805
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 806
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 807
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 808
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 7.69% Indels: 4
RESULT 809
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 810
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 811
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 812
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 813
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 814
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 815
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 816
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 817
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 818
ID ACD90080 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 819
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 820
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 821
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 822
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 823
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 824
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 825
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 826
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 827
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.

PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 828
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 829
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 830
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 831
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 832
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 833
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 834
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 835
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 836
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 837

ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 838
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073174-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 839
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 840
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 841
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104541-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 842
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 843
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 844
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 845
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 846
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032133-A1.

PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 847
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032136-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 848
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036129-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 849
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 850
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040057-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 851
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 852
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044932-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 853
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027270-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 854
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 855
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 856
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 857
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 858
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 859
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049738-A1.
PD 13-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 860
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 861
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 862
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 863
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 864
ID ACF51219 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 865
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 7.69% Indels: 4
RESULT 866
ID ACF25706 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 867
ID ACF39019 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 868
ID ACF28776 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 869
ID ACD90693 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 870
ID ACD86396 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 871
ID ACH05258 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 872
ID ACF65054 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 873
ID ADB20139 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 874
ID ACF43527 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 875

ID ACH08997 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 876
ID ACH09304 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 877
ID ADA78391 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 878
ID ACF09727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 879
ID ACF50912 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 880
ID ACF23806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 881
ID ACD88238 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 882
ID ACH09611 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 883
ID ACH10532 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 884
ID ACD11339 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036126-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 885
ID ACC96389 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044924-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 886
ID ACC98419 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044927-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 887
ID ADA16672 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 888
ID ACF41724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040072-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 889
ID ACF16645 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040073-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 890
ID ADA13101 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 891
ID ACD32165 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 892
ID ACD30323 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 893
ID ACD41194 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 894

ID ACF07578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 895
ID ACF30993 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 896
ID ACF77313 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 897
ID ACF10955 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073170-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 898
ID ACF32835 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 899
ID ACF26013 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 900
ID ACD83326 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 901
ID ACF23499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 902
ID ACF42913 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 903
ID ACF43220 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 904
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 905
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 906
ID ADA41969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 907
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027273-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 908
ID ACF10648 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036119-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 909
ID ACC93463 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036120-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 910
ID ACC96082 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 911
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044921-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 912
ID ADA17316 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4

RESULT 913
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 914
ID ACF21964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 915
ID ACF22578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 916
ID ACF08806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 917
ID ACF33142 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 918
ID ACF54596 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 919
ID ACF48456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 920
ID ACD47246 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 921
ID ACD49088 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 922

ID ACF37791 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 923
ID ACF30004 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 924
ID ACD87317 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 925
ID ACF61906 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104538-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 926
ID ACH10839 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 927
ID ADA42819 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 928
ID ACD10004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 929
ID ACD16729 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 930
ID ACC99026 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040067-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 931
ID ACF00420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054456-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 7.69% Indels: 4
RESULT 932
ID ACD40887 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 933
ID ACF14496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 934
ID ACF22271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 935
ID ACF78848 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 936
ID ACF11569 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 937
ID ACF51526 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 938
ID ACF33449 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 939
ID ACD49702 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 940
ID ACF37484 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068683-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 941

ID ACF28469 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 942
ID ACD88545 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068681-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 943
ID ACF75164 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 944
ID ACF60985 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 945
ID ACF44141 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 946
ID ACH08383 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 947
ID ACC93770 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036122-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 948
ID ACD20875 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 949
ID ACF06657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040065-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 950
ID ACD20568 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044919-A1.
PD 06-MAR-2003.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 951
ID ACD22717 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 952
ID ACF41417 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044928-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 953
ID ACF06964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 954
ID ACD23665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 955
ID ACF77620 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 956
ID ACD46018 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 957
ID ACF46921 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 958
ID ACF54289 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 959
ID ACF45693 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 960

ID ACF45386 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 961
ID ACF38405 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 962
ID ACD89466 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 963
ID ACD85168 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 964
ID ACD85782 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 965
ID ACF75778 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 966
ID ACF60678 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 967
ID ACH05565 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 968
ID ADA82462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 969
ID ACF55824 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068680-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 970
ID ACF55210 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 971
ID ADB77738 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 972
ID ADB74874 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 973
ID ADB85770 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 974
ID ACF56131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 975
ID ACF56438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 976
ID ACF55517 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 977
ID ACF54903 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 978
ID ADC28520 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059772-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 979
ID ADC39720 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 980
ID ADC40234 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 981
ID ADC19058 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 982
ID ADC34358 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 983
ID ADC29413 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 984
ID ADC28944 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 985
ID ADC40829 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 986
ID ADC19486 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 987
ID ADC33934 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073077-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 988
ID ADC13004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 989
ID ADC12456 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 990
ID ADD05500 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 991
ID ADD05011 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 992
ID ADD04017 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 993
ID ADD03593 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 994
ID ADE34845 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 995
ID ADG02495 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 996
ID ADG01202 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 997
ID ADF95377 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 998
ID ADG12192 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 999
ID ADH08852 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1000
ID ADH59328 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1001
ID ADI38107 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1002
ID ABX78541 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1003
ID ACA59070 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1004
ID ACA75513 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1005
ID ACA70993 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1006
ID ACC87521 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003027278-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1007
ID ACC86907 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036159-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1008
ID ACD04080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1009
ID ACA69411 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1010
ID ACA90256 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1011
ID ACA58467 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1012
ID ACC89363 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027264-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1013
ID ACA98154 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1014
ID ACA93796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1015
ID ACD15189 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1016
ID ACD08776 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040062-A1.
PD 27-FEB-2003.

Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1017
ID ACC96696 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040056-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1018
ID ACF15417 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044926-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1019
ID ACA72784 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1020
ID ACD02956 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1021
ID ACD01771 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1022
ID ACA91963 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1023
ID ADJ26375 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1024
ID ADL32633 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1025
ID ADM30167 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1026
ID ADE79290 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003135025-A1.

PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1027
ID ADE79714 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1028
ID ADE73390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1029
ID ADE74164 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003211572-A1.
PD 13-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1030
ID ADE73925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1031
ID ADE74776 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003211574-A1.
PD 13-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1032
ID ADE99479 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1033
ID ADE98598 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1034
ID ADE99025 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1035
ID ADG40495 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1036
ID ADF73889 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1037
ID ADF95989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1038
ID ADF73465 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1039
ID ADG04260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1040
ID ADG00420 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1041
ID ADG82676 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1042
ID ADG92308 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1043
ID ADG92735 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1044
ID ADH25957 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.

PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1045
ID ADH32926 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1046
ID ADH20524 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1047
ID ADH07379 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1048
ID ADH59924 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1049
ID ADH06952 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1050
ID ADI18694 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1051
ID ADI65414 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4

RESULT 1052
ID ADI37677 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1053
ID ADH97473 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1054
ID ADI65841 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1055
ID ADH60584 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1056
ID ADJ99641 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1057
ID ADL08834 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1058
ID ADJ54665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1059
ID ADM25175 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1060
ID ADM29925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.

PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1061
ID ADJ64436 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1062
ID ADM31332 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1063
ID ADM36379 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1064
ID ADM40184 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1065
ID ADO06247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #40.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1066
ID ADN37792 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1067
ID ADR11099 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1068
ID ADT03684 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1069
ID ADS74647 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane cDNA #42.
PN US2004185531-A1.

PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 1070
ID AAD48133 standard; DNA; 2878 BP.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1071
ID ADN38941 standard; cDNA; 2878 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1072
ID ADK67783 standard; DNA; 2878 BP.
DE Human glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYYA) UNIV YALE.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1073
ID ADQ83194 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1074
ID ADQ85107 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1075
ID ACN42086 standard; cDNA; 4353 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1076
ID ACN42083 standard; cDNA; 4545 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1077
ID ACN42082 standard; cDNA; 4659 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 7.69% Indels: 53
RESULT 1078
ID ABK62593 standard; cDNA; 2465 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #500.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 27.14% Mismatches: 69
Query Match: 7.66% Indels: 11
RESULT 1079
ID ADB47730 standard; cDNA; 2753 BP.
DE Novel human secreted protein cDNA #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 20.62% Mismatches: 123
Query Match: 7.63% Indels: 97
RESULT 1080
ID ADJ55285 standard; cDNA; 2753 BP.
DE Novel human secreted protein cDNA #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 20.62% Mismatches: 123
Query Match: 7.63% Indels: 97
RESULT 1081
ID ADQ45337 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 7000.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.60% Indels: 2
RESULT 1082
ID ADQ45257 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6920.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30

Query Match: 7.54% Indels: 2
RESULT 1083
ID ADQ45308 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6971.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1084
ID ADQ45241 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6904.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1085
ID ADQ45225 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6888.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1086
ID ADQ45323 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6986.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1087
ID ADQ45215 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6878.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1088
ID ADQ45264 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1089
ID ADQ45280 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6943.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1090
ID ADQ45298 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6961.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1091
ID ADL13960 standard; DNA; 834 BP.
DE Osteoarthritis-associated polymorphic nucleotide #492.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8

RESULT 1092
ID ABL68341 standard; DNA; 1414 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6678.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1093
ID ABK83989 standard; cDNA; 1414 BP.
DE Human cDNA differentially expressed in granulocytic cells #560.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1094
ID ABX76383 standard; DNA; 1414 BP.
DE Lung cancer-associated polynucleotide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1095
ID ACC72679 standard; cDNA; 1414 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:18.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1096
ID ADL13959 standard; DNA; 1414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #491.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1097
ID ADN38975 standard; cDNA; 1414 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:293.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1098
ID ADO24484 standard; cDNA; 1414 BP.
DE Human PRO87343 encoding cDNA SEQ ID NO:123.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1099
ID ADO24438 standard; cDNA; 1414 BP.
DE Human PRO87335 encoding cDNA SEQ ID NO:77.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1100
ID ADR14116 standard; DNA; 1414 BP.
DE Human NF-kappaB pathway-associated gene SeqID117.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1101

ID ACH45565 standard; cDNA; 474 BP.
DE Human foetal brain cDNA #6290.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 34.52%
Query Match: 7.48%
Mismatches: 41
Indels: 2
RESULT 1102
ID ADM80846 standard; cDNA; 795 BP.
DE Human CADECM-33 encoding cDNA SEQ ID NO:75.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 34.94%
Query Match: 7.33%
Mismatches: 37
Indels: 3
RESULT 1103
ID AAV41923 standard; cDNA; 1587 BP.
DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Best Local Similarity: 24.06%
Query Match: 7.30%
Mismatches: 81
Indels: 48
RESULT 1104
ID AAQ57710 standard; DNA; 5191 BP.
DE Neurocan DNA.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNV) UNIV NEW YORK STATE.
Best Local Similarity: 23.61%
Query Match: 7.27%
Mismatches: 95
Indels: 43
RESULT 1105
ID ABX34625 standard; cDNA; 1761 BP.
DE Human mddt cDNA SEQ ID 186.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 23.87%
Query Match: 7.24%
Mismatches: 95
Indels: 54
RESULT 1106
ID ADQ83195 standard; cDNA; 1771 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #9.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Best Local Similarity: 23.87%
Query Match: 7.24%
Mismatches: 95
Indels: 54
RESULT 1107
ID ADM87060 standard; cDNA; 1783 BP.
DE Human protein encoding cDNA SEQ ID NO:153.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Best Local Similarity: 22.67%
Query Match: 7.15%
Mismatches: 68
Indels: 89
RESULT 1108
ID ABL62702 standard; DNA; 11185 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1039.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1109
ID ABN96814 standard; DNA; 11185 BP.
DE Gene #3312 used to diagnose liver cancer.

PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1110
ID ADN95527 standard; DNA; 11185 BP.
DE Human BEC/LEC-related gene sequence SeqID450.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1111
ID ADJ75063 standard; DNA; 11185 BP.
DE Marker gene SEQ ID NO:315.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1112
ID ADN04530 standard; cDNA; 11185 BP.
DE Antipsoriatic cDNA sequence #467.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1113
ID ADP23737 standard; cDNA; 11185 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:915.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1114
ID AAS94985 standard; DNA; 12319 BP.
DE Human DNA sequence #240 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 25.47%
Query Match: 7.15%
Mismatches: 69
Indels: 27
RESULT 1115
ID ADJ75926 standard; DNA; 7375 BP.
DE Marker gene SEQ ID NO:1178.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Best Local Similarity: 28.93%
Query Match: 7.12%
Mismatches: 57
Indels: 11
RESULT 1116
ID ADP71272 standard; DNA; 573 BP.
DE Human LP2 B-B' domain gene region SeqID7.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 26.45%
Query Match: 7.06%
Mismatches: 63
Indels: 36
RESULT 1117
ID ACH29430 standard; cDNA; 410 BP.
DE Human adult spleen cDNA #449.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 32.39%
Mismatches: 32

Query Match: 6.97% Indels: 1

RESULT 1118

ID ADQ38685 standard; DNA; 7291 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 348.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 24.18%

Mismatches: 82

Indels: 27

Query Match: 6.97%

RESULT 1119

ID ADQ38687 standard; DNA; 7358 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 350.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 24.18%

Mismatches: 82

Indels: 27

Query Match: 6.97%

RESULT 1120

ID ADQ38681 standard; DNA; 12553 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 344.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 24.18%

Mismatches: 82

Indels: 27

Query Match: 6.97%

RESULT 1121

ID ADQ38682 standard; DNA; 12620 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 345.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 24.18%

Mismatches: 82

Indels: 27

Query Match: 6.97%

RESULT 1122

ID ABT42226 standard; DNA; 5191 BP.

DE Toxicity modelling related rat gene SEQ ID No 1928.

PN WO200295000-A2.

PD 28-NOV-2002.

PA (GENE-) GENE LOGIC INC.

Best Local Similarity: 23.15%

Mismatches: 96

Indels: 43

Query Match: 6.91%

RESULT 1123

ID ADO31199 standard; DNA; 5191 BP.

DE Rat neurocan gene for glucosaminoglycan reduction in glial scars.

PN WO2004041197-A2.

PD 21-MAY-2004.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

Best Local Similarity: 23.15%

Mismatches: 96

Indels: 43

Query Match: 6.91%

RESULT 1124

ID ABL07438 standard; cDNA; 8924 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16796.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Best Local Similarity: 22.48%

Mismatches: 85

Indels: 54

Query Match: 6.88%

RESULT 1125

ID AAA63526 standard; DNA; 285 BP.

DE DNA encoding the domain of hyaluronic acid which interacts with CD44.

PN WO200047163-A2.

PD 17-AUG-2000.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Best Local Similarity: 27.10%

Mismatches: 36

Indels: 27

Query Match: 6.85%

RESULT 1126

ID ABA02881 standard; cDNA; 2087 BP.

DE Human versican isoform V3 encoding cDNA SEQ ID NO 1.

PN WO200179284-A2.

PD 25-OCT-2001.

PA (WIGH/) WIGHT T N.

PA (MERR/) MERRILEES M.

Best Local Similarity: 29.75%

Mismatches: 57

Query Match: 6.82% Indels: 11

RESULT 1127

ID ADQ38683 standard; DNA; 4330 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 346.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1128

ID ACH04002 standard; cDNA; 7182 BP.

DE Human cDNA differentially expressed in lung cancer #207.

PN US2003065157-A1.

PD 03-APR-2003.

PA (LASE/) LASEK A W.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1129

ID AAQ12261 standard; cDNA; 8224 BP.

DE Versican gene.

PN WO9108230-A.

PD 13-JUN-1991.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

PA (LJOL-) LA JOLLA CANCER RES FOUND.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1130

ID ABT11088 standard; cDNA; 8224 BP.

DE Human breast cancer associated coding sequence SEQ ID NO: 1222.

PN WO200259271-A2.

PD 01-AUG-2002.

PA (GENE-) GENE LOGIC INC.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1131

ID ACC50121 standard; cDNA; 8224 BP.

DE Breast cancer associated cDNA sequence SEQ ID NO:89.

PN WO2003004989-A2.

PD 16-JAN-2003.

PA (MILL-) MILLENIUM PHARM INC.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1132

ID ADQ38686 standard; DNA; 9592 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 349.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1133

ID ACN89856 standard; DNA; 9647 BP.

DE Breast cancer related marker, seq id 11006.

PN US2003099974-A1.

PD 29-MAY-2003.

PA (MILL-) MILLENIUM PHARM INC.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1134

ID ADQ38684 standard; DNA; 9659 BP.

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 347.

PN WO2004058052-A2.

PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.

Best Local Similarity: 29.75%

Mismatches: 57

Indels: 11

Query Match: 6.82%

RESULT 1135

ID ABA06490 standard; cDNA; 972 BP.

DE Human cDNA SEQ ID NO: 156.

PN WO200154474-A2.

PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Best Local Similarity: 25.66%

Mismatches: 66

Query Match: 6.79% Indels: 25
RESULT 1136
ID ABV83827 standard; cDNA; 972 BP.
DE Human polynucleotide SEQ ID NO 156.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.66% Mismatches: 66
Query Match: 6.79% Indels: 25
RESULT 1137
ID AAQ51157 standard; DNA; 1190 BP.
DE Herpes simplex virus glycoprotein I DNA.
EP568178-A1.
PD 03-NOV-1993.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Best Local Similarity: 21.63% Mismatches: 99
Query Match: 6.76% Indels: 52
RESULT 1138
ID ACA40155 standard; DNA; 1209 BP.
DE Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 22.47% Mismatches: 114
Query Match: 6.73% Indels: 61
RESULT 1139
ID ADP71270 standard; DNA; 600 BP.
DE Human aggrecan B-B' domain gene region SeqID5.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 37.36% Mismatches: 35
Query Match: 6.70% Indels: 14
RESULT 1140
ID AAV34196 standard; DNA; 1720 BP.
DE Human secreted protein gene 43 clone HSXCK41.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.94% Mismatches: 80
Query Match: 6.70% Indels: 49
RESULT 1141
ID ACD08067 standard; cDNA; 1720 BP.
DE cDNA encoding novel human secreted protein #43.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Best Local Similarity: 23.94% Mismatches: 80
Query Match: 6.70% Indels: 49
RESULT 1142
ID AAC76373 standard; cDNA; 1377 BP.
DE Human ORFX ORF1928 polynucleotide sequence SEQ ID NO:3855.

PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 21.12% Mismatches: 121
Query Match: 6.67% Indels: 91
RESULT 1143
ID AAA61263 standard; DNA; 1308 BP.
DE Human secreted protein gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 28.48% Mismatches: 55
Query Match: 6.64% Indels: 42
RESULT 1144
ID AAA57365 standard; DNA; 1259 BP.
DE DNA encoding a human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Best Local Similarity: 24.56% Mismatches: 85
Query Match: 6.61% Indels: 20
RESULT 1145
ID AAD08974 standard; cDNA; 1354 BP.
DE Alternative version of human TNF stimulated gene-6 (TSG-6) cDNA.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Best Local Similarity: 26.79% Mismatches: 78
Query Match: 6.61% Indels: 16
RESULT 1146
ID ACC49518 standard; cDNA; 6310 BP.
DE Tumour-associated antigenic target protein TAT185 cDNA SEQ ID NO:26.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 23.02% Mismatches: 102
Query Match: 6.58% Indels: 62
RESULT 1147
ID ADN38943 standard; cDNA; 6310 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:261.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 23.02% Mismatches: 102
Query Match: 6.58% Indels: 62
RESULT 1148
ID ADO31195 standard; DNA; 6310 BP.
DE Human neurocan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Best Local Similarity: 23.02% Mismatches: 102
Query Match: 6.58% Indels: 62
RESULT 1149
ID ADP71268 standard; DNA; 585 BP.
DE Human LP1 B-B' domain gene region SeqID3.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 33.33% Mismatches: 44
Query Match: 6.52% Indels: 7
RESULT 1150
ID ADL13630 standard; DNA; 1065 BP.
DE Osteoarthritis-associated polymorphic nucleotide #162.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1151
ID ABT43880 standard; DNA; 1492 BP.
DE 151P3D4 v-1 DNA clone-1 from placenta.

PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1152
ID ABT43881 standard; DNA; 1492 BP.
DE DNA derived from mRNA of human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1153
ID AAS28787 standard; cDNA; 1640 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 33.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1154
ID ABA06583 standard; cDNA; 1640 BP.
DE Human cDNA SEQ ID NO: 249.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1155
ID ABV83920 standard; cDNA; 1640 BP.
DE Human polynucleotide SEQ ID NO 249.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1156
ID ADB31512 standard; cDNA; 1640 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 33.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1157
ID AAS28848 standard; cDNA; 1641 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 94.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1158
ID ABA06754 standard; cDNA; 1641 BP.
DE Human cDNA SEQ ID NO: 420.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1159
ID ABV84091 standard; cDNA; 1641 BP.
DE Human polynucleotide SEQ ID NO 420.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22

RESULT 1160
ID ADB31573 standard; cDNA; 1641 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 94.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.83% Mismatches: 74
Query Match: 6.52% Indels: 22
RESULT 1161
ID ADH71347 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9s SEQ ID NO:243.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 44
Query Match: 6.52% Indels: 2
RESULT 1162
ID ADL13629 standard; DNA; 1759 BP.
DE Osteoarthritis-associated polymorphic nucleotide #161.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1163
ID ABL34375 standard; DNA; 1790 BP.
DE Human immune system associated gene SEQ ID NO: 2348.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.42% Mismatches: 52
Query Match: 6.52% Indels: 64
RESULT 1164
ID ABK31533 standard; DNA; 1790 BP.
DE Signal transduction associated gene modified complementary DNA #188.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.42% Mismatches: 52
Query Match: 6.52% Indels: 64
RESULT 1165
ID ABT43866 standard; DNA; 1957 BP.
DE DNA of transcript variant 151P3D4 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1166
ID ABT43869 standard; cDNA; 1957 BP.
DE 151P3D4 v-1 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1167
ID ABT43878 standard; cDNA; 1957 BP.
DE 151P3D4 v-10 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1168
ID ABT43877 standard; cDNA; 1957 BP.
DE 151P3D4 v-9 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1169

ID ABT43879 standard; cDNA; 1957 BP.
DE 151P3D4 v-11 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1170
ID ABT43874 standard; cDNA; 1957 BP.
DE 151P3D4 v-6 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1171
ID ABT43876 standard; cDNA; 1957 BP.
DE 151P3D4 v-8 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1172
ID ABT43871 standard; cDNA; 1957 BP.
DE 151P3D4 v-3 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1173
ID ABT43872 standard; cDNA; 1957 BP.
DE 151P3D4 v-4 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1174
ID ABT43873 standard; cDNA; 1957 BP.
DE 151P3D4 v-5 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1175
ID ABT43875 standard; cDNA; 1957 BP.
DE 151P3D4 v-7 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1176
ID ABT43870 standard; cDNA; 2166 BP.
DE 151P3D4 v-2 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1177
ID ABT43865 standard; DNA; 2166 BP.
DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1178
ID ABT43867 standard; DNA; 2166 BP.

DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1179
ID ADQ24054 standard; DNA; 2538 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6874.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1180
ID ABL07439 standard; cDNA; 6279 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16799.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.18% Mismatches: 90
Query Match: 6.49% Indels: 48
RESULT 1181
ID ADH71333 standard; DNA; 1599 BP.
DE Human gene of the invention NOV91 SEQ ID NO:229.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1182
ID ADH71335 standard; DNA; 1611 BP.
DE Human gene of the invention NOV9m SEQ ID NO:231.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1183
ID ADH71313 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9b SEQ ID NO:209.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1184
ID ADH71353 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9v SEQ ID NO:249.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1185
ID ADH71341 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9p SEQ ID NO:237.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1186
ID ADH71345 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9r SEQ ID NO:241.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1187
ID ADH71339 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9o SEQ ID NO:235.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1188
ID ADH71349 standard; DNA; 1668 BP.
DE Human Gene of the invention NOV9t SEQ ID NO:245.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1189
ID ADH71343 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9q SEQ ID NO:239.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1190
ID ABA83182 standard; DNA; 1851 BP.
DE HOST-4 ovarian tumour marker gene sequence, SEQ ID NO:144.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 33.71% Mismatches: 41
Query Match: 6.46% Indels: 4
RESULT 1191
ID AAF87113 standard; DNA; 2011 BP.
DE NOV2 coding sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.14% Mismatches: 84
Query Match: 6.46% Indels: 22
RESULT 1192
ID ADH71315 standard; DNA; 2011 BP.
DE Human gene of the invention NOV9c SEQ ID NO:211.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 25.14% Mismatches: 84
Query Match: 6.46% Indels: 22
RESULT 1193
ID AAQ71391 standard; DNA; 2589 BP.
DE Yeast 2.6 kB agglutination gene FLO1s.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1194
ID AAQ67360 standard; DNA; 2685 BP.
DE S. cerevisiae FLO1 gene.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1195
ID AAQ54029 standard; DNA; 2685 BP.
DE Flocculation protein coding sequence of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1196

ID ADQ38559 standard; DNA; 3858 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 222.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 22.28% Mismatches: 91
Query Match: 6.46% Indels: 31
RESULT 1197
ID AAQ71390 standard; DNA; 4614 BP.
DE Yeast 4.7 kB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1198
ID AAA95422 standard; DNA; 4614 BP.
DE S. cerevisiae FLO1 coding sequence.
PN WO200058342-A1.
PD 05-OCT-2000.
PA (VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1199
ID ADS46655 standard; cDNA; 4614 BP.
DE Bacterial polynucleotide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1200
ID ADO31201 standard; DNA; 5259 BP.
DE Mouse neurocan gene for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Best Local Similarity: 26.21% Mismatches: 44
Query Match: 6.46% Indels: 16
RESULT 1201
ID ABL25979 standard; DNA; 5388 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29410.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.81% Mismatches: 93
Query Match: 6.46% Indels: 52
RESULT 1202
ID ADR32196 standard; DNA; 5613 BP.
DE Yeast FLO1 open reading frame fragment, SEQ ID NO:1.
PN WO2004067565-A1.
PD 12-AUG-2004.
PA (OSBO-) OSBORNE DISTRIBUIDORA SA.
PA (UYDO/) UNIV DE OLAVIDE PABLO.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1203
ID ADP87474 standard; DNA; 5864 BP.
DE S cerevisiae glucan synthase pathway gene YAR050W (FLO1) SeqID16.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Best Local Similarity: 25.10% Mismatches: 115
Query Match: 6.46% Indels: 38
RESULT 1204
ID ABL25978 standard; DNA; 7782 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.81% Mismatches: 93
Query Match: 6.46% Indels: 52
RESULT 1205
ID ABQ42487 standard; DNA; 1174 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29078.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.35% Mismatches: 84
Query Match: 6.43% Indels: 45
RESULT 1206
ID ABQ42486 standard; DNA; 1174 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29077.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.35% Mismatches: 84
Query Match: 6.43% Indels: 45
RESULT 1207
ID ACA55632 standard; cDNA; 1482 BP.
DE Human signalling pathway polynucleotide probe SEQ ID NO 230.
PN US6500938-B1.
PD 31-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 20.62% Mismatches: 122
Query Match: 6.43% Indels: 98
RESULT 1208
ID ADI55428 standard; DNA; 1482 BP.
DE Human polynucleotide probe #230.
PN US2004010136-A1.
PD 15-JAN-2004.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 20.62% Mismatches: 122
Query Match: 6.43% Indels: 98
RESULT 1209
ID AAZ45836 standard; cDNA; 2455 BP.
DE cDNA of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Best Local Similarity: 27.03% Mismatches: 75
Query Match: 6.43% Indels: 34
RESULT 1210
ID AAZ45837 standard; cDNA; 2821 BP.
DE cDNA of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Best Local Similarity: 27.03% Mismatches: 75
Query Match: 6.43% Indels: 34
RESULT 1211
ID ADQ45269 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1212
ID ADQ45261 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1213
ID ADQ45247 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6910.
PN WO2004058052-A2.
PD 15-JUL-2004.

PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1214
ID ADQ45220 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6883.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1215
ID ADQ45210 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6873.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1216
ID ADQ45303 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6966.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1217
ID ADQ45335 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6998.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1218
ID ADQ45230 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6893.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1219
ID ADQ45293 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6956.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1220
ID ADQ45313 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6976.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 6.40% Indels: 2
RESULT 1221
ID ADP71266 standard; DNA; 600 BP.
DE Human versican B-B' domain gene region SeqID1.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Best Local Similarity: 32.63% Mismatches: 43
Query Match: 6.40% Indels: 9
RESULT 1222
ID ADH71337 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9n SEQ ID NO:233.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Best Local Similarity: 29.21% Mismatches: 46
Query Match: 6.40% Indels: 2
RESULT 1223
ID AAL56704 standard; DNA; 36604 BP.
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Best Local Similarity: 20.96% Mismatches: 106
Query Match: 6.34% Indels: 122
RESULT 1224
ID ACH79577 standard; DNA; 538 BP.
DE Human genome derived single exon probe #12772.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 25.37% Mismatches: 55
Query Match: 6.31% Indels: 25
RESULT 1225
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 34.21% Mismatches: 35
Query Match: 6.31% Indels: 1
RESULT 1226
ID ADR24283 standard; DNA; 484 BP.
DE Breast cancer prognosis marker #144.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Best Local Similarity: 20.71% Mismatches: 61
Query Match: 6.28% Indels: 28
RESULT 1227
ID ADH71351 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9u SEQ ID NO:247.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 46
Query Match: 6.28% Indels: 2
RESULT 1228
ID ADN41609 standard; DNA; 4767 BP.
DE Novel human secreted protein polynucleotide seqid 731.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 25.61% Mismatches: 114
Query Match: 6.28% Indels: 71
RESULT 1229
ID ADN41608 standard; DNA; 4768 BP.
DE Novel human secreted protein polynucleotide seqid 730.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.

PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 25.61% Mismatches: 114
Query Match: 6.28% Indels: 71
RESULT 1230
ID AAS28917 standard; DNA; 5430 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 279.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.46% Mismatches: 70
Query Match: 6.28% Indels: 28
RESULT 1231
ID ADB31758 standard; DNA; 5430 BP.
DE Human novel protein DNA SEQ ID NO 279.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.46% Mismatches: 70
Query Match: 6.28% Indels: 28
RESULT 1232
ID ADI39160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Best Local Similarity: 21.39% Mismatches: 96
Query Match: 6.28% Indels: 133
RESULT 1233
ID ABL27120 standard; DNA; 8433 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32833.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 31.01% Mismatches: 39
Query Match: 6.25% Indels: 42
RESULT 1234
ID ADF80106 standard; DNA; 402 BP.
DE Leukaemia-related DNA sequence #662.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Best Local Similarity: 32.26% Mismatches: 30
Query Match: 6.22% Indels: 0
RESULT 1235
ID AAT01476 standard; cDNA; 1519 BP.
DE Cat brain-enriched hyaluronan binding protein cDNA.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Best Local Similarity: 21.43% Mismatches: 107
Query Match: 6.22% Indels: 83
RESULT 1236
ID AAA34893 standard; DNA; 1696 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2582.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Best Local Similarity: 22.13% Mismatches: 106
Query Match: 6.22% Indels: 125

RESULT 1237
ID AAF21015 standard; DNA; 1696 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2582.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Best Local Similarity: 22.13% Mismatches: 106
Query Match: 6.22% Indels: 125
RESULT 1238
ID ABZ96709 standard; DNA; 1696 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 22.13% Mismatches: 106
Query Match: 6.22% Indels: 125
RESULT 1239
ID ABD20558 standard; DNA; 1696 BP.
DE Human pulmonary and inflammatory target DNA #169.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Best Local Similarity: 22.13% Mismatches: 106
Query Match: 6.22% Indels: 125
RESULT 1240
ID AAV34254 standard; DNA; 1962 BP.
DE Human secreted protein gene 43 clone HSXCK41.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 20.46% Mismatches: 107
Query Match: 6.22% Indels: 89
RESULT 1241
ID ACD08125 standard; cDNA; 1962 BP.
DE cDNA encoding novel human secreted protein #101.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Best Local Similarity: 20.46% Mismatches: 107
Query Match: 6.22% Indels: 89
RESULT 1242
ID ACN42085 standard; cDNA; 4391 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:960.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.00% Mismatches: 51
Query Match: 6.22% Indels: 14
RESULT 1243
ID ACN42084 standard; cDNA; 4536 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.
PN WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Best Local Similarity: 25.00% Mismatches: 51
Query Match: 6.22% Indels: 14
RESULT 1244
ID ADM43175 standard; DNA; 35167 BP.
DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.
PN WO2004018627-A2.
PD 04-MAR-2004.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 23.62% Mismatches: 78
Query Match: 6.22% Indels: 86
RESULT 1245
ID ADS00140 standard; DNA; 35167 BP.
DE Wild-type human adenovirus serotype 24 DNA SEQ ID NO:1.
PN WO2004083418-A1.
PD 30-SEP-2004.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 23.62% Mismatches: 78
Query Match: 6.22% Indels: 86
RESULT 1246
ID ABT23534 standard; DNA; 1341 BP.
DE Cellobiohydrolase I activity polynucleotide SEQ ID No 43.
PN WO2003000941-A2.
PD 03-JAN-2003.
PA (NOVO) NOVOZYMES AS.
Best Local Similarity: 23.68% Mismatches: 125
Query Match: 6.19% Indels: 104
RESULT 1247
ID ABL18341 standard; DNA; 1372 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6496.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 29.69% Mismatches: 54
Query Match: 6.19% Indels: 25
RESULT 1248
ID ABL18340 standard; DNA; 4492 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6493.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 29.69% Mismatches: 54
Query Match: 6.19% Indels: 25
RESULT 1249
ID ABQ81848 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Best Local Similarity: 26.64% Mismatches: 113
Query Match: 6.16% Indels: 29
RESULT 1250
ID ABQ41262 standard; DNA; 1276 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27853.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.53% Mismatches: 95
Query Match: 6.13% Indels: 38
RESULT 1251
ID ABQ41263 standard; DNA; 1276 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27854.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.53% Mismatches: 95
Query Match: 6.13% Indels: 38
RESULT 1252
ID AAA93621 standard; DNA; 2607 BP.
DE Human SLIT protein-like splice variant SECX 3352358-2 DNA.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.

Best Local Similarity: 20.58% Mismatches: 124
Query Match: 6.13% Indels: 79
RESULT 1253
ID ADA23288 standard; cDNA; 2607 BP.
DE cDNA encoding human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Best Local Similarity: 20.58% Mismatches: 124
Query Match: 6.13% Indels: 79
RESULT 1254
ID ABK33981 standard; DNA; 6112 BP.
DE Human DNA for staging of Astrocytomas, complement, #33.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.53% Mismatches: 95
Query Match: 6.13% Indels: 38
RESULT 1255
ID ADA20369 standard; DNA; 6112 BP.
DE Prostate tumour related genomic DNA complement sample #17.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.53% Mismatches: 95
Query Match: 6.13% Indels: 38
RESULT 1256
ID ADA84176 standard; DNA; 6112 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:34.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.53% Mismatches: 95
Query Match: 6.13% Indels: 38
RESULT 1257
ID AAS59543 standard; DNA; 53178 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #38.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 25.00% Mismatches: 91
Query Match: 6.13% Indels: 67
RESULT 1258
ID ACF64472 standard; DNA; 53178 BP.
DE Propionibacterium acnes DNA contig sequence #38.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 25.00% Mismatches: 91
Query Match: 6.13% Indels: 67
RESULT 1259
ID AAT01475 standard; cDNA; 1084 BP.
DE Rat brain-enriched hyaluronan binding protein cDNA.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Best Local Similarity: 25.00% Mismatches: 52
Query Match: 6.10% Indels: 14
RESULT 1260
ID AAH90018 standard; cDNA; 2313 BP.
DE Human bone marrow cDNA, SEQ ID NO: 262.
PN WO200153453-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1261
ID ACD05902 standard; cDNA; 2313 BP.
DE Novel human contig #76.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.

Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1262
ID ADE09790 standard; DNA; 2313 BP.
DE Novel DNA-related contig nucleotide sequence #512.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1263
ID ADE07629 standard; DNA; 2514 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #695.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1264
ID AAH14562 standard; cDNA; 3118 BP.
DE Human cDNA encoding clone SPLEN20087370.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1265
ID ADB63178 standard; cDNA; 3175 BP.
DE Human cDNA encoding clone SPLEN20087370.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 23.23% Mismatches: 87
Query Match: 6.10% Indels: 106
RESULT 1266
ID AAH14010 standard; cDNA; 3499 BP.
DE Human cDNA sequence SEQ ID NO:11101.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1267
ID ADO00911 standard; cDNA; 4011 BP.
DE Human homologue of Fruit fly AD-related cDNA CG1103 #2.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1268
ID ADR07180 standard; cDNA; 5131 BP.
DE Full length human cDNA useful for treating neurological disease Seq 686.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 26.75% Mismatches: 78
Query Match: 6.10% Indels: 55
RESULT 1269
ID ADL13962 standard; DNA; 160198 BP.
DE Osteoarthritis-associated polymorphic nucleotide #494.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 34.55% Mismatches: 23
Query Match: 6.10% Indels: 2
RESULT 1270
ID AAS17594 standard; cDNA; 1209 BP.
DE DNA encoding novel secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 6.07% Indels: 3
RESULT 1271
ID ADF58259 standard; cDNA; 1209 BP.
DE Human polynucleotide sequence SEQ ID NO:626.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 6.07% Indels: 3
RESULT 1272
ID AAA37671 standard; DNA; 1241 BP.
DE Human peptidase, HPEP-15 coding sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 23.50% Mismatches: 76
Query Match: 6.07% Indels: 45
RESULT 1273
ID ABK11078 standard; cDNA; 1475 BP.
DE cDNA encoding LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 6.07% Indels: 3
RESULT 1274
ID ABL24247 standard; DNA; 4140 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24214.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.16% Mismatches: 94
Query Match: 6.07% Indels: 59
RESULT 1275
ID ADF74225 standard; cDNA; 5409 BP.
DE Human novel brain/hippocampus cDNA #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 6.07% Indels: 3
RESULT 1276
ID AAD56128 standard; DNA; 7596 BP.
DE Mouse Notch carcinoma associated (CA) gene coding region.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1277
ID ADA02491 standard; cDNA; 7596 BP.
DE Mouse Notch1 carcinoma associated coding sequence, SEQ ID NO:1009.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1278
ID ADB72229 standard; cDNA; 7596 BP.
DE Mouse Notch1 cDNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1279
ID AAD56127 standard; DNA; 8064 BP.
DE Mouse Notch carcinoma associated (CA) DNA.
PN WO2003035837-A2.
PD 01-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1280
ID ADA02490 standard; cDNA; 8064 BP.
DE Mouse Notch1 carcinoma associated cDNA, SEQ ID NO:1008.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1281
ID ADB72228 standard; mRNA; 8064 BP.
DE Mouse Notch1 mRNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.99% Mismatches: 65
Query Match: 6.07% Indels: 47
RESULT 1282
ID ABQ14105 standard; DNA; 645 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 696.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIC-) EPIGENOMICS AG.
Best Local Similarity: 21.39% Mismatches: 68
Query Match: 6.04% Indels: 64
RESULT 1283
ID ABQ14104 standard; DNA; 645 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 695.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIC-) EPIGENOMICS AG.
Best Local Similarity: 21.39% Mismatches: 68
Query Match: 6.04% Indels: 64
RESULT 1284
ID ADS55917 standard; cDNA; 1386 BP.
DE Bacterial polynucleotide #7904.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.60% Mismatches: 99
Query Match: 6.04% Indels: 64
RESULT 1285
ID ADR46580 standard; DNA; 2453 BP.
DE Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Best Local Similarity: 23.35% Mismatches: 109
Query Match: 6.04% Indels: 132
RESULT 1286
ID ADR99037 standard; DNA; 9487 BP.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, DNA SEQ ID 43.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Best Local Similarity: 20.09% Mismatches: 98
Query Match: 6.04% Indels: 48
RESULT 1287
ID ABZ59662 standard; cDNA; 2622 BP.
DE Human secreted protein SECP-17 encoding cDNA SEQ ID NO:48.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYY/) LU Y.
Best Local Similarity: 30.86% Mismatches: 40
Query Match: 6.00% Indels: 3
RESULT 1288

ID ABO81849 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Best Local Similarity: 23.40% Mismatches: 103
Query Match: 6.00% Indels: 100
RESULT 1289
ID AAV28137 standard; cDNA to mRNA; 1374 BP.
DE Mouse junctional adhesion molecule gene.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Best Local Similarity: 23.75% Mismatches: 104
Query Match: 5.97% Indels: 121
RESULT 1290
ID ABL27121 standard; DNA; 4287 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 28.39% Mismatches: 59
Query Match: 5.97% Indels: 42
RESULT 1291
ID ADO30240 standard; cDNA; 4488 BP.
DE Mouse GPCR GPRC5B polynucleotide, SEQ ID NO:1343.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Best Local Similarity: 22.01% Mismatches: 96
Query Match: 5.97% Indels: 68
RESULT 1292
ID AAF86431 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #1.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Best Local Similarity: 23.50% Mismatches: 51
Query Match: 5.97% Indels: 80
RESULT 1293
ID AAA27366 standard; DNA; 1206 BP.
DE Sinorhizobium meliloti ribc gene.
PN WO200029607-A1.
PD 25-MAY-2000.
PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 27.07% Mismatches: 45
Query Match: 5.94% Indels: 33
RESULT 1294
ID ABL25807 standard; DNA; 3381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28894.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.00% Mismatches: 86
Query Match: 5.94% Indels: 57
RESULT 1295
ID ADS48391 standard; cDNA; 3799 BP.
DE Bacterial polynucleotide #3134.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.61% Mismatches: 64
Query Match: 5.94% Indels: 73
RESULT 1296
ID AAA27364 standard; DNA; 4248 BP.
DE Sinorhizobium meliloti ribc/ribD gene complex.
PN WO200029607-A1.
PD 25-MAY-2000.

PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 27.07% Mismatches: 45
Query Match: 5.94% Indels: 33
RESULT 1297
ID ABL25806 standard; DNA; 5381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.00% Mismatches: 86
Query Match: 5.94% Indels: 57
RESULT 1298
ID ADH69807 standard; DNA; 684973 BP.
DE Human Vbeta gene.
PN US2002150891-A1.
PD 17-OCT-2002.
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
Best Local Similarity: 26.49% Mismatches: 93
Query Match: 5.94% Indels: 25
RESULT 1299
ID ABL68560 standard; DNA; 267156 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6897.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 26.49% Mismatches: 93
Query Match: 5.94% Indels: 25
RESULT 1300
ID ABL07173 standard; cDNA; 6353 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.88% Mismatches: 71
Query Match: 5.91% Indels: 34
RESULT 1301
ID ABL07172 standard; cDNA; 8429 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.88% Mismatches: 71
Query Match: 5.91% Indels: 34
RESULT 1302
ID ABQ51862 standard; DNA; 585 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38453.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.68% Mismatches: 50
Query Match: 5.88% Indels: 72
RESULT 1303
ID ABQ51863 standard; DNA; 585 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38454.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.68% Mismatches: 50
Query Match: 5.88% Indels: 72
RESULT 1304
ID ABQ25506 standard; DNA; 1195 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12097.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 25.29% Mismatches: 77
Query Match: 5.88% Indels: 31
RESULT 1305
ID ABQ25507 standard; DNA; 1195 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12098.
PN WO200218632-A2.
PD 07-MAR-2002.

PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 25.29%
Query Match: 5.88%
RESULT 1306
ID AAX22095 standard; DNA; 1767 BP.
DE Cellobiohydrolase CBH B coding sequence.
PN WO9906574-A1.
PD 11-FEB-1999.
PA (KONN) GIST-BROCADES BV.
Best Local Similarity: 22.03%
Query Match: 5.88%
RESULT 1307
ID AAA81515 standard; DNA; 16878 BP.
DE N. meningitidis partial DNA sequence gnm_62 SEQ ID NO:62.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 19.17%
Query Match: 5.88%
RESULT 1308
Best Local Similarity: 19.17%
Query Match: 5.88%
RESULT 1309
ID AAF21609 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 19.17%
Query Match: 5.88%
RESULT 1310
ID AAF21608 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 19.17%
Query Match: 5.88%
RESULT 1311
ID ACH93277 standard; DNA; 334 BP.
DE Human genome derived single exon probe #26472.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 27.27%
Query Match: 5.85%
RESULT 1312
ID ABQ33971 standard; DNA; 738 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20562.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.94%
Query Match: 5.85%
RESULT 1313
ID ABQ33970 standard; DNA; 738 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20561.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.94%
Query Match: 5.85%
RESULT 1314
ID ABQ41874 standard; DNA; 1347 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28465.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.62%
Query Match: 5.85%
RESULT 1315
ID ABQ41875 standard; DNA; 1347 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28466.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.62%
Query Match: 5.85%
RESULT 1316
ID ACA30865 standard; DNA; 2085 BP.
DE Prokaryotic essential gene #12522.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 21.71%
Query Match: 5.85%
RESULT 1317
ID ADA53056 standard; cDNA; 2751 BP.
DE Human coding sequence, SEQ ID 624.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 24.09%
Query Match: 5.85%
RESULT 1318
Best Local Similarity: 21.71%
Query Match: 5.85%
RESULT 1319
ID ABL27928 standard; DNA; 3161 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35257.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 21.16%
Query Match: 5.82%
RESULT 1320
ID ADS63288 standard; cDNA; 3684 BP.
DE Bacterial polynucleotide #15275.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.77%
Query Match: 5.82%
RESULT 1321
ID ABX77167 standard; DNA; 125653 BP.
DE DNA sequence of human BAC clone RP11-8211.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Best Local Similarity: 33.68%
Query Match: 5.82%
RESULT 1322
ID ADO42013 standard; DNA; 784 BP.
DE Human cell adhesion and extracellular matrix protein 1 gene SeqID42.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 28.07%
Query Match: 5.79%
RESULT 1323
ID AAK94215 standard; cDNA; 1995 BP.
DE Human full-length cDNA, SEQ ID NO: 2788.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 26.32%
Query Match: 5.79%

Query Match: 5.85%
Indels: 68
ID ABL27928 standard; DNA; 3161 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35257.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 21.16%
Query Match: 5.82%
RESULT 1320
ID ADS63288 standard; cDNA; 3684 BP.
DE Bacterial polynucleotide #15275.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 23.77%
Query Match: 5.82%
RESULT 1321
ID ABX77167 standard; DNA; 125653 BP.
DE DNA sequence of human BAC clone RP11-8211.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Best Local Similarity: 33.68%
Query Match: 5.82%
RESULT 1322
ID ADO42013 standard; DNA; 784 BP.
DE Human cell adhesion and extracellular matrix protein 1 gene SeqID42.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 28.07%
Query Match: 5.79%
RESULT 1323
ID AAK94215 standard; cDNA; 1995 BP.
DE Human full-length cDNA, SEQ ID NO: 2788.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 26.32%
Query Match: 5.79%
Indels: 66
Mismatches: 90
Indels: 66
Mismatches: 89
Indels: 97
Mismatches: 90
Indels: 66
Mismatches: 93
Indels: 53
Mismatches: 57
Indels: 114
Mismatches: 31
Indels: 21
Mismatches: 48
Indels: 14
Mismatches: 79
Indels: 55

RESULT 1324
ID ADL30755 standard; cDNA; 1995 BP.
DE Full length human cDNA clone SeqID 2788.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 26.32% Mismatches: 79
Query Match: 5.79% Indels: 55
RESULT 1325
ID ABQ70959 standard; DNA; 4562 BP.
DE Listeria monocytogenes 4b contig DNA sequence #901.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 19.94% Mismatches: 114
Query Match: 5.79% Indels: 126
RESULT 1326
ID ABD15716 standard; DNA; 1665 BP.
DE Pseudomonas aeruginosa polynucleotide #14320.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 25.49% Mismatches: 74
Query Match: 5.76% Indels: 82
RESULT 1327
ID AAX60539 standard; DNA; 4435 BP.
DE C. trachomatis LGV L2 HMW protein encoding DNA.
PN WO9917741-A1.
PD 15-APR-1999.
PA (ANTE-) ANTEX BIOLOGICS INC.
Best Local Similarity: 23.39% Mismatches: 70
Query Match: 5.76% Indels: 95
RESULT 1328
ID AAS46385 standard; DNA; 12781 BP.
DE Tumour suppressor gene derived chemically modified sequence #107.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.35% Mismatches: 51
Query Match: 5.76% Indels: 81
RESULT 1329
ID ABL92228 standard; DNA; 12781 BP.
DE Chemically treated DNA repair gene fragment#19.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.35% Mismatches: 51
Query Match: 5.76% Indels: 81
RESULT 1330
ID ADB54127 standard; DNA; 12781 BP.
DE Pretreated genomic DNA region 51.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.35% Mismatches: 51
Query Match: 5.76% Indels: 81
RESULT 1331
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.

Best Local Similarity: 26.39% Mismatches: 57
Query Match: 5.76% Indels: 32
RESULT 1332
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Best Local Similarity: 26.39% Mismatches: 57
Query Match: 5.76% Indels: 32
RESULT 1333
ID ADE36593 standard; cDNA; 1440 BP.
DE Human NOV1b encoding cDNA SEQ ID NO:3.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 23.67% Mismatches: 120
Query Match: 5.73% Indels: 72
RESULT 1334
ID ADN38983 standard; cDNA; 1440 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:301.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 23.67% Mismatches: 120
Query Match: 5.73% Indels: 72
RESULT 1335
ID ACA30126 standard; DNA; 1455 BP.
DE Prokaryotic essential gene #11783.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 19.69% Mismatches: 119
Query Match: 5.73% Indels: 151
RESULT 1336
ID ABL12707 standard; cDNA; 2211 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32603.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.89% Mismatches: 127
Query Match: 5.73% Indels: 116
RESULT 1337
ID ADB63598 standard; cDNA; 2304 BP.
DE Human cDNA encoding clone THYMU20044100.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.90% Mismatches: 88
Query Match: 5.73% Indels: 106
RESULT 1338
ID ADA53796 standard; cDNA; 2803 BP.
DE Human coding sequence, SEQ ID 1364.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 21.93% Mismatches: 128
Query Match: 5.73% Indels: 58
RESULT 1339
ID ABL12706 standard; cDNA; 4678 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32600.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.89% Mismatches: 127
Query Match: 5.73% Indels: 116
RESULT 1340
ID ADM47088 standard; DNA; 5615 BP.
DE Ogataea minuta LEU2 gene.
PN WO2003091431-A1.
PD 06-NOV-2003.
PA (KIRI) KIRIN BEER KK.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Best Local Similarity: 23.72% Mismatches: 80
Query Match: 5.73% Indels: 81
RESULT 1341
ID AAS08693 standard; DNA; 109519 BP.
DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
Best Local Similarity: 21.21% Mismatches: 152
Query Match: 5.73% Indels: 63
RESULT 1342
ID ABQ20581 standard; DNA; 1026 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7172.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.78% Mismatches: 66
Query Match: 5.70% Indels: 47
RESULT 1343
ID ABQ20580 standard; DNA; 1026 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7171.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.78% Mismatches: 66
Query Match: 5.70% Indels: 47
RESULT 1344
ID ABQ35719 standard; DNA; 1032 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22310.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.78% Mismatches: 66
Query Match: 5.70% Indels: 47
RESULT 1345
ID ABQ35718 standard; DNA; 1032 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22309.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.78% Mismatches: 66
Query Match: 5.70% Indels: 47
RESULT 1346
ID AAZ38579 standard; cDNA; 1608 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1608 coding strand.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1347
ID AAZ38580 standard; cDNA; 1608 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1608 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1348
ID ABK69575 standard; cDNA; 1608 BP.
DE Der HMW-map polynucleotide #5.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.

Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1349
ID ABK69576 standard; cDNA; 1608 BP.
DE Der HMW-map polynucleotide #6.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1350
ID AAZ38577 standard; cDNA; 1665 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1665 coding strand.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1351
ID AAZ38578 standard; cDNA; 1665 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1665 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1352
ID ABK69573 standard; cDNA; 1665 BP.
DE Der HMW-map polynucleotide #3.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1353
ID ABK69574 standard; cDNA; 1665 BP.
DE Der HMW-map polynucleotide #4.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1354
ID AAZ38576 standard; cDNA; 1752 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1752 complement.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1355
ID AAZ38575 standard; cDNA; 1752 BP.
DE D. farinae mite allergen protein (map) gene nDerf98-1752 coding strand.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1356
ID ABK69572 standard; cDNA; 1752 BP.
DE Der HMW-map polynucleotide #2.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98
Query Match: 5.70% Indels: 81
RESULT 1357
ID ABK69571 standard; cDNA; 1752 BP.
DE Der HMW-map polynucleotide #1.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Best Local Similarity: 23.02% Mismatches: 98

Query Match: 5.70% Indels: 81
RESULT 1358
ID ADH12800 standard; cDNA; 2207 BP.
DE Abalone (Haliotis discus hannai) cellulase-encoding cDNA, SEQ ID NO:1.
PN JP2003235552-A.
PD 26-AUG-2003.
PA (HOKK-) HOKKAIDO TLO KK.
Best Local Similarity: 24.09% Mismatches: 62
Query Match: 5.70% Indels: 78
RESULT 1359
ID ADQ64957 standard; cDNA; 2438 BP.
DE Novel human cDNA sequence #2118.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.59% Mismatches: 110
Query Match: 5.70% Indels: 66
RESULT 1360
ID ADA70755 standard; DNA; 2784 BP.
DE Rice gene, SEQ ID 4078.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 19.60% Mismatches: 114
Query Match: 5.70% Indels: 154
RESULT 1361
ID ABQ76313 standard; cDNA; 3401 BP.
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 51.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Best Local Similarity: 20.78% Mismatches: 85
Query Match: 5.70% Indels: 80
RESULT 1362
ID ACC50985 standard; cDNA; 4209 BP.
DE Human bladder cancer associated cDNA sequence SEQ ID NO:63.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 23.28% Mismatches: 119
Query Match: 5.70% Indels: 77
RESULT 1363
ID ABD13413 standard; DNA; 1179 BP.
DE Pseudomonas aeruginosa polynucleotide #12017.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 27.60% Mismatches: 63
Query Match: 5.67% Indels: 59
RESULT 1364
ID ABQ46961 standard; DNA; 1199 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33552.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.49% Mismatches: 63
Query Match: 5.67% Indels: 31
RESULT 1365
ID ABO46960 standard; DNA; 1199 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33551.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 24.49% Mismatches: 63
Query Match: 5.67% Indels: 31
RESULT 1366
ID ABL12433 standard; cDNA; 1946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31781.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.08% Mismatches: 72
Query Match: 5.67% Indels: 63

RESULT 1367
ID AAS57123 standard; cDNA; 1946 BP.
DE cDNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.08% Mismatches: 72
Query Match: 5.67% Indels: 63
RESULT 1368
ID ADC35825 standard; cDNA; 1946 BP.
DE Drosophila G protein coupled receptor cDNA seq id 27.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 23.08% Mismatches: 72
Query Match: 5.67% Indels: 63
RESULT 1369
ID ABL12432 standard; cDNA; 3946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31778.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.77% Mismatches: 104
Query Match: 5.67% Indels: 99
RESULT 1370
ID AAS57122 standard; DNA; 3946 BP.
DE DNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.77% Mismatches: 104
Query Match: 5.67% Indels: 99
RESULT 1371
ID ADC35824 standard; DNA; 3946 BP.
DE Drosophila G protein coupled receptor genomic DNA seq id 26.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 20.77% Mismatches: 104
Query Match: 5.67% Indels: 99
RESULT 1372
ID ADP04444 standard; cDNA; 4849 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 39.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Best Local Similarity: 24.06% Mismatches: 99
Query Match: 5.67% Indels: 77
RESULT 1373
ID ABL33459 standard; DNA; 6047 BP.
DE Human immune system associated gene SEQ ID NO: 1432.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 20.67% Mismatches: 112
Query Match: 5.67% Indels: 110
RESULT 1374
ID ABL23194 standard; DNA; 6313 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21055.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 20.72% Mismatches: 104
Query Match: 5.67% Indels: 119
RESULT 1375
ID ABQ52389 standard; DNA; 739 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38980.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.98% Mismatches: 93
Query Match: 5.64% Indels: 35
RESULT 1376

ID ABQ52388 standard; DNA; 739 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38979.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 23.98% Mismatches: 93
Query Match: 5.64% Indels: 35
RESULT 1377
ID ADE36591 standard; cDNA; 1017 BP.
DE Human NOV1a encoding cDNA SEQ ID NO:1.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 23.08% Mismatches: 113
Query Match: 5.64% Indels: 71
RESULT 1378
ID ADE36617 standard; DNA; 1017 BP.
DE Plasmid pCR2.1-CG57008-03-S843 15B nucleotide insert SEQ ID NO:27.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 23.08% Mismatches: 113
Query Match: 5.64% Indels: 71
RESULT 1379
ID ACC72709 standard; cDNA; 1080 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:48.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 23.08% Mismatches: 113
Query Match: 5.64% Indels: 71
RESULT 1380
ID ABZ68333 standard; DNA; 1080 BP.
DE Nucleotide sequence of human TIM-1 allele 2.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 23.08% Mismatches: 113
Query Match: 5.64% Indels: 71
RESULT 1381
ID ABZ68332 standard; DNA; 1080 BP.
DE Nucleotide sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 23.08% Mismatches: 113
Query Match: 5.64% Indels: 71
RESULT 1382
ID AAS65697 standard; cDNA; 1082 BP.
DE DNA encoding novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 23.19% Mismatches: 73
Query Match: 5.64% Indels: 57
RESULT 1383
ID ABQ52391 standard; DNA; 1185 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38982.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.43% Mismatches: 84
Query Match: 5.64% Indels: 43
RESULT 1384
ID ABQ52390 standard; DNA; 1185 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38981.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.43% Mismatches: 84
Query Match: 5.64% Indels: 43
RESULT 1385
ID ABQ44576 standard; DNA; 1190 BP.

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31167.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.43% Mismatches: 84
Query Match: 5.64% Indels: 43
RESULT 1386
ID ABQ44577 standard; DNA; 1190 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31168.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.43% Mismatches: 84
Query Match: 5.64% Indels: 43
RESULT 1387
ID AAS72110 standard; cDNA; 1242 BP.
DE DNA encoding novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 23.19% Mismatches: 73
Query Match: 5.64% Indels: 57
RESULT 1388
ID ADQ63160 standard; cDNA; 2176 BP.
DE Novel human cDNA sequence #321.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.76% Mismatches: 84
Query Match: 5.64% Indels: 89
RESULT 1389
ID ACC84451 standard; DNA; 6166 BP.
DE Glucanucrase nucleotide sequence from strain KG15.
PN WO2003008618-A2.
PD 30-JAN-2003.
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
Best Local Similarity: 23.28% Mismatches: 92
Query Match: 5.64% Indels: 77
RESULT 1390
ID AAS46336 standard; DNA; 7348 BP.
DE Tumour suppressor gene derived chemically modified sequence #58.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 22.65% Mismatches: 93
Query Match: 5.64% Indels: 55
RESULT 1391
ID AAS80823 standard; cDNA; 7568 BP.
DE DNA encoding novel human diagnostic protein #16627.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1392
ID ADL12996 standard; cDNA; 8146 BP.
DE Human steroid-induced C3a liver cell cDNA #725.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1393
ID ADL61871 standard; DNA; 9169 BP.
DE Human ovarian cancer DNA marker #20083.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1394
ID ABV24414 standard; cDNA; 9220 BP.
DE Human prostate expression marker cDNA 24405.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1395
ID ABV25265 standard; cDNA; 9220 BP.
DE Human prostate expression marker cDNA 25256.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1396
ID ABK83800 standard; cDNA; 9416 BP.
DE Human cDNA differentially expressed in granulocytic cells #371.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1397
ID ACF34559 standard; DNA; 9416 BP.
DE Gene encoding angiogenesis protein BNO382.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1398
ID ADN05259 standard; cDNA; 9416 BP.
DE Antipsoriatic cDNA sequence #849.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1399
ID ADRI4613 standard; DNA; 9416 BP.
DE Human NF-kappaB pathway-associated gene SeqID614.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1400
ID ADI61664 standard; cDNA; 11917 BP.
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 475473.1.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1401
ID ADE53871 standard; cDNA; 11950 BP.
DE Human prostate cancer cDNA #218.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1402
ID ADF90735 standard; DNA; 11965 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 197.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1403
ID ADN04560 standard; cDNA; 12004 BP.
DE Antipsoriatic cDNA sequence #484.

PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 21.50% Mismatches: 77
Query Match: 5.64% Indels: 55
RESULT 1404
ID ADA02891 standard; DNA; 34570 BP.
DE Mouse Blrl carcinoma associated gene, SEQ ID NO:1409.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.38% Mismatches: 67
Query Match: 5.64% Indels: 63
RESULT 1405
ID ADB72629 standard; DNA; 34570 BP.
DE Mouse Blrl gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.38% Mismatches: 67
Query Match: 5.64% Indels: 63
RESULT 1406
ID ADC85370 standard; DNA; 34570 BP.
DE Human Blm coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 25.38% Mismatches: 67
Query Match: 5.64% Indels: 63
RESULT 1407
ID ADM74486 standard; DNA; 34570 BP.
DE Murine carcinoma associated (CA) nucleic acid #79.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Best Local Similarity: 25.38% Mismatches: 67
Query Match: 5.64% Indels: 63
RESULT 1408
ID ADR66967 standard; DNA; 34571 BP.
DE Mouse cancer associated gene genomic sequence SEQ ID NO:13.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Best Local Similarity: 25.38% Mismatches: 67
Query Match: 5.64% Indels: 63
RESULT 1409
ID ABQ81848 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Best Local Similarity: 23.68% Mismatches: 62
Query Match: 5.64% Indels: 57
RESULT 1410
ID ADK53470 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #853.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.37% Mismatches: 50
Query Match: 5.61% Indels: 26
RESULT 1411
ID ADK56638 standard; DNA; 971 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4021.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.37% Mismatches: 50
Query Match: 5.61% Indels: 26
RESULT 1412

ID ADQ16561 standard; DNA; 1089 BP.
DE Dog calcitonin gene-related peptide (CGRP) receptor CGRP-R DNA.
PN US2004110170-A1.
PD 10-JUN-2004.
PA (REGC) UNIV CALIFORNIA.
Best Local Similarity: 23.15% Mismatches: 72
Query Match: 5.61% Indels: 50
RESULT 1413
ID ABQ17861 standard; DNA; 1128 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4452.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 25.93% Mismatches: 80
Query Match: 5.61% Indels: 45
RESULT 1414
ID ABQ17860 standard; DNA; 1128 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4451.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 25.93% Mismatches: 80
Query Match: 5.61% Indels: 45
RESULT 1415
ID AAT29035 standard; cDNA; 1321 BP.
DE Endoglucanase (60 kDa Family 5 cellulase) cDNA sequence.
PN WO9611262-A1.
PD 18-APR-1996.
PA (NOVO) NOVO-NORDISK AS.
Best Local Similarity: 30.00% Mismatches: 32
Query Match: 5.61% Indels: 22
RESULT 1416
ID AAS73740 standard; cDNA; 1365 BP.
DE DNA encoding novel human diagnostic protein #9544.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 20.49% Mismatches: 102
Query Match: 5.61% Indels: 92
RESULT 1417
ID ADO07822 standard; cDNA; 1962 BP.
DE Mouse polynucleotide #40.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Best Local Similarity: 22.64% Mismatches: 101
Query Match: 5.61% Indels: 96
RESULT 1418
ID AAT10117 standard; cDNA; 2032 BP.
DE Drosophila scavenger receptor class CI cDNA.
PN WO9600288-A2.
PD 04-JAN-1996.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Best Local Similarity: 19.92% Mismatches: 96
Query Match: 5.61% Indels: 74
RESULT 1419
ID ABS53745 standard; cDNA; 2032 BP.
DE cDNA encoding fruit fly scavenger receptor type CI (dSR-CI).
PN US6429289-B1.
PD 06-AUG-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Best Local Similarity: 19.92% Mismatches: 96
Query Match: 5.61% Indels: 74
RESULT 1420
ID AAD33916 standard; cDNA; 2032 BP.
DE Drosophila melanogaster scavenger receptor class CI (dSR-CI) cDNA.
PN US6350859-B1.
PD 26-FEB-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Best Local Similarity: 19.92% Mismatches: 96
Query Match: 5.61% Indels: 74
RESULT 1421
ID ABX10897 standard; DNA; 2050 BP.

DE DNA encoding human orphan chemokine receptor RDC1.
PN US2002166133-A1.
PD 07-NOV-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 23.15% Mismatches: 72
Query Match: 5.61% Indels: 50
RESULT 1422
ID ADK66235 standard; DNA; 2050 BP.
DE Human NEOKINE-1 receptor RDC1 DNA.
PN US2004019917-A1.
PD 29-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 23.15% Mismatches: 72
Query Match: 5.61% Indels: 50
RESULT 1423
ID ABL16152 standard; cDNA; 3004 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42938.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 22.32% Mismatches: 114
Query Match: 5.61% Indels: 90
RESULT 1424
ID ABL25205 standard; DNA; 5931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.65% Mismatches: 34
Query Match: 5.61% Indels: 13
RESULT 1425
ID ADQ79681 standard; DNA; 6312 BP.
DE Benzoate catabolic enzyme gene cluster #1.
PN KR2003082683-A.
PD 23-OCT-2003.
PA (KIME/) KIM E S.
Best Local Similarity: 24.70% Mismatches: 121
Query Match: 5.61% Indels: 96
RESULT 1426
ID ABL25204 standard; DNA; 7931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 32.65% Mismatches: 34
Query Match: 5.61% Indels: 13
RESULT 1427
ID ABQ14148 standard; DNA; 647 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 739.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 27.27% Mismatches: 82
Query Match: 5.58% Indels: 41
RESULT 1428
ID ABQ14149 standard; DNA; 647 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 740.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 27.27% Mismatches: 82
Query Match: 5.58% Indels: 41
RESULT 1429
ID ADR60062 standard; cDNA; 907 BP.
DE Cotton cDNA sequence, SEQ ID 843.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Best Local Similarity: 23.58% Mismatches: 82
Query Match: 5.58% Indels: 50
RESULT 1430

ID ABZ68337 standard; DNA; 1099 BP.
DE Nucleotide sequence of human TIM-1 allele 6.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 22.34% Mismatches: 113
Query Match: 5.58% Indels: 74
RESULT 1431
ID ABZ78250 standard; cDNA; 1185 BP.
DE A. niger aspergillopepsin I cDNA.
PN WO200268623-A2.
PD 06-SEP-2002.
PA (STAM) DSM NV.
Best Local Similarity: 23.57% Mismatches: 106
Query Match: 5.58% Indels: 61
RESULT 1432
ID ACA42210 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #23867.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 25.49% Mismatches: 74
Query Match: 5.58% Indels: 82
RESULT 1433
ID ABX94893 standard; DNA; 1275 BP.
DE P. auroginosa PAO DNA variant SEQ ID 3.
PN WO2003022881-A2.
PD 20-MAR-2003.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
PA (TUEM/) TUEMMLER B.
Best Local Similarity: 25.49% Mismatches: 74
Query Match: 5.58% Indels: 82
RESULT 1434
ID AAH15685 standard; cDNA; 1709 BP.
DE Human cDNA sequence SEQ ID NO:14050.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1435
ID ACA36388 standard; DNA; 1710 BP.
DE Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 21.41% Mismatches: 135
Query Match: 5.58% Indels: 67
RESULT 1436
ID ABZ11710 standard; cDNA; 2096 BP.
DE Human polynucleotide SEQ ID NO 592.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1437
ID ADM44228 standard; cDNA; 2096 BP.
DE Novel human arginine-rich protein cDNA #592.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1438
ID ADS46773 standard; cDNA; 2985 BP.
DE Bacterial polynucleotide #1516.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 19.70% Mismatches: 139
Query Match: 5.58% Indels: 85
RESULT 1439
ID ABN79988 standard; DNA; 6113 BP.
DE Human chemically modified disease associated gene SEQ ID NO 5.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 20.45% Mismatches: 71
Query Match: 5.58% Indels: 108
RESULT 1440
ID ABA16168 standard; DNA; 6838 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8499.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.18% Mismatches: 99
Query Match: 5.58% Indels: 76
RESULT 1441
Best Local Similarity: 23.08% Mismatches: 79
Query Match: 5.58% Indels: 84
RESULT 1442
Best Local Similarity: 21.41% Mismatches: 135
Query Match: 5.58% Indels: 67
RESULT 1443
ID ABS77501 standard; cDNA; 736 BP.
DE Frog embryonic gene sequence Q9925909.
PN US2002081610-A1.
PD 27-JUN-2002.
PA (UYRQ) UNIV ROCKEFELLER.
Best Local Similarity: 21.83% Mismatches: 76
Query Match: 5.55% Indels: 94
RESULT 1444
ID ADK55629 standard; DNA; 747 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3012.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.60% Mismatches: 54
Query Match: 5.55% Indels: 20
RESULT 1445
ID ADK57771 standard; DNA; 747 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5154.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.60% Mismatches: 54
Query Match: 5.55% Indels: 20
RESULT 1446
ID ABZ68336 standard; DNA; 1095 BP.
DE Nucleotide sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 21.65% Mismatches: 114
Query Match: 5.55% Indels: 76
RESULT 1447
ID ADR85331 standard; DNA; 1110 BP.
DE Aspergillus fumigatus essential gene with introns #555.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 24.80% Mismatches: 94
Query Match: 5.55% Indels: 62
RESULT 1448
ID AAS59778 standard; DNA; 1389 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #273.

PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 24.58% Mismatches: 89
Query Match: 5.55% Indels: 66
RESULT 1449
ID ACF64707 standard; DNA; 1389 BP.
DE Propionibacterium acnes DNA contig sequence #273.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 24.58% Mismatches: 89
Query Match: 5.55% Indels: 66
RESULT 1450
ID AAI67205 standard; DNA; 1905 BP.
DE Nucleotide sequence of GSK gene Id 239881.
PN WO200172961-A2.
PD 04-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Best Local Similarity: 24.09% Mismatches: 89
Query Match: 5.55% Indels: 97
RESULT 1451
ID ADR84744 standard; DNA; 3110 BP.
DE Aspergillus fumigatus essential gene genomic sequence #555.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 24.80% Mismatches: 94
Query Match: 5.55% Indels: 62
RESULT 1452
ID ADR32198 standard; DNA; 4893 BP.
DE Yeast FLO11 open reading frame, SEQ ID NO:3.
PN WO2004067565-A1.
PD 12-AUG-2004.
PA (OSBO-) OSBORNE DISTRIBUIDORA SA.
PA (UYDO/) UNIV DE OLAVIDE PABLO.
Best Local Similarity: 21.75% Mismatches: 114
Query Match: 5.55% Indels: 71
RESULT 1453
ID ADS89638 standard; DNA; 5087 BP.
DE Oligonucleotide of the invention SEQ ID NO:654.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.13% Mismatches: 69
Query Match: 5.55% Indels: 68
RESULT 1454
ID ADS89578 standard; DNA; 5087 BP.
DE Oligonucleotide of the invention SEQ ID NO:594.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 21.13% Mismatches: 69
Query Match: 5.55% Indels: 68
RESULT 1455
ID ABL06739 standard; cDNA; 5269 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14699.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 28.28% Mismatches: 55
Query Match: 5.55% Indels: 29
RESULT 1456
ID ABL06738 standard; cDNA; 7740 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 28.28% Mismatches: 55
Query Match: 5.55% Indels: 29
RESULT 1457

ID AAV58939 standard; DNA; 9960 BP.
DE Mycobacterium smegmatis embCAB operon.
PN WO9841533-A1.
PD 24-SEP-1998.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Best Local Similarity: 21.62% Mismatches: 87
Query Match: 5.55% Indels: 111
RESULT 1458
ID ADJ41911 standard; cDNA; 632 BP.
DE Plant cDNA #2911.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Best Local Similarity: 23.33% Mismatches: 77
Query Match: 5.52% Indels: 43
RESULT 1459
ID AAS28824 standard; cDNA; 697 BP.
DE Human immunoglobulin encoding cDNA SEQ ID No 70.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 5.52% Indels: 7
RESULT 1460
ID ABA06691 standard; cDNA; 697 BP.
DE Human cDNA SEQ ID NO: 357.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 5.52% Indels: 7
RESULT 1461
ID ABV84028 standard; cDNA; 697 BP.
DE Human polynucleotide SEQ ID NO 357.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 5.52% Indels: 7
RESULT 1462
ID ADB31549 standard; cDNA; 697 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 70.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 5.52% Indels: 7
RESULT 1463
ID ABQ67928 standard; DNA; 777 BP.
DE Listeria monocytogenes EGD DNA sequence #52.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1464
ID AAI17172 standard; DNA; 1050 BP.
DE ActA protein fragment #2 coding sequence.
PN WO200171356-A2.
PD 27-SEP-2001.

PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1465
ID ABZ68334 standard; DNA; 1098 BP.
DE Nucleotide sequence of human TIM-1 allele 3.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 22.60% Mismatches: 112
Query Match: 5.52% Indels: 77
RESULT 1466
ID AAI71771 standard; DNA; 1128 BP.
DE ActA protein fragment #1 coding sequence.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1467
ID ABL24493 standard; DNA; 1344 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 25.12% Mismatches: 77
Query Match: 5.52% Indels: 44
RESULT 1468
ID ADB58239 standard; DNA; 1548 BP.
DE Toxicity-related gene, SEQ ID 3265.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.17% Mismatches: 96
Query Match: 5.52% Indels: 88
RESULT 1469
ID ADB52767 standard; DNA; 1548 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3309.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.17% Mismatches: 96
Query Match: 5.52% Indels: 88
RESULT 1470
ID ABT41946 standard; DNA; 1548 BP.
DE Toxicity modelling related rat gene SEQ ID No 1648.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 21.17% Mismatches: 96
Query Match: 5.52% Indels: 88
RESULT 1471
ID AAI71770 standard; DNA; 1830 BP.
DE ActA protein coding sequence.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1472
ID ABK89028 standard; DNA; 1869 BP.
DE Synthetic P. falciparum AMA-1 ectodomain (FVO Pf83syn) gene.
PN WO200252014-A2.
PD 04-JUL-2002.
PA (BIOM-) STICHTING BIOMEDICAL PRIMATE RES CENT.
Best Local Similarity: 20.87% Mismatches: 107
Query Match: 5.52% Indels: 132
RESULT 1473
ID AAV37026 standard; DNA; 1920 BP.
DE Listeria monocytogenes sequence used to design primers and probes.

PN WO9820157-A2.
PD 14-MAY-1998.
PA (IDII-) IDI INFECTIO DIAGNOSTIC INC.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1474
ID ABQ69832 standard; DNA; 1920 BP.
DE Listeria monocytogenes EGD DNA sequence #44.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1475
ID ABQ67930 standard; DNA; 1920 BP.
DE Listeria monocytogenes EGD DNA sequence #54.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1476
ID ADS56805 standard; cDNA; 2535 BP.
DE Bacterial polynucleotide #8792.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.15% Mismatches: 115
Query Match: 5.52% Indels: 36
RESULT 1477
ID ACC59291 standard; DNA; 2618 BP.
DE P tetraurelia adenylate cyclase/ ion channel protein expression cassette.
PN WO2003040295-A2.
PD 15-MAY-2003.
PA (GENO-) GENOPIA BIOMEDICAL GMBH.
Best Local Similarity: 25.45% Mismatches: 83
Query Match: 5.52% Indels: 59
RESULT 1478
ID ABQ14764 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1355.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 5.52% Indels: 24
RESULT 1479
ID ABQ14765 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1356.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 5.52% Indels: 24
RESULT 1480
ID ADS48485 standard; cDNA; 3309 BP.
DE Bacterial polynucleotide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.27% Mismatches: 59
Query Match: 5.52% Indels: 67
RESULT 1481
ID AAQ22986 standard; DNA; 3502 BP.

DE Sequence of ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBS-) WEBSTER A PTY LTD.
Best Local Similarity: 28.49% Mismatches: 58.
Query Match: 5.52% Indels: 46
RESULT 1482
ID ADQ67427 standard; cDNA; 3538 BP.
DE Novel human cDNA sequence #2400.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 28.29% Mismatches: 55
Query Match: 5.52% Indels: 39
RESULT 1483
ID ADS49082 standard; cDNA; 3873 BP.
DE Bacterial polynucleotide #3825.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.12% Mismatches: 65
Query Match: 5.52% Indels: 66
RESULT 1484
ID ADR07198 standard; cDNA; 3932 BP.
DE Full length human cDNA useful for treating neurological disease Seq 704.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.76% Mismatches: 84
Query Match: 5.52% Indels: 89
RESULT 1485
ID ACC42734 standard; DNA; 6210 BP.
DE Geldanamycin PKS module 1 DNA sequence, SEQ ID 1.
PN WO2003013430-A2.
PD 20-FEB-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Best Local Similarity: 22.11% Mismatches: 63
Query Match: 5.52% Indels: 77
RESULT 1486
ID AAD61810 standard; DNA; 6210 BP.
DE Streptomyces geldanus polyketide synthase (PKS) gene #1.
PN US2003114450-A1.
PD 19-JUN-2003.
PA (SANT/) SANTI D.
PA (MYLE/) MYLES D C.
PA (TIAN/) TIAN Z.
PA (HUTC/) HUTCHINSON C R.
PA (JOHN/) JOHNSON R.
PA (ZHOU/) ZHOU Y.
PA (FENG/) FENG L.
Best Local Similarity: 22.11% Mismatches: 63
Query Match: 5.52% Indels: 77
RESULT 1487
ID ACC71562 standard; DNA; 6902 BP.
DE VRC6703(pVR1012x/s Marburgdelta TM/h (codon optimised)) plasmid.
PN WO2003028632-A2.
PD 10-APR-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 19.17% Mismatches: 120
Query Match: 5.52% Indels: 181
RESULT 1488
ID ABL33119 standard; DNA; 8758 BP.
DE Human immune system associated gene SEQ ID NO: 1092.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 20.59% Mismatches: 77
Query Match: 5.52% Indels: 82
RESULT 1489

ID ADM48345 standard; DNA; 19112 BP.
DE Marburg virus viral protein genomic DNA.
PN US2003215794-A1.
PD 20-NOV-2003.
PA (KAWA/) KAWAOKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Best Local Similarity: 19.17% Mismatches: 120
Query Match: 5.52% Indels: 181
RESULT 1490
ID ADQ97577 standard; DNA; 73930 BP.
DE Human cancer associated sequence HD10-007, SEQ ID 554.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Best Local Similarity: 22.27% Mismatches: 76
Query Match: 5.52% Indels: 71
RESULT 1491
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Best Local Similarity: 22.11% Mismatches: 63
Query Match: 5.52% Indels: 77
RESULT 1492
Best Local Similarity: 23.53% Mismatches: 98
Query Match: 5.52% Indels: 91
RESULT 1493
Best Local Similarity: 21.98% Mismatches: 57
Query Match: 5.52% Indels: 65
RESULT 1494
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 28.68% Mismatches: 70
Query Match: 5.52% Indels: 15
RESULT 1495
ID AAF21610 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 23.53% Mismatches: 98
Query Match: 5.52% Indels: 91
RESULT 1496
ID ABQ68913 standard; DNA; 1112 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1679.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 20.73% Mismatches: 91
Query Match: 5.49% Indels: 76
RESULT 1497
ID ACA51121 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #32778.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 26.40% Mismatches: 44
Query Match: 5.49% Indels: 30
RESULT 1498
ID ABL21703 standard; DNA; 1380 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16582.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.50% Mismatches: 76

Query Match:	5.49%	Indels:	67
RESULT 1499			
ID ABK51913 standard; cDNA; 1558 BP.			
DE cDNA encoding mouse Cacng2.			
PN US6365337-B1.			
PD 02-APR-2002.			
PA (IOWA) UNIV IOWA RES FOUND.			
PA (JACK-) JACKSON LAB.			
Best Local Similarity: 22.95%		Mismatches:	66
Query Match:	5.49%	Indels:	102
RESULT 1500			
ID ADC92346 standard; DNA; 2028 BP.			
DE E. faecium DNA sequence SEQ ID 1973.			
PN US6583275-B1.			
PD 24-JUN-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Best Local Similarity: 23.26%		Mismatches:	96
Query Match:	5.49%	Indels:	66

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 08:19:48 ; Search time 7719 Seconds
 (without alignments)
 11696.910 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaaatccggatgtc.....ttaaaagcatttagaaaaactt 2372

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query [†]			DB ID	Description	
	Score	Match	Length			
1	1900	80.1	1911	3	CR614790 full-leng	
2	1895	79.9	1925	3	CR595979 full-leng	
3	1883	79.4	1945	3	CR605021 full-leng	
4	1868	78.8	1898	3	CR597409 full-leng	
5	1820	76.7	1820	3	CR612000 full-leng	
6	1797	75.8	1797	3	CR604450 full-leng	
7	1786	75.3	1786	3	CR614245 full-leng	
8	1781	75.1	1781	3	CR598862 full-leng	
9	1765	74.4	1765	3	CR622723 full-leng	
10	1608	67.8	1823	3	CR599107 full-leng	
11	1113	46.9	1113	3	CR598440 full-leng	
C	12	1053.4	44.4	1130	1	AL574194 AL574194
	13	1043.8	44.0	1091	1	AL550279 AL550279
14	1000	42.2	1101	1	AL541927 AL541927	
15	991.6	41.8	1045	1	AL550621 AL550621	
16	976.6	41.2	1117	5	BX397211 BX397211	
C	17	969.6	40.9	1041	1	AL547901 AL547901
C	18	950	40.1	1013	1	AL546590 AL546590
19	943.8	39.8	965	1	AL552299 AL552299	
C	20	943.6	39.8	1007	1	AL552625 AL552625
21	933.4	39.4	977	5	BX366718 BX366718	
C	22	930.8	39.2	1135	1	AL574436 AL574436
C	23	927	39.1	993	1	AL575633 AL575633
24	925	39.0	1090	1	AL546669 AL546669	

C 98	588.2	24.8	618	6	CA419045	CA419045 UI-H-EZ1-	C 171	373.4	15.7	375	1	AI160641
99	584.2	24.6	859	6	CB985681	CB985681 AGENCOURT	172	372.4	15.7	459	7	W03670
100	583	24.6	583	5	BP291949	BP291949 BP291949	173	371.2	15.6	682	5	BP434862
101	582	24.5	582	5	BP198472	BP198472 BP198472	174	370.6	15.6	721	7	CK976672
102	580	24.5	580	5	BP341529	BP341529 BP341529	175	369.4	15.6	415	1	AA463325
C 103	572.8	24.1	594	5	BM972462	BM972462 UI-CF-EC1	176	367.4	15.5	624	1	AV733213
104	572.6	24.1	607	2	AW956729	AW956729 EST368799	C 177	363	15.3	363	1	AA693904
C 105	572.4	24.1	574	2	AW183039	AW183039 xJ66b03.x	178	362.6	15.3	564	1	AL570408
106	569	24.0	581	5	BP197816	BP197816 BP197816	179	361.8	15.3	696	7	CV111589
107	568	23.9	580	5	BP339718	BP339718 BP339718	C 180	358	15.1	358	2	BF438812
108	567.8	23.9	582	5	BP320362	BP320362 BP320362	181	357	15.1	470	7	R76756
109	567.2	23.9	794	4	BG566260	BG566260 602585128	C 182	356.4	15.0	358	2	BF197662
C 110	567	23.9	584	5	BU731554	BU731554 UI-E-C11-	C 183	355.4	15.0	370	7	W87483
C 111	563.4	23.8	582	5	BM984915	BM984915 UI-CF-EC1	184	354.6	14.9	667	7	CF176921
112	561.2	23.7	885	2	BF107215	BF107215 601824293	185	353.8	14.9	579	1	AI391129
113	557.8	23.5	581	5	BP197366	BP197366 BP197366	186	349.6	14.7	670	2	BB611620
114	543	22.9	543	4	BM708892	BM708892 UI-E-C11-	C 187	347.4	14.6	349	1	AA704407
C 115	538.2	22.7	847	1	AL544161	AL544161 AL544161	C 188	346.4	14.6	400	7	N80143
116	535.6	22.6	709	4	BG539893	BG539893 602563781	C 189	346.2	14.6	540	4	BM253102
117	531	22.4	584	5	BP345245	BP345245 BP345245	190	342	14.4	368	4	BG012717
118	529	22.3	529	6	CD671330	CD671330 fG03C09.y	C 191	339	14.3	735	7	CK364727
119	528	22.3	581	5	BP320205	BP320205 BP320205	C 192	338.2	14.3	621	7	CK949311
120	526	22.2	596	1	AA046671	AA046671 zf12d09.r	193	338	14.2	361	7	H59965
121	524	22.1	898	5	BP159588	BP159588 BP159588	C 194	337.4	14.2	618	7	CK957778
C 122	521	22.0	589	5	BX391823	BX391823 BX391823	195	336.4	14.2	841	4	BI730362
C 123	520	21.9	531	1	AI708530	AI708530 as98a06.x	C 196	334	14.1	339	1	AA340162
C 124	514.8	21.7	534	1	AA081351	AA081351 zn33h09.s	C 197	333.8	14.1	356	4	BI492322
C 125	500.2	21.1	516	1	AA046747	AA046747 zf12d09.s	198	333.8	14.1	357	2	AW021291
126	496.2	20.9	1023	6	BY704927	BY704927 BY704927	199	333.8	14.1	456	7	H93850
C 127	492	20.7	494	1	AI453527	AI453527 tj57a07.x	C 200	333.4	14.1	374	6	CA449932
128	489.6	20.6	581	5	BP344636	BP344636 BP344636	201	332.8	14.0	392	7	D63041
C 129	487.4	20.5	489	1	AI151441	AI151441 qc88g11.x	C 202	329.4	13.9	392	7	R76413
C 130	484.4	20.4	486	1	AA682494	AA682494 zj18e06.s	203	329.2	13.9	428	7	W87511
131	479.2	20.2	974	6	CB988195	CB988195 AGENCOURT	204	328.2	13.8	333	7	D79275
132	474.4	20.0	707	7	CK836545	CK836545 4061500 B	205	323	13.6	581	5	BP338802
C 133	474	20.0	474	1	AI342481	AI342481 qt28c08.x	206	320.6	13.5	556	5	BM935573
C 134	473.8	20.0	779	7	CK773274	CK773274 961895 MA	C 207	316	13.3	316	1	AA576601
C 135	470	19.8	474	1	AI480375	AI480375 tm51f03.x	208	316	13.3	535	2	BE756611
136	463	19.5	473	6	CB269023	CB269023 1007930 H	209	314.8	13.3	471	7	H72432
C 137	461	19.4	461	1	AI470227	AI470227 tj92c03.x	C 210	314	13.2	556	5	BX434334
C 138	459	19.4	798	5	BX373340	BX373340 BX373340	C 211	310.8	13.1	474	7	H02824
139	453.6	19.1	751	7	CO737890	CO737890 SL1H03c18	212	307.8	13.0	325	6	CB054311
C 140	452.2	19.1	751	7	CK775586	CK775586 966716 MA	213	306	12.9	318	7	R71437
141	449.8	19.0	673	7	CK949504	CK949504 4074881 B	214	305.8	12.9	390	7	H78909
142	448.8	18.9	675	7	CK958011	CK958011 4098647 B	215	305.2	12.9	499	2	BE198670
C 143	443	18.7	443	1	AI091530	AI091530 oo23d02.x	216	305	12.9	328	1	AA297240
C 144	442	18.6	442	7	N69434	N69434 za35e10.s1	217	304.8	12.8	392	7	R93368
145	439.2	18.5	487	6	CA407758	CA407758 1003907 H	C 218	297.6	12.5	308	7	D63040
C 146	439	18.5	439	1	AI087965	AI087965 oo20h12.x	C 219	290.4	12.2	307	7	H93538
147	437	18.4	437	6	CA406980	CA406980 1003129 H	220	290	12.2	411	7	H02823
148	420.6	17.7	465	7	H69328	H69328 yu19a09.r1	C 221	288.4	12.2	398	7	H80143
C 149	420	17.7	420	7	W69477	W69477 zd45b09.s1	C 222	287.4	12.1	291	7	T40526
C 150	420	17.7	427	1	AA693935	AA693935 zi53b05.s	C 223	284.2	12.0	453	7	T96905
C 151	417.4	17.6	438	2	BF940071	BF940071 nac67c07.	224	279.4	11.8	287	7	D62918
C 152	412.4	17.4	443	2	BE439808	BE439808 HTM1-670F	225	276	11.6	288	1	AA135754
153	408	17.2	793	9	AY411057	AY411057 Homo sapi	C 226	272.8	11.5	289	1	AI378999
154	398.4	16.8	433	7	W03259	W03259 za35e10.r1	227	271	11.4	377	7	D62168
C 155	395.4	16.7	397	1	AI032588	AI032588 ow70h11.s	C 228	264.4	11.1	279	7	H72343
156	394.8	16.6	910	6	CA786491	CA786491 AGENCOURT	229	263.8	11.1	776	7	CO567156
157	393.2	16.6	1070	6	CB989089	CB989089 AGENCOURT	C 230	263.6	11.1	447	7	R71091
C 158	392.4	16.5	403	1	AA923465	AA923465 ol47f01.s	231	263.4	11.1	277	7	W69476
159	392.4	16.5	964	5	BU504417	BU504417 AGENCOURT	232	263	11.1	380	1	AA081350
160	391.6	16.5	1298	7	CF1110966	CF1110966 Shultzomi	233	256.4	10.8	871	4	BG173551
161	389.6	16.4	642	6	CB442342	CB442342 692918 MA	234	255.8	10.8	474	7	CF791146
C 162	388.6	16.4	653	5	BX373038	BX373038 BX373038	235	255.4	10.8	437	1	AJ686473
163	387.6	16.3	753	7	CK949012	CK949012 4074228 B	236	254.8	10.7	444	7	T96904
164	387.2	16.3	409	2	AW961536	AW961536 EST373608	237	252.6	10.6	371	2	BE684197
165	386.6	16.3	790	9	AY411058	AY411058 Pan trogl	238	251.4	10.6	455	1	AI006667
C 166	386	16.3	391	1	AI052329	AI052329 oy93h08.x	239	251.2	10.6	301	7	T39345
C 167	385.2	16.2	392	1	AA693582	AA693582 zi51f06.s	240	251	10.6	564	9	CE284850
C 168	381.4	16.1	398	7	H57840	H57840 yr16e07.s1	241	244.4	10.3	800	9	AY411059
C 169	380.4	16.0	397	2	AW293109	AW293109 UI-H-B12-	242	244	10.3	366	7	R24376
C 170	377.4	15.9	408	1	AI470914	AI470914 ti91a10.x	243	243.4	10.3	337	7	R81462

AI160641 qc84h12.x	W03670 za65c08.r1	BP434862 BP434862	CK976672 4108064 B	AA463325 zx71f04.r	AV733213 AV733213	AA693904 zi49e07.s	AL570408 AL570408	CV111589 AGENCOURT	BF438812 nab54d01.	R76756 yi63e08.r1	BF197662 7m95d08.x	W87483 zh65c03.s1	CF176921 805349 MA	AI391129 mc02a12.y	BB611620 BB611620	AA704407 zj21g08.s	N80143 za65c08.s1	BM253102 512458 MA	BG012717 IL5-GN023	CK364727 AGENCOURT	CK949311 4074497 B	H59965 yr16e07.r1	CK957778 4098263 B	BI730362 603349860	AA340162 EST45327	BI492322 df22f10.w	AW021291 df22f10.y	H93850 yv08a03.r1	CA449932 UI-H-E11-	D63041 HUM354C11B	R76413 yi63e08.s1	W87511 zh65c03.r1	D79275 HUM213B01B	BP338802 BP338802	BM935573 UI-M-BH3-	AA576601 nm66h09.s	BE756611 210798 MA	H72432 ys04b04.r1	BX434334 BX434334	H02824 yJ41h11.s1	CB054311 NISC_gm03	R71437 yi51e04.r1	H78909 yulld03.r1	BE198670 ug81c01.y	AA297240 EST112782	R93568 yq34e10.r1	D63040 HUM354C11A	H93538 yv08h10.s1	H02823 yJ41h11.r1	H80143 yul1e03.s1	T40526 ya04e11.s2	T96905 ye52g09.s1	D62918 HUM339H04B	AA135754 zl11a04.r	AI378999 tc40g03.x	D62168 HUM243C10B	H72343 ys04b05.s1	CO567156 AGENCOURT	R71091 yi51e04.s1	W69476 zd45b09.r1	AA081350 zn33h09.r	BG173551 602336969	CF791146 879311 MA	AJ686473 AJ686473	T96904 ye52g09.r1	BE684197 184504 MA	AI006667 ue16b07.y	T39345 ya04e11.r2	CE284850 tigr-gss-	AY411059 Mus muscu	R24376 yh30e08.r1	R81462 yJ02f03.r1
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244	242.8	10.2	569	2	BE627175	BE627175 uu16h04.y	C 317	107.4	4.5	434	1	AI137643	AI137643 UI-R-CO-h
C 245	239.4	10.1	241	1	AA029421	AA029421 ze96c11.s	C 318	107.4	4.5	473	2	BE105106	BE105106 UI-R-BX0-
246	238.6	10.1	479	2	BE847124	BE847124 uw22b07.y	C 319	107.4	4.5	641	6	CB576450	CB576450 AMGNNUC:U
C 247	238	10.0	308	7	D56989	D56989 HUM243C10A	C 320	107.4	4.5	707	5	BQ192476	BQ192476 UI-R-DZ0-
C 248	236.8	10.0	371	7	R81660	R81660 yj02f03.s1	C 321	106.2	4.5	496	2	BF018032	BF018032 uw96e06.x
C 249	234.8	9.9	340	5	BQ417943	BQ417943 ik53a10.y	C 322	105.8	4.5	480	2	BF284836	BF284836 EST449427
C 250	233	9.8	345	7	R96867	R96867 yq61c10.s1	C 323	105.4	4.4	897	6	BY704426	BY704426 BY704426
251	228.8	9.6	418	6	CB765478	CB765478 AMGNNUC:N	C 324	104.8	4.4	692	1	AV172790	AV172790 AV172790
252	228.6	9.6	449	2	BF041814	BF041814 BP250014B	C 325	104.4	4.4	291	5	BP104206	BP104206 BP104206
253	227	9.6	229	1	AA347305	AA347305 EST53585	C 326	104.4	4.4	465	1	AA986883	AA986883 ue16b07.x
C 254	226.2	9.5	239	1	AA297532	AA297532 EST113232	C 327	104.4	4.4	880	3	AK004182	AK004182 Mus muscu
C 255	224	9.4	237	1	AI057367	AI057367 oz06G08.x	C 328	104	4.4	329	2	BB139788	BB139788 BB139788
C 256	221.4	9.3	605	7	CF175580	CF175580 799547 MA	C 329	103.8	4.4	434	2	BB677237	BB677237 BB677237
C 257	219.6	9.3	426	1	AJ688809	AJ688809 AJ688809	C 330	103.6	4.4	291	1	AV228844	AV228844 AV228844
C 258	218.4	9.2	413	7	R24267	R24267 yh30e08.s1	C 331	102.2	4.3	411	1	AI035630	AI035630 ue19f07.x
C 259	216.4	9.1	424	1	AJ689190	AJ689190 AJ689190	C 332	102.2	4.3	415	1	AA849043	AA849043 EST191805
260	215.4	9.1	469	2	BF471572	BF471572 UI-M-BH3-	C 333	99.6	4.2	298	1	AV364722	AV364722 AV364722
C 261	213	9.0	213	1	AA054727	AA054727 zk68e07.s	C 334	98.8	4.2	520	2	AW488356	AW488356 UI-M-BH3-
C 262	211.6	8.9	650	4	BI183818	BI183818 UNL-P-FN-	C 335	96.8	4.1	467	1	AI179260	AI179260 EST222952
263	211.2	8.9	690	6	CB449214	CB449214 703398 MA	C 336	96.8	4.1	807	5	BU125818	BU125818 603150355
264	206.2	8.7	227	1	AA029420	AA029420 ze96c11.r	C 337	96	4.0	283	1	AV252674	AV252674 AV252674
C 265	205	8.6	205	2	BF086058	BF086058 CM3-GN004	C 338	96	4.0	330	2	BB121286	BB121286 BB121286
C 266	205	8.6	266	5	BX357010	BX357010 BX357010	C 339	96	4.0	420	2	BE767810	BE767810 CM3-GN004
267	204.6	8.6	677	6	CB422343	CB422343 595441 MA	C 340	95.4	4.0	876	6	CB321038	CB321038 AGENCOURT
C 268	204	8.6	206	1	AA135665	AA135665 zl11a04.s	341	94.6	4.0	292	1	AV013247	AV013247 AV013247
C 269	203.2	8.6	660	7	CK948680	CK948680 4073844 B	342	92.8	3.9	268	2	BB121667	BB121667 BB121667
270	202.8	8.5	321	7	CO261322	CO261322 4133483 B	343	91.6	3.9	321	2	BB114586	BB114586 BB114586
271	200.4	8.4	385	7	W29485	W29485 mc02a12.r1	344	91	3.8	301	1	AV239004	AV239004 AV239004
272	197.6	8.3	674	6	CB426075	CB426075 601215 MA	345	89.8	3.8	295	1	AV025307	AV025307 AV025307
273	196	8.3	676	6	CB422955	CB422955 596120 MA	346	86.8	3.7	745	7	CF520494	CF520494 AGENCOURT
C 274	195.4	8.2	211	2	BE767809	BE767809 CM3-GN004	347	86.4	3.6	313	2	BB448071	BB448071 BB448071
C 275	189.2	8.0	642	6	CB449936	CB449936 704550 MA	348	86.2	3.6	739	7	CF110338	CF110338 Shultzomi
C 276	186.8	7.9	627	6	CB442706	CB442706 693510 MA	349	86.2	3.6	747	5	BU324601	BU324601 603492075
C 277	185.2	7.8	634	6	CB426417	CB426417 601599 MA	350	85.8	3.6	652	7	CF250037	CF250037 esa007_f1
C 278	179	7.5	378	7	CO948073	CO948073 UMC-p8mm3	C 351	83.4	3.5	237	1	AA800067	AA800067 EST189564
279	168.2	7.1	606	6	CB434168	CB434168 610759 MA	C 352	80.2	3.4	705	9	CC482801	CC482801 CH240_311
280	162.8	6.9	351	6	CB780898	CB780898 AMGNNUC:C	C 353	80	3.4	257	1	AV230818	AV230818 AV230818
281	161.6	6.8	353	5	BY318491	BY318491 BY318491	354	79.8	3.4	744	5	BU376182	BU376182 603808158
282	160.6	6.8	354	5	BY107653	BY107653 BY107653	C 355	77.8	3.3	406	1	AA880234	AA880234 vx39d06.r
C 283	160.4	6.8	265	7	R93569	R93569 yq34e10.s1	C 356	77.4	3.3	1225	9	CNS0161D	AL106171 Drosophil
284	158.6	6.7	405	6	BY766304	BY766304 BY766304	357	77.2	3.3	553	2	BE632373	BE632373 uv55c09.y
285	153	6.5	305	1	AV749159	AV749159 AV749159	C 358	77	3.2	423	2	AW419846	AW419846 fj84c10.y
286	151.6	6.4	813	5	BU388030	BU388030 603582582	359	77	3.2	639	1	AV734145	AV734145 AV734145
287	151.4	6.4	463	4	BM445953	BM445953 11L1H10.a	C 360	77	3.2	801	7	CK030244	CK030244 AGENCOURT
C 288	150.2	6.3	485	7	CK976252	CK976252 4107680 B	361	77	3.2	895	6	CA474635	CA474635 AGENCOURT
289	148.2	6.2	232	7	D62882	D62882 HUM336D08B	362	76.6	3.2	599	6	CB515759	CB515759 ssalrgb51
290	147	6.2	158	7	F35420	F35420 HSPD31546 H	363	76.6	3.2	600	6	CB512734	CB512734 ssalrgb54
291	147	6.2	424	2	AW482448	AW482448 43882 MAR	C 364	75.8	3.2	230	1	AV369277	AV369277 AV369277
292	141.6	6.0	883	5	BU239567	BU239567 603322730	C 365	75	3.2	598	6	CA367101	CA367101 642837 NC
C 293	139.2	5.9	824	9	CC551496	CC551496 CH240_436	366	73.8	3.1	248	1	AV230434	AV230434 AV230434
294	138.8	5.9	582	2	BB611006	BB611006 BB611006	C 367	73.8	3.1	596	8	AZ393106	AZ393106 1M0156H04
C 295	135.4	5.7	652	6	CB431732	CB431732 607740 MA	368	73.4	3.1	245	1	AV229154	AV229154 AV229154
296	135.2	5.7	359	6	BY788232	BY788232 BY788232	C 369	72.6	3.1	274	2	BB002268	BB002268 BB002268
C 297	133.8	5.6	434	5	BP104909	BP104909 BP104909	370	72	3.0	230	1	AV231922	AV231922 AV231922
C 298	133.8	5.6	654	6	CB441998	CB441998 692542 MA	371	71	3.0	913	7	CK410366	CK410366 AUF_IpHdk
299	131.6	5.5	627	5	BU241066	BU241066 603321257	C 372	71	3.0	974	7	CK404422	CK404422 AUF_IpHdk
300	131.4	5.5	358	6	BY770042	BY770042 BY770042	373	70.8	3.0	294	1	AV228851	AV228851 AV228851
C 301	130	5.5	642	9	CE016545	CE016545 tigr-ges-	374	70.6	3.0	1101	9	CNS00EVL	AL069706 Drosophil
C 302	127.4	5.4	434	6	CB421993	CB421993 595057 MA	C 375	70.4	3.0	336	7	CO990587	CO990587 UMC-pd3ov
303	125.4	5.3	127	7	T83800	T83800 yd65g09.r1	C 376	69.4	2.9	318	6	CB054310	CB054310 NISC_gm03
C 304	124.8	5.3	242	2	AW318386	AW318386 um96a08.y	377	69.2	2.9	238	1	AV254112	AV254112 AV254112
C 305	124.8	5.3	537	5	BP100492	BP100492 BP100492	C 378	68	2.9	240	2	BE929936	BE929936 CM3-GN004
306	122.6	5.2	442	1	AI226003	AI226003 uj08b06.y	379	67.8	2.9	1101	9	CNS0039G	AL063921 Drosophil
307	121.2	5.1	289	5	BY145458	BY145458 BY145458	380	67	2.8	563	2	AW918716	AW918716 EST350020
308	120.6	5.1	441	2	BB674620	BB674620 BB674620	381	66.2	2.8	454	6	CB784811	CB784811 AMGNNUC:N
309	109.6	4.6	656	4	BM426481	BM426481 pgf2n.pk0	C 382	66	2.8	259	2	BB570771	BB570771 BB570771
C 310	109.4	4.6	425	2	BE634695	BE634695 uv84h08.x	383	65.4	2.8	1101	9	CNS00EO7	AL069440 Drosophil
C 311	109.4	4.6	455	2	BE200162	BE200162 ug74c08.x	C 384	65.2	2.7	567	9	CG806751	CG806751 1118073E0
C 312	109.4	4.6	525	2	BE691106	BE691106 uv55h07.x	C 385	65.2	2.7	661	9	CNS02QVJ	AL209800 Tetraodon
C 313	109.4	4.6	541	2	BE691061	BE691061 uv55c09.x	386	64.8	2.7	1146	9	CNS02IG2	AL176843 Tetraodon
C 314	108.4	4.6	429	4	BG229926	BG229926 mac24d06.	C 387	64.6	2.7	418	1	AL835535	AL835535 AL835535
315	108.4	4.6	461	4	BG091529	BG091529 mac24d06.	388	64.2	2.7	1241	9	AG448181	AG448181 Mus muscu
316	107.6	4.5	726	1	AV235047	AV235047 AV235047	389	64.2	2.7	1489	9	AG350139	AG350139 Mus muscu

C 317	107.4	4.5	434	1	AI137643
C 318	107.4	4.5	473	2	BE105106
C 319	107.4	4.5	641	6	CB576450
C 320	107.4	4.5	707	5	BQ192476
C 321	106.2	4.5	496	2	BF018032
C 322	105.8	4.5	480	2	BF284836
C 323	105.4	4.4	897	6	BY704426
C 324	104.8	4.4	692	1	AV172790
C 325	104.4	4.4	291	5	BP104206
C 326	104.4	4.4	465	1	AA986883
C 327	104.4	4.4	880	3	AK004182
C 328	104	4.4	329	2	BB139788
C 329	103.8	4.4	434	2	BB677237
C 330	103.6	4.4	291	1	AV228844
C 331	102.2	4.3	411	1	AI035630
C 332	102.2	4.3	415	1	AA849043
C 333	99.6	4.2	298	1	AV364722
C 334	98.8	4.2	520	2	AW488356
C 335	96.8	4.1	467	1	AI179260
C 336	96.8	4.1	807	5	BU125818
C 337	96	4.0	283	1	AV252674
C 338	96	4.0	330	2	BB121286
C 339	96	4.0	420	2	BE767810
C 340	95.4	4.0	876	6	CB321038
C 341	94.6	4.0	292	1	AV013247
C 342	92.8	3.9	268	2	BB121667
C 343	91.6	3.9	321	1	BB114586
C 344	91	3.8	301	1	AV239004
C 345	89.8	3.8	295	1	AV025307
C 346	86.8	3.7	745	7	CF520494
C 347	86.4	3.6	313	2	BB448071
C 348	86.2	3.6	739	7	CF110338
C 349	86.2	3.6	747	5	BU324601
C 350	85.8	3.6	652	7	CF250037
C 351	83.4	3.5	237	1	AA800067
C 352	80.2	3.4	705	9	CC482801
C 353	80	3.4	257	1	AV230818
C 354	79.8	3.4	744	5	BU376182
C 355	77.8	3.3	406	1	AA880234
C 356	77.4	3.3	1225	9	CNS0161D
C 357	77.2	3.3	553	2	BE632373
C 358	77	3.2	423	2	AW419846
C 359	77	3.2	639	1	AV734145
C 360	77	3.2	801	7	CK030244
C 361	77	3.2	895	6	CA474635
C 362	76.6	3.2	599	6	CB515759
C 363	76.6	3.2	600	6	CB512734
C 364	75.8	3.2	230	1	AV369277
C 365	75	3.2	598	6	CA367101
C 366	73.8	3.1	248	1	AV230434
C 367	73.8	3.1	596	8	AZ393106
C 368	73.4	3.1	245	1	AV229154
C 369	72.6	3.1	274	2	BB002268
C 370	72	3.0	230	1	AV231922
C 371	71	3.0	913	7	CK410366
C 372	71	3.0	974	7	CK404422
C 373	70.8	3.0	294	1	AV228851
C 374	70.6	3.0	1101	9	CNS00EVL
C 375	70.4	3.0	336	7	CO990587
C 376	69.4	2.9	318	6	CB054310
C 377	69.2	2.9	238	1	AV254112
C 378	68	2.9	240	2	BE929936
C 379	67.8	2.9	1101	9	CNS0039G
C 380	67	2.8	563	2	AW918716
C 381	66.2	2.8	454	6	CB784811
C 382	66	2.8	259	2	BB570771
C 383	65.4	2.8	1101	9	CNS00EO7
C 384	65.2	2.7	567	9	CG806751
C 385	65.2	2.7	661	9	CNS02QVJ
C 386	64.8	2.7	1146	9	CNS021G2
C 387	64.6	2.7	418	1	AL835535
C 388	64.2	2.7	1241	9	AG448181
C 389	64.2	2.7	1489	9	AG350139

536	55.4	2.3	571	9	CG732194	1119146F0	609	54	2.3	572	6	CB016588
537	55.4	2.3	575	9	CG803705	1118045B1	610	54	2.3	867	9	CNS075BG
538	55.4	2.3	582	7	CF256984	pha005_c0	C 611	54	2.3	987	9	CNS014PQ
539	55.4	2.3	596	9	CG726927	1119092C0	C 612	54	2.3	1038	9	CNS01TL7
540	55.4	2.3	608	7	CF257313	pha009_f1	C 613	54	2.3	1101	9	CNS00EMH
541	55.4	2.3	739	1	AJ450624	AJ450624	614	54	2.3	1187	9	AG381847
542	55.4	2.3	775	7	CN218866	RJA040G05	C 615	54	2.3	1193	9	CG745316
543	55.4	2.3	811	1	AL514901	AL514901	616	53.8	2.3	509	9	CG721684
544	55.4	2.3	855	7	CF257095	pha006_g0	617	53.8	2.3	530	9	CG731340
545	55.4	2.3	859	7	CF257757	pha015_a1	618	53.8	2.3	601	9	CG727094
546	55.4	2.3	885	7	CF257093	pha006_f1	619	53.8	2.3	609	9	CG726983
547	55.4	2.3	889	7	CF251893	hdm005_f1	620	53.8	2.3	616	4	BJ117778
548	55.4	2.3	1101	9	CNS003BB	AL064089	621	53.8	2.3	758	1	AV756150
549	55.4	2.3	1388	5	BQ279227	AGENCOURT	622	53.8	2.3	881	7	CF251803
550	55.4	2.3	2300	3	CR734152	Tetraodon	623	53.8	2.3	886	7	CF251786
551	55.2	2.3	332	6	CD584497	CD584497	C 624	53.8	2.3	961	9	CNS008HI
552	55.2	2.3	478	9	CG730972	1119131F0	C 625	53.8	2.3	969	6	CD048933
553	55.2	2.3	530	9	CG731251	1119138B0	C 626	53.8	2.3	1038	9	CNS06L7M
554	55.2	2.3	958	9	CNS0074D	AL066801	C 627	53.8	2.3	1101	9	CNS00EJ4
555	55.2	2.3	1013	9	CNS06RPFQ	AL412260	C 628	53.8	2.3	1350	9	CG744271
556	55.2	2.3	1032	9	CL1144058	ISB1-124E	629	53.8	2.3	1696	9	AG346840
557	55.2	2.3	1132	8	BZ695089	SP_Ba005	630	53.6	2.3	458	9	CG727107
558	55.2	2.3	1169	9	CNS05KHQ	AL402900	631	53.6	2.3	495	9	CG803905
559	55.2	2.3	2142	3	CR730230	Tetraodon	632	53.6	2.3	636	9	CG727329
560	55	2.3	407	9	CG727336	1119094D0	C 633	53.6	2.3	641	8	BZ400247
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562	55	2.3	598	9	CG727121	1119093C0	C 635	53.6	2.3	665	9	CG730213
563	55	2.3	598	9	CG727121	1119093C0	C 636	53.6	2.3	687	5	BP179101
564	55	2.3	825	4	BM358161	GA_Ea000	C 637	53.6	2.3	799	9	AG137960
565	55	2.3	914	9	CNS00ZJY	AL097768	C 638	53.6	2.3	843	9	CNS00CS1
566	55	2.3	1101	9	CNS00FVE	AL071298	C 639	53.6	2.3	850	8	BH512733
567	55	2.3	1664	3	CR721909	Tetraodon	C 640	53.6	2.3	910	9	CNS01G8P
568	55	2.3	1780	9	AG320553	Mus muscu	C 641	53.6	2.3	938	9	CNS006TJ
569	54.8	2.3	411	9	CG731085	1119133D0	C 642	53.6	2.3	973	9	CNS071LE
570	54.8	2.3	498	1	AU087066	AU087066	643	53.6	2.3	1038	9	CNS01TL7</

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683 53.2 2.2 1038 6 CD388242 CD388242 AGENCOURT
684 53.2 2.2 1091 9 CL504270 SAIL_734
685 53 2.2 417 9 CG721114 CG721114 1119065E0
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687 53 2.2 571 8 B88488 B88488 CpG0226B Cp
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694 53 2.2 1332 9 AG429508 AG429508 Mus muscu
695 53 2.2 1352 9 AG381852 AG381852 Mus muscu
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716 52.6 2.2 903 9 CNS02WVM AL217579 Tetraodon
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736 52.4 2.2 1091 9 CNS007OF AL067422 Drosophil
737 52.4 2.2 1101 9 CNS00Z6Z AL097301 Drosophil
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CG807610 1118085C1 501 2.2 51.6 c 806
CG731135 1119134C1 504 2.2 51.6 807
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BH177277 008_L_22- 773 2.2 51.6 c 816
AL614235 T3_end of 886 2.2 51.6 817
CD387611 AGENCOURT 886 2.2 51.6 818
AL064580 Drosophil 1013 2.2 51.6 c 819
AG337989 Mus muscu 1101 2.2 51.6 c 820
BZ555610 pacs1-60_ 1187 2.2 51.6 c 821
AG333887 Mus muscu 1303 2.2 51.6 c 822
CG803223 1118040B1 2087 2.2 51.6 c 823
CG727192 1119093F0 475 2.2 51.4 c 824
CG732575 1119149D0 487 2.2 51.4 c 825
CG727387 1119094F0 500 2.2 51.4 c 826
CG727387 1119094F0 502 2.2 51.4 c 827

828 51.4 2.2 581 9 CNS034DK AL227297 Tetraodon 901 50.8 2.1 791 8 BH551361
829 51.4 2.2 603 9 CG730227 CG730227 Tetraodon 902 50.8 2.1 821 7 CF885572
C 830 51.4 2.2 605 9 CG731359 CG731359 903 50.8 2.1 826 9 AG579614 Mus muscu
C 831 51.4 2.2 646 1 AV399905 AV399905 904 50.8 2.1 828 8 AQ739398
832 51.4 2.2 650 9 CE195951 CE195951 tigr-gss- 905 50.8 2.1 831 9 AG477668 Mus muscu
833 51.4 2.2 691 8 BH941093 BH941093 odfl6b06. 906 50.8 2.1 880 9 CNS001L8
834 51.4 2.2 843 9 CNS00CS1 AL059666 Drosophil 907 50.8 2.1 921 9 CL100769
C 835 51.4 2.2 887 9 AG526041 Mus muscu 908 50.8 2.1 939 6 CD387952
836 51.4 2.2 911 9 CL478691 CL478691 SAIL_294 909 50.8 2.1 952 6 CD051140
C 837 51.4 2.2 1101 9 CNS00D1 AL065414 Drosophil 910 50.8 2.1 961 7 CK230311 ILLUMIGEN
838 51.4 2.2 1101 9 CNS016LI AL106896 Drosophil 911 50.8 2.1 1012 9 CL044464
C 839 51.4 2.2 1160 8 BZ579469 BZ579469 msh2_637. 912 50.8 2.1 1065 9 CL040367
840 51.4 2.2 1200 9 CNS016CO AL106578 Drosophil 913 50.8 2.1 1101 9 CNS00ESI
C 841 51.4 2.2 1335 9 CL646802 CL646802 CH213-123 914 50.8 2.1 1146 9 CNS021G2
C 842 51.4 2.2 1715 9 AG288305 AG288305 Mus muscu 915 50.8 2.1 1196 3 CR734775
843 51.2 2.2 348 9 AG2337623 AG2337623 Lotus cor 916 50.8 2.1 1348 9 CG749499
844 51.2 2.2 434 9 CG723260 CG723260 1119075E0 917 50.8 2.1 1388 9 AG278124 Mus muscu
845 51.2 2.2 453 9 CG730298 CG730298 1119124B0 918 50.8 2.1 1392 9 CG757503
C 846 51.2 2.2 480 9 CG721323 CG721323 1119066D0 919 50.8 2.1 1592 9 CG750135
847 51.2 2.2 488 9 CG731260 CG731260 1119138C0 920 50.6 2.1 367 9 CG730984
C 848 51.2 2.2 505 9 CG807903 CG807903 1118087G1 921 50.6 2.1 413 9 CG727412
C 849 51.2 2.2 510 8 BH766152 BH766152 BMBAC359H 922 50.6 2.1 464 9 CG803917
850 51.2 2.2 520 9 CG723442 CG723442 1119076D0 923 50.6 2.1 491 9 CG730328
851 51.2 2.2 556 9 CL341275 CL341275 RPCI44_26 924 50.6 2.1 513 9 CG803105
852 51.2 2.2 568 9 CG803931 CG803931 1118046H0 925 50.6 2.1 562 8 B68654
C 853 51.2 2.2 628 9 CG721223 CG721223 1119066A0 926 50.6 2.1 571 9 CG732209
854 51.2 2.2 631 9 CG731287 CG731287 1119138E0 927 50.6 2.1 593 9 CG732537
C 855 51.2 2.2 675 9 CG807781 CG807781 1118086H0 928 50.6 2.1 613 9 CG721572
856 51.2 2.2 831 8 B19844 B19844 T2J23-T7 TA 929 50.6 2.1 628 9 CG807906
857 51.2 2.2 900 8 AZ678198 AZ678198 ENTGV60TF 930 50.6 2.1 646 9 CG807859
858 51.2 2.2 1101 9 CNS017ZQ AL108704 Drosophil 931 50.6 2.1 651 9 CG807569
859 51.2 2.2 1542 9 AG386981 AG386981 Mus muscu 932 50.6 2.1 656 9 CG807672
C 860 51.2 2.2 2588 9 CL468223 CL468223 SAIL_1282 933 50.6 2.1 673 8 BH565747
861 51 2.2 415 9 CG731289 CG731289 1119138E0 934 50.6 2.1 694 9 CG807674
C 862 51 2.2 508 9 CG728850 CG728850 1119104C0 935 50.6 2.1 704 9 BX193580
863 51 2.2 523 9 CG721571 CG721571 1119068A0 936 50.6 2.1 806 8 B20782
864 51 2.2 558 4 BM276395 BM276395 PfESToaa8 937 50.6 2.1 830 8 BH248163
865 51 2.2 581 5 BP202818 BP202818 938 50.6 2.1 939 6 BY720774
C 866 51 2.2 610 9 CG806846 CG806846 1118074F0 939 50.6 2.1 970 6 CB208406
C 867 51 2.2 628 9 CG807906 CG807906 1118087H0 940 50.6 2.1 982 4 BM415348
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C 869 51 2.2 638 9 CG803213 CG803213 1118040A0 942 50.6 2.1 1101 9 CNS0022U
C 870 51 2.2 659 9 CG732143 CG732143 1119146D0 943 50.6 2.1 1174 9 CL110860
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C 873 51 2.2 826 7 CV483860 CV483860 AGENCOURT 946 50.4 2.1 442 9 CG804073
C 874 51 2.2 828 8 AZ693244 AZ693244 AGENCOURT 947 50.4 2.1 461 9 CG730244
875 51 2.2 893 8 BH188563 BH188563 036_O_12- 948 50.4 2.1 481 9 CG803819
876 51 2.2 893 9 CNS07SJW AL625502 T3_end of 949 50.4 2.1 567 9 CG806751
C 877 51 2.2 920 4 BM816394 BM816394 HCL14G06 950 50.4 2.1 576 9 CG807740
C 878 51 2.2 1007 9 CNS06X9S AL419462 T3_end of 951 50.4 2.1 685 8 BZ030069
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C 880 51 2.2 1165 3 CR677611 CR677611 Tetraodon 953 50.4 2.1 814 7 CK478557
881 51 2.2 1178 9 CL111035 CL111035 ISB1-54K1 954 50.4 2.1 829 9 AG528710
C 882 51 2.2 1214 7 CK211400 CK211400 FGAS02324 955 50.4 2.1 1085 9 CNS016YR
C 883 51 2.2 1254 3 CR720510 CR720510 Tetraodon 956 50.4 2.1 1091 9 CNS007OF
884 51 2.2 1943 9 AG333983 AG333983 Mus muscu 957 50.4 2.1 1101 9 CNS0039L
885 50.8 2.1 380 9 CG723457 CG723457 1119076E0 958 50.4 2.1 1101 9 CNS00DT7
886 50.8 2.1 430 9 CG730971 CG730971 1119131F0 959 50.4 2.1 1101 9 CNS000T7
887 50.8 2.1 441 9 CG730243 CG730243 1119123D1 960 50.2 2.1 356 5 BU495248
888 50.8 2.1 469 9 CG731872 CG731872 1119144B1 961 50.2 2.1 367 5 BQ451328
C 889 50.8 2.1 473 9 CG803682 CG803682 1118045A0 962 50.2 2.1 440 5 BW528256
C 890 50.8 2.1 473 9 CG803682 CG803682 1118045A0 963 50.2 2.1 456 9 CG801855
891 50.8 2.1 481 9 CG727147 CG727147 1119093D1 964 50.2 2.1 482 9 CG732472
892 50.8 2.1 482 9 CG807733 CG807733 1118086D0 965 50.2 2.1 501 9 CG807610
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894 50.8 2.1 509 9 CG721196 CG721196 1119065H0 967 50.2 2.1 519 9 CNS006PJ
895 50.8 2.1 523 9 CG731328 CG731328 1119139C0 968 50.2 2.1 522 9 CG803757
C 896 50.8 2.1 550 9 CG803095 CG803095 1118038D0 969 50.2 2.1 592 9 CG729361
897 50.8 2.1 593 9 CG807914 CG807914 1118087H1 970 50.2 2.1 601 9 CG727094
898 50.8 2.1 609 9 CNS025K1 AL182171 Tetraodon 971 50.2 2.1 629 9 CG717882
899 50.8 2.1 627 8 BH724093 BH724093 BOHUS58TF 972 50.2 2.1 644 6 CB935757
C 900 50.8 2.1 714 8 BH981072 BH981072 odd66h10. 973 50.2 2.1 647 6 CB935758

BH551361 BOGCE09TF
CF885572 tric082xa
AG579614 Mus muscu
AQ739398 HS_5482_B
AG477668 Mus muscu
AL053817 Drosophil
CL100769 ISB1-36F1
CD387952 AGENCOURT
CD051140 AGENCOURT
CK230311 ILLUMIGEN
CL044464 CH216-49K
CL040367 CH216-49K
AL069797 Drosophil
AL176843 Tetraodon
CR734775 Tetraodon
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AG278124 Mus muscu
CG757503 P052-4-C0
CG750135 P044-3-D0
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CG727412 1119094G0
CG803917 1118046G0
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CG803105 1118038E1
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CG807859 1118087E0
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B20782 T7H16-T7 TA
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BM415348 OP20422 M
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AL097152 Drosophil
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CG730244 1119123D1
CG803819 1118046B0
CG806751 1118073E0
CG807740 1118086D0
BZ030069 oed2a10.
BH178455 011_J_02-
AL615412 T3_end of
CK478557 AGENCOURT
AG528710 Mus muscu
AL107373 Drosophil
AL067422 Drosophil
AL063926 Drosophil
AL075293 Drosophil
BU495248 PfESToab7
BQ451328 PfESToaa9
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CG803757 1118045E1
CG729361 1119111B1
CG727094 1119093B0
CG717882 1119050F0
CB935757 tab95f10.
CB935758 tab95f11.

974	50.2	2.1	719	6	CD835864	CD835864	BN45.046P	1047	49.8	2.1	991	9	CL139092	CL139092	ISB1-111O
975	50.2	2.1	770	8	AQ740708	AQ740708	HS_5507_A	1048	49.8	2.1	1101	9	CNS004ZW	AL055440	Drosophil
976	50.2	2.1	780	9	AG291100	AG291100	Mus muscu	c1049	49.8	2.1	1101	9	CNS016LI	AL106896	Drosophil
977	50.2	2.1	793	9	AG591322	AG591322	Mus muscu	c1050	49.8	2.1	1152	9	CL499024	CL499024	SAIL_662
978	50.2	2.1	836	9	CNS01120	AL099642	Drosophil	1051	49.8	2.1	1201	9	CNS016E1	AL106627	Drosophil
c 979	50.2	2.1	876	8	AZ677905	AZ677905	ENTKD58TF	1052	49.8	2.1	1253	9	CL036722	CL036722	CH216-42D
c 980	50.2	2.1	889	9	AG362888	AG362888	Mus muscu	1053	49.8	2.1	1896	9	CG753083	CG753083	P048-1-CO
981	50.2	2.1	999	9	CNS06RCL	AL411787	T7 end of	1054	49.6	2.1	403	9	CG732151	CG732151	1119146D1
c 982	50.2	2.1	1001	9	CNS01400	AL103554	Drosophil	1055	49.6	2.1	522	9	CG730299	CG730299	1119124B0
983	50.2	2.1	1254	3	CR720510	CR720510	Tetraodon	c1056	49.6	2.1	560	5	BP179243	BP179243	BP179243
984	50.2	2.1	1294	9	AG448672	AG448672	Mus muscu	c1057	49.6	2.1	615	9	CG807731	CG807731	1118086D0
985	50.2	2.1	1313	7	CK997149	CK997149	ip15c02.b	1058	49.6	2.1	656	9	CG807672	CG807672	1118085H0
c 986	50.2	2.1	1616	3	CR734259	CR734259	Tetraodon	c1059	49.6	2.1	706	8	BH992021	BH992021	oen97g04.
987	50.2	2.1	1715	9	AG288305	AG288305	Mus muscu	c1060	49.6	2.1	718	7	CO720184	CO720184	tai40a11.
c 988	50.2	2.1	1896	3	CR722884	CR722884	Tetraodon	c1061	49.6	2.1	724	5	BP178533	BP178533	BP178533
989	50	2.1	416	9	CG730241	CG730241	1119123D0	1062	49.6	2.1	726	8	BI8951	BI8951	F6I1-Sp6 IG
990	50	2.1	443	9	CG726802	CG726802	1119091F1	c1063	49.6	2.1	749	1	AV400884	AV400884	AV400884
991	50	2.1	467	9	CG732152	CG732152	1119146D1	c1064	49.6	2.1	780	7	CK595444	CK595444	AGENCOURT
c 992	50	2.1	492	9	CG808373	CG808373	1118091G0	1065	49.6	2.1	837	9	AG480808	AG480808	Mus muscu
c 993	50	2.1	508	1	AU001161	AU001161	AU001161	c1066	49.6	2.1	856	9	AG544460	AG544460	Mus muscu
c 994	50	2.1	521	1	AU001371	AU001371	AU001371	1067	49.6	2.1	858	9	BX907266	BX907266	Leishmani
c 995	50	2.1	522	1	AV399582	AV399582	AV399582	c1068	49.6	2.1	867	8	AZ675186	AZ675186	ENTKU40TR
c 996	50	2.1	528	1	AU001040	AU001040	AU001040	c1069	49.6	2.1	945	9	CNS005WY	AL062612	Drosophil
c 997	50	2.1	542	5	BP177610	BP177610	BP177610	1070	49.6	2.1	1118	5	BX462896	BX462896	BX462896
c 998	50	2.1	549	5	BP178615	BP178615	BP178615	1071	49.6	2.1	1233	9	AG278952	AG278952	Mus muscu
999	50	2.1	572	9	CG807807	CG807807	1118087B0	1072	49.6	2.1	1242	9	CL068807	CL068807	CH216-115
c1000	50	2.1	591	9	CG807037	CG807037	1118076H0	1073	49.6	2.1	1364	9	CG757986	CG757986	P053-2-D0
c1001	50	2.1	607	9	CG721216	CG721216	1119066A0	1074	49.6	2.1	1391	9	CG754863	CG754863	P050-2-G0
c1002	50	2.1	628	1	AV404749	AV404749	AV404749	c1075	49.6	2.1	2201	9	AG310854	AG310854	Mus muscu
c1003	50	2.1	639	9	CG721246	CG721246	1119066B0	1076	49.6	2.1	2736	9	AY402613	AY402613	Pan trogl
c1004	50	2.1	647	1	AV399591	AV399591	AV399591	1077	49.4	2.1	415	7	R21312	R21312	Yg48g10.r1
1005	50	2.1	663	9	CG721115	CG721115	1119065E0	1078	49.4	2.1	462	1	AU087611	AU087611	AU087611
c1006	50	2.1	682	8	BZ646791	BZ646791	OGCBS18TM	1079	49.4	2.1	463	9	CG805664	CG805664	1118061B0
c1007	50	2.1	692	5	BP177891	BP177891	BP177891	1080	49.4	2.1	552	9	CG732218	CG732218	1119146G0
c1008	50	2.1	692	8	BH430772	BH430772	BOHTX76TF	c1081	49.4	2.1	556	9	CG800480	CG800480	1118013A0
c1009	50	2.1	701	5	BP121539	BP121539	BP121539	c1082	49.4	2.1	592	9	CG727098	CG727098	1119093B0
c1010	50	2.1	704	5	BP177739	BP177739	BP177739	1083	49.4	2.1	648	8	AZ527257	AZ527257	266PB0D1
c1011	50	2.1	723	5	BP178342	BP178342	BP178342	c1084	49.4	2.1	656	8	BH809580	BH809580	Gm_ISB001
c1012	50	2.1	728	7	CO388065	CO388065	AGENCOURT	1085	49.4	2.1	727	5	BU384897	BU384897	603856373
c1013	50	2.1	742	5	BX462820	BX462820	BX462820	c1086	49.4	2.1	802	8	BH681367	BH681367	BOMCI93TR
c1014	50	2.1	759	5	BP121009	BP121009	BP121009	c1087	49.4	2.1	872	8	AZ680887	AZ680887	ENTHU38TF
c1015	50	2.1	770	1	AV399357	AV399357	AV399357	c1088	49.4	2.1	917	5	BU515694	BU515694	AGENCOURT
c1016	50	2.1	771	8	BZ438776	BZ438776	BONSBO8TR	1089	49.4	2.1	987	9	CNS014PQ	AL104456	Drosophil
1017	50	2.1	819	9	AG401866	AG401866	Mus muscu	c1090	49.4	2.1	994	9	CNS04NOJ	AL298972	Tetraodon
c1018	50	2.1	849	1	AU005735	AU005735	AU005735	1091	49.4	2.1	996	9	CNS00FUH	AL071063	Drosophil
1019	50	2.1	908	7	CF257407	CF257407	pha010_g0	c1092	49.4	2.1	1032	9	CNS0201P	AL206746	Tetraodon
1020	50	2.1	935	8	B10881	B10881	F24H6-Sp6.1	1093	49.4	2.1	1101	9	CNS00B01	AL057419	Drosophil
c1021	50	2.1	988	9	CL087333	CL087333	ISB1-9A17	1094	49.4	2.1	1167	9	CNS07360	AL427102	clone BA0
c1022	50	2.1	997	6	CD049644	CD049644	AGENCOURT	1095	49.4	2.1	1272	8	CC264939	CC264939	CH261-19L
c1023	50	2.1	1101	9	CNS00GDR	AL072060	Drosophil	1096	49.4	2.1	1352	9	CL648187	CL648187	CH213-166
c1024	50	2.1	1101	9	CNS00YWL	AL096927	Drosophil	1097	49.2	2.1	471	9	CG732128	CG732128	1119146C0
1025	50	2.1	1205	9	CL509381	CL509381	SAIL_811	c1098	49.2	2.1	481	9	CG803819	CG803819	1118046B0
c1026	50	2.1	1210	9	CG749728	CG749728	P044-1-C0	1099	49.2	2.1	489	9	CG727334	CG727334	1119094D0
c1027	49.8	2.1	443	9	CG729064	CG729064	1119107C0	1100	49.2	2.1	505	9	CG730263	CG730263	1119123F0
1028	49.8	2.1	450	9	CG799178	CG799178	1118001B0	1101	49.2	2.1	507	9	CG721167	CG721167	1119065G0
1029	49.8	2.1	452	9	CG730252	CG730252	1119123E0	1102	49.2	2.1	509	9	CG721574	CG721574	1119068A0
1030	49.8	2.1	485	9	CG732429	CG732429	1119148D1	1103	49.2	2.1	521	9	CG807764	CG807764	1118086F1
c1031	49.8	2.1	487	9	CG730305	CG730305	1119124B1	c1104	49.2	2.1	543	9	CG730256	CG730256	1119123E1
c1032	49.8	2.1	498	9	CG721172	CG721172	1119065G0	c1105	49.2	2.1	549	9	CG807268	CG807268	1118080A0
1033	49.8	2.1	540	9	CG726775	CG726775	1119091E0	c1106	49.2	2.1	550	9	CG808239	CG808239	1118090F0
1034	49.8	2.1	558	9	CG806837	CG806837	1118074E0	c1107	49.2	2.1	559	9	CG807049	CG807049	1118077B0
c1035	49.8	2.1	572	9	CG807807	CG807807	1118087B0	c1108	49.2	2.1	662	1	AV398694	AV398694	AV398694
c1036	49.8	2.1	576	9	CG807740	CG807740	1118086D0	c1109	49.2	2.1	766	4	BG309119	BG309119	HVSMec000
1037	49.8	2.1	582	5	BP229649	BP229649	BP229649	1110	49.2	2.1	768	8	BZ394392	BZ394392	EINBM19TR
1038	49.8	2.1	673	8	BH510309	BH510309	BOHJA93TF	1111	49.2	2.1	830	8	BH687659	BH687659	BOMMX94TR
c1039	49.8	2.1	722	8	BH947077	BH947077	obv12e08.	c1112	49.2	2.1	907	1	AL553912	AL553912	AL553912
1040	49.8	2.1	786	9	CNS009A5	AL053317	Drosophil	1113	49.2	2.1	959	8	AZ540580	AZ540580	ENTDR43TR
1041	49.8	2.1	849	8	AZ539019	AZ539019	ENTDV05TF	c1114	49.2	2.1	965	9	CL505797	CL505797	SAIL_755
c1042	49.8	2.1	914	9	CNS00ZJY	AL097768	Drosophil	c1115	49.2	2.1	999	9	CL038485	CL038485	CH216-46D
1043	49.8	2.1	952	9	CNS01016	AL098388	Drosophil	1116	49.2	2.1	1101	9	CNS00HD9	AL073338	Drosophil
c1044	49.8	2.1	958	6	CD385091	CD385091	AGENCOURT	c1117	49.2	2.1	1101	9	CNS00282	AL097340	Drosophil
c1045	49.8	2.1	964	9	CNS006N9	AL065781	Drosophil	1118	49.2	2.1	1101	9	CNS0152S	AL106114	Drosophil
c1046	49.8	2.1	976	9	CNS04E5M	AL286627	Tetraodon	c1119	49.2	2.1	1277	8	CC253231	CC253231	CH261-180

c1120	49.2	2.1	1350	9	CL019486	CH216-5G1	1193	48.8	2.1	1206	9	CL027076	CH216-25A
1121	49.2	2.1	1354	9	CG744717	P037-2-F0	1194	48.6	2.0	349	9	CG807125	1118078A0
1122	49.2	2.1	1962	9	AG390999	Mus muscu	1195	48.6	2.0	409	9	CG731919	1119144E1
1123	49	2.1	411	6	CB802631	AMGNNUC:M	1196	48.6	2.0	426	9	CG732171	1119146E0
1124	49	2.1	415	9	CG726747	1119091D0	1197	48.6	2.0	445	9	CG721283	1119066C0
1125	49	2.1	425	9	CG803718	1118045C0	1198	48.6	2.0	457	9	CG721709	1119068F0
1126	49	2.1	480	9	CG727295	1119094B0	1199	48.6	2.0	468	9	CG732170	1119146E0
1127	49	2.1	480	9	CG730265	1119123F1	1200	48.6	2.0	471	9	CG803897	1118046F0
c1128	49	2.1	507	9	CG731596	1119142B1	c1201	48.6	2.0	475	9	CG807289	1118080C0
c1129	49	2.1	521	9	CG807764	1118086F1	1202	48.6	2.0	488	9	CG730332	1119124E0
c1130	49	2.1	551	9	CG803090	1118038D0	c1203	48.6	2.0	499	9	CG807727	1118086C1
c1131	49	2.1	611	8	BH570603	BOGO079TR	1204	48.6	2.0	501	9	CG732556	1119149C1
c1132	49	2.1	613	9	CG721572	1119068A0	1205	48.6	2.0	503	9	CG727101	1119093B1
c1133	49	2.1	615	9	CG807731	1118086D0	c1206	48.6	2.0	505	9	CG729349	1119111A0
c1134	49	2.1	624	9	CG721168	1119065G0	1207	48.6	2.0	507	9	CG731596	1119142B1
c1135	49	2.1	658	5	BU948212	io52a02.X	1208	48.6	2.0	530	9	CG803796	1118046A0
c1136	49	2.1	663	9	CG721115	1119065E0	c1209	48.6	2.0	543	1	AU001085	AU001085
c1137	49	2.1	724	8	BZ614777	ig46e07.G	c1210	48.6	2.0	553	9	CG806061	1118065A0
c1138	49	2.1	772	8	BH480795	BOHJM11TR	c1211	48.6	2.0	663	9	CG807905	1118087H0
c1139	49	2.1	831	9	CNS002BX	AL097479 Drosophil	1212	48.6	2.0	675	8	BH969561	odh60h04.
c1140	49	2.1	832	9	CNS06SQE	AL413580 T7 end of	1213	48.6	2.0	694	5	BP506178	BP506178
1141	49	2.1	897	9	CNS07ABZ	AL436389 T7 end of	c1214	48.6	2.0	736	1	AU001091	AU001091
c1142	49	2.1	932	9	CL479576	CL479576 SAIL_308	c1215	48.6	2.0	758	9	AG547036	Mus muscu
c1143	49	2.1	938	9	CNS011LO	AL100422 Drosophil	1216	48.6	2.0	793	9	CNS01GMC	AL143317 Anopheles
c1144	49	2.1	945	9	CL483400	CL483400 SAIL_37b	1217	48.6	2.0	834	9	CNS008CK	AL051502 Drosophil
1145	49	2.1	961	9	CNS00M86	AL079258 Drosophil	c1218	48.6	2.0	840	8	BH433039	BOHNF56TF
c1146	49	2.1	1002	9	CNS011RP	AL100639 Drosophil	1219	48.6	2.0	842	8	AZ670364	ENTLN21TR
c1147	49	2.1	1010	6	CD171719	CF171719 AGENCOURT	c1220	48.6	2.0	855	9	CNS04P5D	AL300874 Tetraodon
c1148	49	2.1	1113	7	CF994845	CF994845 AGENCOURT	c1221	48.6	2.0	865	8	AZ546251	ENTDU61TR
c1149	49	2.1	1152	4	BG309087	BG309087 HVSMEC000	c1222	48.6	2.0	876	8	AZ533593	AZ533593 ENTDO47TF
c1150	49	2.1	1153	6	CD389859	CD389859 AGENCOURT	1223	48.6	2.0	893	5	BP507314	BP507314
1151	49	2.1	1202	9	AG338379	AG338379 Mus muscu	c1224	48.6	2.0	919	8	AZ688396	AZ688396 ENTKN14TR
c1152	49	2.1	1320	9	CL103881	CL103881 ISB1-42C8	c1225	48.6	2.0	945	9	CL072136	CL072136 CH216-122
c1153	49	2.1	1624	9	CL466243	CL466243 SAIL_1253	c1226	48.6	2.0	971	9	CNS005KU	AL059324 Drosophil
c1154	49	2.1	1877	3	CR721531	CR721531 Tetraodon	c1227	48.6	2.0	976	9	CL516956	CL516956 SAIL_98 C
c1155	48.8	2.1	360	7	CN079773	CN079773 EC2BBA17A	1228	48.6	2.0	991	6	CD248081	CD248081 AGENCOURT
c1156	48.8	2.1	404	9	CG713828	CG713828 1119033F0	c1229	48.6	2.0	1017	9	CNS04UKH	AL307898 Tetraodon
c1157	48.8	2.1	450	9	CG799178	CG799178 1118001B0	1230	48.6	2.0	1101	9	CNS00240	AL061823 Drosophil
1158	48.8	2.1	462	1	AJ696357	AJ696357 AJ696357	c1231	48.6	2.0	1101	9	CNS003B0	AL064078 Drosophil
c1159	48.8	2.1	463	9	CG803217	CG803217 1118040B0	c1232	48.6	2.0	1121	9	CL508918	CL508918 SAIL_805
c1160	48.8	2.1	476	9	CG726749	CG726749 1119091D0	c1233	48.6	2.0	1124	9	AG279040	AG279040 Mus muscu
c1161	48.8	2.1	480	9	CG807661	CG807661 1118085G0	1234	48.6	2.0	1192	9	CNS03Y36	AL265803 Tetraodon
c1162	48.8	2.1	568	9	CG803931	CG803931 1118046H0	c1235	48.6	2.0	1205	9	CNS0165A	AL106312 Drosophil
c1163	48.8	2.1	632	9	CG721033	CG721033 1119065B0	1236	48.6	2.0	1214	9	CL646783	CL646783 CH213-123
c1164	48.8	2.1	643	4	BM159684	BM159684 EST562207	c1237	48.6	2.0	1242	8	BZ695766	BZ695766 SP_Ba006
c1165	48.8	2.1	643	4	BM160648	BM160648 EST563171	1238	48.6	2.0	1263	9	AG396942	AG396942 Mus muscu
c1166	48.8	2.1	646	9	CG807859	CG807859 1118087E0	1239	48.6	2.0	1364	9	CG757970	CG757970 P053-2-C0
c1167	48.8	2.1	653	7	CN075506	CN075506 EC2BBA10B	c1240	48.6	2.0	1372	9	AG390627	AG390627 Mus muscu
c1168	48.8	2.1	683	4	BM159163	BM159163 EST561686	1241	48.6	2.0	1375	9	CL646465	CL646465 CH213-116
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1171	48.8	2.1	699	8	BH929444	BH929444 odh68a03.	1244	48.4	2.0	431	9	CG721541	CG721541 1119067G1
c1172	48.8	2.1	700	4	BM170161	BM170161 EST572684	1245	48.4	2.0	463	9	CG729377	CG729377 1119111D1
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c1174	48.8	2.1	784	8	BH446645	BH446645 BOHKS77TR	1247	48.4	2.0	479	9	CG805662	CG805662 1118061B0
c1175	48.8	2.1	790	1	AL664486	AL664486	1248	48.4	2.0	480	9	CG726949	CG726949 1119092D0
c1176	48.8	2.1	800	9	CNS06PYX	AL409999 T7 end of	c1249	48.4	2.0	508	9	CG801552	CG801552 1118022D1
c1177	48.8	2.1	812	8	BH477956	BH477956 BOHQM35TR	c1250	48.4	2.0	519	9	CG802630	CG802630 1118032F0
c1178	48.8	2.1	815	8	BZ037267	BZ037267 oef92e08.	c1251	48.4	2.0	548	1	AU001244	AU001244 AU001244
c1179	48.8	2.1	872	7	CK022958	CK022958 AGENCOURT	1252	48.4	2.0	553	9	CG732166	CG732166 1119146E0
c1180	48.8	2.1	886	8	AZ532704	AZ532704 ENTBO40TF	c1253	48.4	2.0	579	9	CG807571	CG807571 1118085A0
1181	48.8	2.1	891	8	BH160327	BH160327 ENTRZ18TF	c1254	48.4	2.0	633	1	AU004482	AU004482 AU004482
c1182	48.8	2.1	891	8	AG526131	AG526131 Mus muscu	c1255	48.4	2.0	643	5	BU546971	BU546971 GM880011B
c1183	48.8	2.1	910	9	CNS01XIW	AL171761 Tetraodon	1256	48.4	2.0	675	9	CG807781	CG807781 1118086H0
c1184	48.8	2.1	913	9	CNS0102F	AL098433 Drosophil	1257	48.4	2.0	697	9	CNS04707	AL278224 Tetraodon
c1185	48.8	2.1	928	9	CD387866	CD387866 AGENCOURT	c1258	48.4	2.0	705	8	BH461803	BH461803 BOHJV67TR
c1186	48.8	2.1	949	6	CL461494	CL461494 SAIL_1148	c1259	48.4	2.0	724	5	BP178072	BP178072 BP178072
c1187	48.8	2.1	1042	9	CL461494	CL461494 SAIL_1148	1260	48.4	2.0	749	8	AQ361974	AQ361974 mgxb00050
c1188	48.8	2.1	1101	9	CNS00ETW	AL069847 Drosophil	1261	48.4	2.0	755	9	BX150378	BX150378 Danio rer
c1189	48.8	2.1	1101	9	CNS00HD9	AL073338 Drosophil	c1262	48.4	2.0	757	4	BJ130908	BJ130908 BJ130908
c1190	48.8	2.1	1101	9	CNS0100X	AL098379 Drosophil	1263	48.4	2.0	780	7	CK595444	CK595444 AGENCOURT
c1191	48.8	2.1	1131	9	CNS034FO	AL227373 Tetraodon	1264	48.4	2.0	812	6	CA918125	CA918125 EST642272
c1192	48.8	2.1	1201	9	CNS015ZZ	AL106121 Drosophil	c1265	48.4	2.0	852	8	AQ894184	AQ894184 HS_3072_A

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c1269 48.4 2.0 905 9 CNS00KHX AL077798 Drosophil
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c1271 48.4 2.0 973 9 CNS071LE AL425064 clone BA0
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c1277 48.4 2.0 1101 9 CNS00LT2 AL078714 Drosophil
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c1279 48.4 2.0 1206 8 BZ695529 BZ695529 SP_Ba006
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c1284 48.4 2.0 2108 9 AG390640 AG390640 Mus muscu
c1285 48.2 2.0 328 5 BM930129 BM930129 UI-E-EJ1-
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c1313 48.2 2.0 584 5 BP250707 BP250707 BP250707
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c1413	47.8	2.0	452	9	CG729156	1119108E1	CG729156	1119108E1	c1486	47.4	2.0	311	1	AI965701	sc77c09.Y
1414	47.8	2.0	461	6	BY551983	BY551983	BY551983	BY551983	1487	47.4	2.0	413	9	CG727364	1119094E0
1415	47.8	2.0	466	9	CG807825	CG807825	CG807825	1118087C0	1488	47.4	2.0	419	9	CG721562	1119067H1
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1417	47.8	2.0	503	5	BU480294	603844970	BU480294	603844970	1490	47.4	2.0	452	9	CG727090	1119093B0
c1418	47.8	2.0	503	9	CG804059	1118047E1	CG804059	1118047E1	c1491	47.4	2.0	453	9	CG730298	1119124B0
c1419	47.8	2.0	552	9	CG724997	CG724997	1119083E0	1119083E0	1492	47.4	2.0	454	9	CG804111	1118047H0
c1420	47.8	2.0	620	8	BH068361	CG724997	BH068361	RPCI-24-2	1493	47.4	2.0	464	9	CG732153	1119146D1
1421	47.8	2.0	661	9	CNS02QVJ	AL209800	Tetraodon	AL209800	c1494	47.4	2.0	468	9	CG806831	1118074D0
1422	47.8	2.0	702	5	EX841013	EX841013	EX841013	EX841013	1495	47.4	2.0	475	9	CG807289	1118080C0
1423	47.8	2.0	759	8	BZ089333	BZ089333	11kx38e08	11kx38e08	1496	47.4	2.0	476	9	CG727365	1119094E0
c1424	47.8	2.0	773	9	EX236086	BX236086	Danio rer	Danio rer	c1497	47.4	2.0	488	9	CG731260	1119138C0
1425	47.8	2.0	776	8	BH711762	BH711762	BOMHG73TF	BOMHG73TF	1498	47.4	2.0	500	1	AU087594	AU087594
c1426	47.8	2.0	810	9	CNS06GOD	AL397955	T3 end of	T3 end of	c1499	47.4	2.0	540	5	BP179089	BP179089
c1427	47.8	2.0	821	1	AV758661	AV758661	AV758661	AV758661	c1500	47.4	2.0	544	9	BX128251	Danio rer
c1428	47.8	2.0	834	8	AZ667977	AZ667977	ENTGJ36TF	ENTGJ36TF							
1429	47.8	2.0	843	7	CO389145	CO389145	AGENCOURT	AGENCOURT							
c1430	47.8	2.0	854	9	CNS024OG	AL181033	Tetraodon	AL181033							
1431	47.8	2.0	886	8	BH153730	BH153730	ENTRJ16TF	ENTRJ16TF							
1432	47.8	2.0	891	5	BU484122	BU484122	603471770	603471770							
1433	47.8	2.0	907	8	BH165866	BH165866	ENTTC13TF	ENTTC13TF							
c1434	47.8	2.0	926	4	BM358145	BM358145	GA_Ea000	GA_Ea000							
c1435	47.8	2.0	928	7	CK406657	CK406657	AUF_iflvr	AUF_iflvr							
1436	47.8	2.0	1087	3	CR721616	CR721616	Tetraodon	Tetraodon							
1437	47.8	2.0	1101	9	CNS0039Q	AL063931	Drosophil	Drosophil							
c1438	47.8	2.0	1101	9	CNS00FVE	AL071298	Drosophil	Drosophil							
c1439	47.8	2.0	1101	9	CNS00KAE	AL077628	Drosophil	Drosophil							
c1440	47.8	2.0	1227	9	AG4330010	AG4330010	Mus muscu	Mus muscu							
1441	47.8	2.0	1265	1	AJ537929	AJ537929	AJ537929	AJ537929							
1442	47.8	2.0	1292	4	BM463105	BM463105	AGENCOURT	AGENCOURT							
c1443	47.8	2.0	1542	9	AG386981	AG386981	Mus muscu	Mus muscu							
1444	47.8	2.0	1837	9	AG381859	AG381859	Mus muscu	Mus muscu							
c1445	47.6	2.0	300	6	C32453	C32453	C32453	C32453							
1446	47.6	2.0	426	9	CG721421	CG721421	C32453	C32453							
1447	47.6	2.0	430	9	CG732195	CG732195	1119067A0	1119067A0							
1448	47.6	2.0	439	9	CG730281	CG730281	1119146F0	1119146F0							
1449	47.6	2.0	448	9	CG730282	CG730282	1119123G0	1119123G0							
c1450	47.6	2.0	460	9	CG730210	CG730210	1119123B0	1119123B0							
1451	47.6	2.0	476	9	CG807890	CG807890	1118087G0	1118087G0							
1452	47.6	2.0	482	9	CG721052	CG721052	1119065B0	1119065B0							
1453	47.6	2.0	489	9	CG731039	CG731039	1119132F0	1119132F0							
1454	47.6	2.0	490	9	CG803859	CG803859	1118046D0	1118046D0							
1455	47.6	2.0	502	9	CG727077	CG727077	1119093A0	1119093A0							
c1456	47.6	2.0	534	9	CG806296	CG806296	1118068A0	1118068A0							
1457	47.6	2.0	549	9	CG807268	CG807268	1118080A0	1118080A0							
1458	47.6	2.0	552	9	CG724997	CG724997	1119083E0	1119083E0							
c1459	47.6	2.0	556	9	CG803777	CG803777	1118045H0	1118045H0							
c1460	47.6	2.0	567	9	CG803178	CG803178	1118039F1	1118039F1							
c1461	47.6	2.0	574	9	CG730254	CG730254	1119123E1	1119123E1							
c1462	47.6	2.0	592	5	BP119084	BP119084	BP119084	BP119084							
1463	47.6	2.0	601	9	CG806848	CG806848	1118074F0	1118074F0							
1464	47.6	2.0	657	8	BZ385948	BZ385948	EINDR93TR	EINDR93TR							
c1465	47.6	2.0	693	1	AV682300	AV682300	AV682300	AV682300							
c1466	47.6	2.0	715	8	BH927413	BH927413	odi61a10	odi61a10							
c1467	47.6	2.0	739	8	BZ078915	BZ078915	11k12f12	11k12f12							
1468	47.6	2.0	740	8	BH513221	BH513221	BOGYR19TR	BOGYR19TR							
1469	47.6	2.0	770	7	CK478641	CK478641	AGENCOURT	AGENCOURT							
c1470	47.6	2.0	806	4	BG309137	BG309137	HVSMEC000	HVSMEC000							
1471	47.6	2.0	820	7	CO930994	CO930994	AGENCOURT	AGENCOURT							
1472	47.6	2.0	860	8	AZ682680	AZ682680	ENTLJ28TR	ENTLJ28TR							
c1473	47.6	2.0	866	7	CV482428	CV482428	AGENCOURT	AGENCOURT							
c1474	47.6	2.0	882	8	BH167593	BH167593	ENTTM02TF	ENTTM02TF							
c1475	47.6	2.0	905	9	CL460252	CL460252	SAIL_102	SAIL_102							
c1476	47.6	2.0	935	9	CNS010G4	AL098926	Drosophi	Drosophi							
1477	47.6	2.0	939	6	BY720774	BY720774	BY720774	BY720774							
1478	47.6	2.0	978	8	BH155923	BH155923	ENTSH70TR	ENTSH70TR							
c1479	47.6	2.0	994	9	CNS015XG	AL106030	Drosophil	Drosophil							
c1480	47.6	2.0	1067	3	CR733733	CR733733	Tetraodon	Tetraodon							
1481	47.6	2.0	1164	8	CC218891	CC218891	CH261-14M	CH261-14M							
1482	47.6	2.0	1168	9	CL078758	CL078758	CH216-153	CH216-153							
1483	47.6	2.0	1415	9	CL646438	CL646438	CH213-115	CH213-115							
1484	47.6	2.0	1454	9	CL646440	CL646440	CH213-115	CH213-115							

ALIGNMENTS

RESULT 1
CR614790
LOCUS
DEFINITION
full-length cDNA clone CS0DI018YG12 of Placenta Cot 25-normalized of Homo sapiens (human) .
ACCESSION
CR614790
VERSION
CR614790.1 GI:50495597
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 1911)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue

REFERENCE
2 (bases 1 to 1911)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
Location/Qualifiers
1..1911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI018YG12"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 80.1%; Score 1900; DB 3; Length 1911;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
|||||
Db 12 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 71
Qy 61 GTTCCAGAACTCCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
|||||
Db 72 GTTCCAGAACTCCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 13

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source 1..1925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI059YA12"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match		79.9%;	Score 1895;	DB 3;	Length 1925;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1895;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60		
Db	31	AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	90		
QY	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120		
Db	91	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	150		
QY	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180		
Db	151	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	210		
QY	181	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA	240		
Db	211	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA	270		
QY	241	GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGGATCACCCTTGTGAGCAAAAAG	300		
Db	271	GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGGATCACCCTTGTGAGCAAAAAG	330		
QY	301	CGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT	360		
Db	331	CGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT	390		
QY	361	TTGGCCGGCAAGCAACCAAGTTGAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420		
Db	391	TTGGCCGGCAAGCAACCAAGTTGAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	450		
QY	421	GGCTGGGTTGGAGATGGATTCTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	480		
Db	451	GGCTGGGTTGGAGATGGATTCTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	510		
QY	481	AAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540		
Db	511	AAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	570		
QY	541	TGTTACAACCTATCTGATACCTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAA	600		
Db	571	TGTTACAACCTATCTGATACCTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAA	630		
QY	601	GATCCCATATTCAACACTCAAACTGCAACACAAACAACAGAAATTTATTGTCAGTGACAGT	660		
Db	631	GATCCCATATTCAACACTCAAACTGCAACACAAACAACAGAAATTTATTGTCAGTGACAGT	690		
QY	661	ACCTACTCGGTGGATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT	720		
Db	691	ACCTACTCGGTGGATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT	750		
QY	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG	780		
Db	751	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG	810		
QY	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTTCAAG	840		

Db	811	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG	870
QY	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCACCGGCTCTGCTAGTGTCTTGTCTCTCTTC	900
Db	871	AATGAAGCTGCTGGGTTTGGAGGTGTCCACCGGCTCTGCTAGTGTCTTGTCTCTCTTC	930
QY	901	TTTGGTGTCTGAGCTGGTCTTGGATTTTGGTATGTCAAAGGTATGTGAAGCCTTCCCT	960
Db	931	TTTGGTGTCTGAGCTGGTCTTGGATTTTGGTATGTCAAAGGTATGTGAAGCCTTCCCT	990
QY	961	TTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAAG	1020
Db	991	TTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAAG	1050
QY	1021	GCCAATGATAGCAACCTTAATGAGGAATCAAAAGAAAAACTGATAAAAAACCAGAGAGTCC	1080
Db	1051	GCCAATGATAGCAACCTTAATGAGGAATCAAAAGAAAAACTGATAAAAAACCAGAGAGTCC	1110
QY	1081	AAGAGTCCAAACAAAAACTACCGTGCATGCGTGGAAAGCTGAAAGTTTAGATGAGACAGAAA	1140
Db	1111	AAGAGTCCAAACAAAAACTACCGTGCATGCGTGGAAAGCTGAAAGTTTAGATGAGACAGAAA	1170
QY	1141	TGAGGAGACACACTGAGGCTGGTTTCTTTCATGCTCCTTACCCCTGCCCCAGCTGGGAA	1200
Db	1171	TGAGGAGACACACTGAGGCTGGTTTCTTTCATGCTCCTTACCCCTGCCCCAGCTGGGAA	1230
QY	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCCTAACTGGAAATCAGC	1260
Db	1231	ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCCTAACTGGAAATCAGC	1290
QY	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTATTGTAAC	1320
Db	1291	TCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTATTGTAAC	1350
QY	1321	CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCACGGCCTTCTAGCCTGGCTAT	1380
Db	1351	CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCACGGCCTTCTAGCCTGGCTAT	1410
QY	1381	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAAAACATC	1440
Db	1411	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAAAACATC	1470
QY	1441	TCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1500
Db	1471	TCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC	1530
QY	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA	1560
Db	1531	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA	1590
QY	1561	GCTCTGAAAGAGAAAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA	1620
Db	1591	GCTCTGAAAGAGAAAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA	1650
QY	1621	AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
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QY	1681	TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1711	TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA	1770
QY	1741	GCAGGGACTGTAAAAACAGACAGGGTCAAAGTGTCTCTCTGAACACATGAGTTGGAAT	1800
Db	1771	GCAGGGACTGTAAAAACAGACAGGGTCAAAGTGTCTCTCTGAACACATGAGTTGGAAT	1830
QY	1801	CACCTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCCACTGCTGATATTTCTCT	1860
Db	1831	CACCTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCCACTGCTGATATTTCTCT	1890
QY	1861	AGGAAATATACTTTTACAAGTAACAAAAATAAAAA	1895
Db	1891	AGGAAATATACTTTTACAAGTAACAAAAATAAAAA	1925

RESULT 3
CR605021
LOCUS CR605021 1945 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI029YM23 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR605021 GI:50485828
VERSION HTC; CNSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1945)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 1945)
Genoscope.
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YM23"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 79.4%; Score 1883; DB 3; Length 1945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1883; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Db |||
63 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 122
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db |||
123 GTTCCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 182
QY 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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183 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 242
QY 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTTTTGC GTGCA 240
Db |||
243 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTTTTGC GTGCA 302
QY 241 GAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 300
Db |||
303 GAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 362
QY 301 GCGAACCAGCAGCTGAATTTTCACAGAAGCTTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360
Db |||
363 GCGAACCAGCAGCTGAATTTTCACAGAAGCTTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 422
QY 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db |||
423 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTTGAACCTTGCAGCTAT 482

QY 421 GGCTGGGTTGGAGATGGATTCTGTTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 480
Db |||
483 GGCTGGGTTGGAGATGGATTCTGTTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 542
QY 481 AAAAAATGGGGTGGGTGTCCTGATTTTGAAGGTTCCAGTGAGCGCAGACAGTTTGCAGCCTAT 540
Db |||
543 AAAAAATGGGGTGGGTGTCCTGATTTGAAGGTTCCAGTGAGCGCAGACAGTTTGCAGCCTAT 602
QY 541 TGTTACAACTCATCTGATACACTTGGACTAACTCGTGCAATTCAGAAATTTATGTGACGACAGT 600
Db |||
603 TGTTACAACTCATCTGATACACTTGGACTAACTCGTGCAATTCAGAAATTTATCACCAACCAA 662
QY 601 GATCCATATTCAACACTCAAACTGCAACACACAAACACAGAAATTTATGTGAGTGACAGT 660
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663 GATCCCATATTCAACACTCAAACTGCAACACACAAACACAGAAATTTATGTGAGTGACAGT 722
QY 661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCGCT 720
Db |||
723 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCGCT 782
QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTACAGAAAGTTTATTATG 780
Db |||
783 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTACAGAAAGTTTATTATG 842
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 840
Db |||
843 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 902
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCACGGCTCTGCTGAGTGTGCTCTCCTCTTC 900
Db |||
903 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCACGGCTCTGCTGAGTGTGCTCTCCTCTTC 962
QY 901 TTTGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960
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963 TTTGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 1022
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1023 TTTTACAAACAAGAATCAGCAGAAAGAAATGATCGAAACCAAACTAGTAAAGGAGGAGAAG 1082
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1083 GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACTGATAAAAAACCCAGAAGAGTCC 1142
QY 1081 AAGAGTCCAAGCAAAAACCTACCGTGGCATGCCTGGAAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db |||
1143 AAGAGTCCAAGCAAAAACCTACCGTGGCATGCCTGGAAAGCTGAAGTTTAGATGAGACAGAAA 1202
QY 1141 TGAGGAGACACACCTGAGGCTGGFTTCTTTTCATGCTCCTTACCTGCCCCCAGCTGGGGAA 1200
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1203 TGAGGAGACACACCTGAGGCTGGFTTCTTTTCATGCTCCTTACCTGCCCCCAGCTGGGGAA 1262
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1263 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAAGTGAATCAGC 1322
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1323 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1382
QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380
Db |||
1383 CCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1442
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAAGTGCAAGGACCTAAAAACATC 1440
Db |||
1443 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAAGTGCAAGGACCTAAAAACATC 1502
QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTGTGAAAGC 1500
Db |||
1503 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTGTGAAAGC 1562

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QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA 1560
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1563 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA 1622
QY 1561 GCTCTGAAAGAGAAACACGTTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAA 1620
Db GCTCTGAAAGAGAAACACGTTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAA 1682
QY 1621 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1742
QY 1681 TCTCTGTAAAGCTAAATAAGAAATAGAACAGCGCTGAGGATACGACAGTACACTGTCA 1740
Db TCTCTGTAAAGCTAAATAAGAAATAGAACAGCGCTGAGGATACGACAGTACACTGTCA 1802
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAAT 1800
Db GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAAT 1862
QY 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1922
QY 1861 AGGAAATATACTTTTACAAGTAA 1883
Db |||||||||||||||||||||||||||
1923 AGGAAATATACTTTTACAAGTAA 1945
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RESULT 4
CR597409
LOCUS CR597409 1898 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI067YG15 of Placenta Cot 25-normalized
of Homo sapiens (human) .
ACCESSION CR597409
VERSION CR597409.1 GI:50478216
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1898)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
```

```
REFERENCE 2 (bases 1 to 1898)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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FEATURES
Location/Qualifiers
source 1..1898
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YG15"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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ORIGIN

Query Match 78.8%; Score 1868; DB 3; Length 1898;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTAGCCTCAACATA 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
31 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTAGCCTCAACATA 90
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
91 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 150
QY 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
151 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 210
QY 181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
211 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 270
QY 241 GAAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGGGATCACCCCTTGAGCAAAAAG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
271 GAAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGGGATCACCCCTTGAGCAAAAAG 330
QY 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
331 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 390
QY 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
391 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 450
QY 421 GGCTGGGTTGAGATGGATTCTGGTCACTCTTAGGATTAGCCCAAACCCCAAGTGTGGG 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
451 GGCTGGGTTGAGATGGATTCTGGTCACTCTTAGGATTAGCCCAAACCCCAAGTGTGGG 510
QY 481 AAAAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
511 AAAAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 570
QY 541 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTTATGTGAGTGACAGT 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
571 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTTATGTGAGTGACAGT 630
QY 601 GATCCCATATTCAACACACTCAAACCTGCAACACACAAACAGAAATTTATGTGAGTGACAGT 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
631 GATCCCATATTCAACACACTCAAACCTGCAACACACAAACAGAAATTTATGTGAGTGACAGT 690
QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
691 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 750
QY 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATGATTTGTGCACAGAAAGTTTATG 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
751 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATGATTTGTGCACAGAAAGTTTATG 810
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG 840
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
811 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG 870
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTTGTCTCTCTTC 900
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
871 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTTGTCTCTCTTC 930
QY 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTTATGTGAAGGCCTTCCCT 960
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
931 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTTATGTGAAGGCCTTCCCT 990
QY 961 TTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAG 1020
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
991 TTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAG 1050
QY 1021 GCCAATGATAGCAACCCTAATGAGGAATCAAAAGAAACTGATAAAACCCAGAGAGTCC 1080
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1051 GCCAATGATAGCAACCCTAATGAGGAATCAAAAGAAACTGATAAAACCCAGAGAGTCC 1110
QY 1081 AAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAAGCTGGAAGCTTAAGATGAGACAGAAA 1140
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Db	1111	AAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCTGAAGTTAGATGAGACAGAAA	1170
Qy	1141	TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA	1200
Db	1171	TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA	1230
Qy	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGAGTCCACCCTTGGTTCCCTAAACTGGAATCAGC	1260
Db	1231	ATCAAAAGGGCCAAAGAACCAAGAAAGAGTCCACCCTTGGTTCCCTAAACTGGAATCAGC	1290
Qy	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC	1320
Db	1291	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC	1350
Qy	1321	CCTGTCTGGATCCTATCCTCCTACCTCCAAAAGCTTCCCACGGCCTTCTTAGCCTGGCTAT	1380
Db	1351	CCTGTCTGGATCCTATCCTCCTACCTCCAAAAGCTTCCCACGGCCTTCTTAGCCTGGCTAT	1410
Qy	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAAGTGCAAAGGACCTTAAACATC	1440
Db	1411	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAAAGTGCAAAGGACCTTAAACATC	1470
Qy	1441	TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGCTAGGTGGTTGAAAGC	1500
Db	1471	TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGCTAGGTGGTTGAAAGC	1530
Qy	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGTATCCGAGCTCAGACCCCTTCTTCA	1560
Db	1531	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGTATCCGAGCTCAGACCCCTTCTTCA	1590
Qy	1561	GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCCGGTAAGAGCAA	1620
Db	1591	GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCCGGTAAGAGCAA	1650
Qy	1621	AGAATGSGAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Db	1651	AGAATGSGAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1710
Qy	1681	TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGCTGAGGATACGACAGTACACTGTCA	1740
Db	1711	TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGCTGAGGATACGACAGTACACTGTCA	1770
Qy	1741	GCAGGACTGTAAACACAGACAGGTCAAAGTGTTTTCTCTGAAACACATTGAGTTGGAAT	1800
Db	1771	GCAGGACTGTAAACACAGACAGGTCAAAGTGTTTTCTCTGAAACACATTGAGTTGGAAT	1830
Qy	1801	CACGTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Db	1831	CACGTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1890
Qy	1861	AGGAAATA	1868
Db	1891	AGGAAATA	1898

RESULT 5
CR612000
LOCUS CR612000 1820 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI069YN02 of Placentia Cot 25-normalized of Homo sapiens (human).
ACCESSION CR612000
VERSION CR612000.1 GI:50492807
KEYWORDS HTC; CNSLT CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1820)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

REFERENCE	http://fulllength.invitrogen.com/ InvitroGen Corporation 1600		
AUTHORS	Faraday Avenue		
TITLE	2 (bases 1 to 1820)		
JOURNAL	Genoscope.		
	Direct Submission		
	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :		
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
FEATURES	Location/Qualifiers		
source	1..1820		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DI069YN02"		
	/tissue_type="Placentia Cot 25-normalized"		
	/plasmid="pCMVSPORT_6"		
ORIGIN			
	Query Match	76.7%;	Score 1820; DB 3; Length 1820;
	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 1820; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	63	TCAGAAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCA	122
Db	1	TCCGAAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCA	60
Qy	123	TCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTGGT	182
Db	61	TCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTGGT	120
Qy	183	GTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGA	242
Db	121	GTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGA	180
Qy	243	AGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGC	302
Db	181	AGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGC	240
Qy	303	GAACCAGCAGCTGAAATTTACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTT	362
Db	241	GAACCAGCAGCTGAAATTTACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTT	300
Qy	363	GGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAGCTATGG	422
Db	301	GGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAGCTATGG	360
Qy	423	CTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAA	482
Db	361	CTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAA	420
Qy	483	AAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTG	542
Db	421	AAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTG	480
Qy	543	TTACAACCTCATCTGATACTTGGACTTAACCTCGTGCATTCAGAAATATCACCACCAAAGA	602
Db	481	TTACAACCTCATCTGATACTTGGACTTAACCTCGTGCATTCAGAAATATCACCACCAAAGA	540
Qy	603	TCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTTATTGTAGTGACAGTAC	662
Db	541	TCCCATATTCAACACTCAAACCTGCAACACAAAACAGAAATTTATTGTAGTGACAGTAC	600
Qy	663	CTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTCTACTACTCCTCTGCTCC	722
Db	601	CTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTCTACTACTCCTCTGCTCC	660
Qy	723	AGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCAGAAAGTTTTTATGGA	782

Db 661 AGCTTCCACTTCTATTCCACGGAGAAAAAATTGAATTGTGTACAGAAAGTTTTTATGGA 720

QY 783 AACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAGCAGCATTCAGAA 842

Db 721 AACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAAAAATAAGCAGCATTCAGAA 780

QY 843 TGAAGCTGCTGGGTTTGAGAGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCTTCTT 902

Db 781 TGAAGCTGCTGGGTTTGAGAGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCTTCTT 840

QY 903 TGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTT 962

Db 841 TGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTT 900

QY 963 TACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGAGAGGC 1022

Db 901 TACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGAGAGGC 960

QY 1023 CAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACGTATAAAAAACCCAGAGAGTCCAA 1082

Db 961 CAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACGTATAAAAAACCCAGAGAGTCCAA 1020

QY 1083 GAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATG 1142

Db 1021 GAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATG 1080

QY 1143 AGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCCTGCCCCAGCTGGGGAAT 1202

Db 1081 AGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCCTGCCCCAGCTGGGGAAT 1140

QY 1203 CAAAAGGGCCAAAGAACCAAAGAAAGAAAGTCCACCCCTGGTTCCCTAACTGGGAATCAGCTC 1262

Db 1141 CAAAAGGGCCAAAGAACCAAAGAAAGAAAGTCCACCCCTGGTTCCCTAACTGGGAATCAGCTC 1200

QY 1263 AGGACTGCCATTTGGACTATGGAGTGCACCAAGAGAGATGCCCTTCTCCTTATTTGTAACCC 1322

Db 1201 AGGACTGCCATTTGGACTATGGAGTGCACCAAGAGAGATGCCCTTCTCCTTATTTGTAACCC 1260

QY 1323 TGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTATGT 1382

Db 1261 TGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTATGT 1320

QY 1383 CCTAATAATATCCCACCTGGGAGAAAGGAGTTTGGCAAAGTCAAGGACCTTAAACATCTC 1442

Db 1321 CCTAATAATATCCCACCTGGGAGAAAGGAGTTTGGCAAAGTCAAGGACCTTAAACATCTC 1380

QY 1443 ATCAGTATCCAGTGTGTAAGAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCA 1502

Db 1381 ATCAGTATCCAGTGTGTAAGAGAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCA 1440

QY 1503 AGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCOGCAGCTCAGACCCCTTCTTTCAGC 1562

Db 1441 AGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTCTTTCAGC 1500

QY 1563 TCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGCAAAAG 1622

Db 1501 TCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGCAAAAG 1560

QY 1623 AATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTTGAGACCTAATC 1682

Db 1561 AATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTTGAGACCTAATC 1620

QY 1683 TCTGTAAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTTCAGC 1742

Db 1621 TCTGTAAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTTCAGC 1680

QY 1743 AGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTCTGAACACATTTAGTTGGAATCA 1802

Db 1681 AGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTCTGAACACATTTAGTTGGAATCA 1740

QY 1803 CTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGTCTGATATTTTCTCTAG 1862

Db 1741 CTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGTCTGATATTTTCTCTAG 1800

QY 1863 GAAATATACTTTTACAAGTA 1882

Db 1801 GAAATATACTTTTACAAGTA 1820

RESULT 6

CR604450

LOCUS

DEFINITION

CR604450 1797 bp mRNA linear HTC 21-JUL-2004

full-length cDNA clone CS0DI065YD17 of Placenta Cot 25-normalized of Homo sapiens (human) .

ACCESSION

CR604450

VERSION

CR604450.1 GI:50485257

KEYWORDS

HTC; CNSLT_cDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1797)

AUTHORS

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue

REFERENCE

2 (bases 1 to 1797)

Genoscope.

AUTHORS

Direct Submission

TITLE

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

1..1797

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI065YD17"

/tissue type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 75.8%; Score 1797; DB 3; Length 1797;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 GAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTG 126

Db 1 GAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTG 60

QY 127 AGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACCATGGCCAGGTGCTTCAGCCTGGTGTG 186

Db 61 AGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACCATGGCCAGGTGCTTCAGCCTGGTGTG 120

QY 187 CTTCTCATTCCATCTGGACCACGAGGCTCTTGGTCCAAGGCTCTTTGGTGCAGAAAG 246

Db 121 CTTCTCATTCCATCTGGACCACGAGGCTCTTGGTCCAAGGCTCTTTGGTGCAGAAAG 180

QY 247 CTTTCCATCCAGGTGTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAAC 306

Db 181 CTTTCCATCCAGGTGTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAAC 240

QY 307 CAGCAGCTGAATTTACAGAAAGCTAAGAGGSCCTGTAGGCTGTGGACTGAAGTTTGGCC 366

Db 241 CAGCAGCTGAATTTACAGAAAGCTAAGAGGSCCTGTAGGCTGTGGGACTAAGTTTGGCC 300

QY 367 GGCAAGGACCAAGTTGAAACAGCCCTTGAAGAGCTAGCTTTGAAACTTGCAGCTATGGCTGG 426

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division of Invitrogen.

Location/Qualifiers

1. .1781

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="CS0DI039YJ06"

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ORIGIN

Query Match 75.1%; Score 1781; DB 3; Length 1781;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1781; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	102	CTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGAT	161
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QY	162	GGCCAGGTGCTTCAGCCTGGTGTTCCTTCACATTCCATCTGGACACGAGGCTCCTGGT	221
Db	61	GGCCAGGTGCTTCAGCCTGGTGTTCCTTCACATTCCATCTGGACACGAGGCTCCTGGT	120
QY	222	CCAAGGCTCTTTCGCGTCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGAT	281
Db	121	CCAAGGCTCTTTCGCGTCAGAAAGAGCTTTCATCCAGGTGTCAIGCAGAAATTATGGGGAT	180
QY	282	CACCCCTGTGAGCAAAAAGCGAACACGAGCTGAATTTTCACAGAAGCTAAGGAGGCGCTG	341
Db	181	CACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCGCTG	240
QY	342	TAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG	401
Db	241	TAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG	300
QY	402	CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAG	461
Db	301	CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAG	360
QY	462	CCCAAAACCCCAAGTGTGGGAAAAAATGGGTTGGGTGTCCTGATTTGGAAGGTTCCAGTGAG	521
Db	361	CCCAAAACCCCAAGTGTGGGAAAAAATGGGTTGGGTGTCCTGATTTGGAAGGTTCCAGTGAG	420
QY	522	CCGACAGTTTGACGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAATTCC	581
Db	421	CCGACAGTTTGACGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAATTCC	480
QY	582	AGAAATTATCACACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACAGA	641
Db	481	AGAAATTATCACACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACAGA	540
QY	642	ATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCC	701
Db	541	ATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCC	600
QY	702	TACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATTG	761
Db	601	TACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATTG	660
QY	762	TGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGA	821
Db	661	TGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGA	720
QY	822	AAATAAAGCAGCAATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGCT	881
Db	721	AAATAAAGCAGCAATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGCT	780
QY	882	AGTGCTTGCTCTCCTCTCTCTTTGGTGCTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAG	941
Db	781	AGTGCTTGCTCTCCTCTCTCTTTGGTGCTGCAGCTGGTCTTTGGAATTTTGCTATGTCAAAAG	840
QY	942	GTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACCAA	1001

Db	841	GTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAA	900
QY	1002	AGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATAGGGAATCAAAAGAAAACTGA	1061
Db	901	AGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATAGGGAATCAAAAGAAAACTGA	960
QY	1062	TAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACACTACCGTGCATGCTGGAAGCTGA	1121
Db	961	TAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACACTACCGTGCATGCTGGAAGCTGA	1020
QY	1122	AGTTTAGATGAGACAGAAAAATGAGGAGACACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTA	1181
Db	1021	AGTTTAGATGAGACAGAAAAATGAGGAGACACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTA	1080
QY	1182	CCCTGCCCCAGCTGGGGAAATCAAAAAGGGCCAAAAGAACCAAAAGAAAAGTCCACCCTTG	1241
Db	1081	CCCTGCCCCAGCTGGGGAAATCAAAAAGGGCCAAAAGAACCAAAAGAAAAGTCCACCCTTG	1140
QY	1242	GTTCTTAAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATG	1301
Db	1141	GTTCTTAAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATG	1200
QY	1302	CCCTTCTCCTTATTGTAACCCCTGCTGGATCCTATCCTCCTACCTCCAAAAGCTTCCCACG	1361
Db	1201	CCCTTCTCCTTATTGTAACCCCTGCTGGATCCTATCCTCCTACCTCCAAAAGCTTCCCACG	1260
QY	1362	GCCTTTCTAGCCTGGCTATGTCTCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGCAAAG	1421
Db	1261	GCCTTTCTAGCCTGGCTATGTCTCTAATAATATCCCACCTGGGAGAAAGGAGTTTTCGCAAAG	1320
QY	1422	TGCAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGA	1481
Db	1321	TGCAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGA	1380
QY	1482	GGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGC	1541
Db	1381	GGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGC	1440
QY	1542	AGCTCAGACCCCTTCTTTCAGCTCTGAAAAGAGAAAAACACGTATCCACCTGACATGTCTTTC	1601
Db	1441	AGCTCAGACCCCTTCTTTCAGCTCTGAAAAGAGAAAAACACGTATCCACCTGACATGTCTTTC	1500
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Db	1501	TGAGCCCGGTAAGAGCAAAAAGAAATGCGCAGAAAAAGTTTAGCCCTCGAAAAGCCATGGAGATT	1560
QY	1662	CTCATAACTTGAGACCTTAATCTCTGTAAAGCTAAAAATAAAGAATAAGAACCAAGGCTGAGG	1721
Db	1561	CTCATAACTTGAGACCTTAATCTCTGTAAAGCTAAAAATAAAGAATAAGAACCAAGGCTGAGG	1620
QY	1722	ATACGACAGTACACTGTCTCAGCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTCT	1781
Db	1621	ATACGACAGTACACTGTCTCAGCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTCT	1680
QY	1782	GAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTAC	1841
Db	1681	GAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTAC	1740
QY	1842	CACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAAGTA	1882
Db	1741	CACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAAGTA	1781
RESULT 9			
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LOCUS			
DEFINITION			
full-length cDNA clone CS0DI079YK19 of Placenta Cot 25-normalized			
of Homo sapiens (human).			
ACCESSION			
CR622723			
VERSION			
CR622723.1 GI:50503530			
KEYWORDS			
HTC; CNSLT_cDNA.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 1765)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE	2 (bases 1 to 1765)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/clone="CSODI079YK19"
	/tissue_type="Placenta Cot 25-normalized"
	/plasmid="pCMVSPORT_6"
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Best Local Similarity 100.0%; Pred. No. 0;	
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 CAGAAATTATCACCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAG 60
Qy	641 AATTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 700
Db	61 AATTATTGTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 120
Qy	701 CTACTACTACTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTT 760
Db	121 CTACTACTACTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTT 180
Qy	761 GTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCAATTGTTG 820
Db	181 GTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCAATTGTTG 240
Qy	821 AAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTTGCCCCACGGCTCTGC 880
Db	241 AAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTTGCCCCACGGCTCTGC 300
Qy	881 TAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAAA 940
Db	301 TAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAAA 360
Qy	941 GGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCA 1000
Db	361 GGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCA 420
Qy	1001 AAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCATATGAGGAATCAAAGAAACTG 1060
Db	421 AAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCATATGAGGAATCAAAGAAACTG 480
Qy	1061 ATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTG 1120
Db	481 ATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTG 540
Qy	1121 AAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTT 1180
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Qy	1181 ACCCTGCCCCAGCTGGGAAATCAAAGGGGCCAAAGAACCAAAAGAAAGAAAGTCCACCCTT 1240
Db	601 ACCCTGCCCCAGCTGGGAAATCAAAGGGGCCAAAGAACCAAAAGAAAGAAAGTCCACCCTT 660
Qy	1241 GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCACAAAGAGAAAT 1300
Db	661 GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCACAAAGAGAAAT 720
Qy	1301 GCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCAC 1360
Db	721 GCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCAC 780
Qy	1361 GGCTTTCTAGCCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTTTGCAAA 1420
Db	781 GGCTTTCTAGCCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTTTGCAAA 840
Qy	1421 GTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTG 1480
Db	841 GTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTG 900
Qy	1481 AGGCTAGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTTCTCTACTGATCCG 1540
Db	901 AGGCTAGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTTCTCTACTGATCCG 960
Qy	1541 CAGCTCAGACCCCTTTCTTCAGCTCTGAAAAGAGAAACACGTATCCCACCTGACATGTCCTT 1600
Db	961 CAGCTCAGACCCCTTTCTTCAGCTCTGAAAAGAGAAACACGTATCCCACCTGACATGTCCTT 1020
Qy	1601 CTGAGCCCGGTAAAGCAAAAAGATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGAT 1660
Db	1021 CTGAGCCCGGTAAAGCAAAAAGATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGAT 1080
Qy	1661 TCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACCAAGGCTGAG 1720
Db	1081 TCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACCAAGGCTGAG 1140
Qy	1721 GATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGGTCAAAGTGTTCCTC 1780
Db	1141 GATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGGTCAAAGTGTTCCTC 1200
Qy	1781 TGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTA 1840
Db	1201 TGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTA 1260
Qy	1841 CCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTT 1900
Db	1261 CCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTT 1320
Qy	1901 ATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAT 1960
Db	1321 ATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAT 1380
Qy	1961 TTGTTTAAAAAGTAATAAAATTCACACAAACATTTGCTGAATAGCTACTATATGTCAGTG 2020
Db	1381 TTGTTTAAAAAGTAATAAAATTCACACAAACATTTGCTGAATAGCTACTATATGTCAGTG 1440
Qy	2021 CTGTGCAAGGTATTACACTCTGTAATTGAATATATTCTCCTCAAAAAATTGCACATAGTAG 2080
Db	1441 CTGTGCAAGGTATTACACTCTGTAATTGAATATATTCTCCTCAAAAAATTGCACATAGTAG 1500
Qy	2081 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAAA 2140
Db	1501 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAAA 1560
Qy	2141 CTAATTTTATTTTTTTCAGACTAATCTTTATTCATTTTCTCTAATATGSCAACCATTAT 2200
Db	1561 CTAATTTTATTTTTTTCAGACTAATCTTTATTCATTTTCTCTAATATGSCAACCATTAT 1620
Qy	2201 AACCTTAATTTTATTTAATACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCA 2260
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QY 2261 CATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCCTTTTTCACAAAGAAGGGA 2320
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RESULT 10
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LOCUS
DEFINITION
full-length cDNA clone CS0DI030YC09 of Placenta Cot 25-normalized
of Homo sapiens (human) .
CR599107
ACCESSION
VERSION
CR599107.1 GI:50479914
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1823)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue

REFERENCE
2 (bases 1 to 1823)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
Location/Qualifiers
source
1. .1823
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI030YC09"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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Best Local Similarity 92.8%; Pred. No. 0;
Matches 1741; Conservative 0; Mismatches 55; Indels 80; Gaps 2;
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61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
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QY 481 AAAATGGGTTGGTGTCTCTGATTTCGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
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Qy 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db 1748 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1807
Qy 1861 AGGAAATATACTTTTA 1876
Db 1808 AGGAAATATACTTTTA 1823
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RESULT 11
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LOCUS
DEFINITION
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ACCESSION
    CR598440
VERSION
    CR598440.1 GI:50479247
KEYWORDS
    HTC; CNSLT cDNA.
SOURCE
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ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 1113)
    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
    Full-length cDNA libraries and normalization
    Unpublished
    Contact : Feng Liang Email : fliang@lifetech.com URL :
    http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
    Faraday Avenue
REFERENCE
    2 (bases 1 to 1113)
    Genoscope.
    Direct Submission
    Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
    BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
    - web : www.genoscope.cns.fr)
COMMENT
    1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime
    end enriched, double-strand cDNA was digested with Not I and cloned
    into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
    was normalized. Library was constructed by Life Technologies, a
    division of Invitrogen.
    Location/Qualifiers
FEATURES
    source
    1..1113
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DE007YF17"
    /tissue_type="Placenta"
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/plasmid="pCMVSPORT_6"
ORIGIN
    Query Match 46.9%; Score 1113; DB 3; Length 1113;
    Best Local Similarity 100.0%; Pred. No. 4.2e-265;
    Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1240 TGGTTCTTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAA 1299
Db 1 TGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAA 60
Qy 1300 TGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTTACCTCCAAAGCTTCCCA 1359
Db 61 TGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTTACCTCCAAAGCTTCCCA 120
Qy 1360 CGGCCTTTCTAGCCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 1419
Db 121 CGGCCTTTCTAGCCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 180
Qy 1420 AGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCT 1479
Db 181 AGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCT 240
Qy 1480 GAGGCTAGTGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCC 1539
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Qy 1540 GCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAAAACACGTATCCCACCTGACATGCTCCT 1599
Db 301 GCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAAAACACGTATCCCACCTGACATGCTCCT 360
Qy 1600 TCTGAGCCCGGTAAAGACCAAGAAATGGCAGAAAAAGTTTAGCCCCCTGAAAAGCCATGGAGA 1659
Db 361 TCTGAGCCCGGTAAAGACCAAGAAATGGCAGAAAAAGTTTAGCCCCCTGAAAAGCCATGGAGA 420
Qy 1660 TTCTCATAACTTTGAGACCTTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACAGGCTGA 1719
Db 421 TTCTCATAACTTTGAGACCTTAATCTCTGTAAAGCTAAAAATAAGAAATAGAACAGGCTGA 480
Qy 1720 GGATACGACAGTACACTGTGAGAGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCT 1779
Db 481 GGATACGACAGTACACTGTGAGAGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCT 540
Qy 1780 CTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCT 1839
Db 541 CTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCT 600
Qy 1840 ACCACTGCTGATATTTTCTCTAGGAAATATACCTTTTACAAGTAACAAAAATAAAAACTCT 1899
Db 601 ACCACTGCTGATATTTTCTCTAGGAAATATACCTTTTACAAGTAACAAAAATAAAAACTCT 660
Qy 1900 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAA 1959
Db 661 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAA 720
Qy 1960 TTTGTTTAAAAAGTAATAAAAAATTCACAAAAATTTGCTGAAATAGCTACTATATGTCAAGT 2019
Db 721 TTTGTTTAAAAAGTAATAAAAAATTCACAAAAATTTGCTGAAATAGCTACTATATGTCAAGT 780
Qy 2020 GCTGTGCAAGGTATTACACTCTGTAATTGAATATATTCTCTCAAAAAATTGCACATAGTA 2079
Db 781 GCTGTGCAAGGTATTACACTCTGTAATTGAATATATTCTCTCAAAAAATTGCACATAGTA 840
Qy 2080 GAACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAA 2139
Db 841 GAACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAA 900
Qy 2140 ACTAATTTTTTATTTTGTCTGAGACTAATCTTATTCATTTTTCTCTAATATGGCAACCATTA 2199
Db 901 ACTAATTTTTTATTTTGTCTGAGACTAATCTTATTCATTTTTCTCTAATATGGCAACCATTA 960
Qy 2200 TAACCTTAATTTATTTAATAACATACCTTAAGAGTACATTGTTACCTCTATATACCAAGC 2259
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Db 961 TAACCTTAATTATTATTAAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGC 1020

QY 2260 ACATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGG 2319

Db 1021 ACATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGG 1080

QY 2320 ACTGAGAGATCGAATAATATTGTGACAAAAA 2352

Db 1081 ACTGAGAGATCGAATAATATTGTGACAAAAA 1113

RESULT 12

AL574194/c

LOCUS

DEFINITION

AL574194 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI039YJ06 3-PRIME, mRNA sequence.

ACCESSION

AL574194

VERSION

AL574194.3 GI:46247285

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1130)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:31295529.

Contact: Genoscope

Genoscope - Centre National de Sequencage

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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DI039DE03NP1&c=5952.r.

FEATURES

source

1..1130

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI039YJ06"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.4%; Score 1053.4; DB 1; Length 1130;

Best Local Similarity 97.3%; Pred. No. 2.7e-250;

Matches 1083; Conservative 8; Mismatches 20; Indels 2; Gaps 2;

QY 746 GAAAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAA 805

Db 1130 GAGAAAAAAATTGAATTKTKACAGAAG-TTTTATGRAAACTAGCACCATGTCTACAGAAA 1072

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QY 866 TCCCCACGGCTCTGCTAGTGTCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGAT 925

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QY 926 TTTTGCTATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAG 985

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Db 832 AATCAAGAAGAAACTGATAAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC 773

QY 1106 GATGCCTGGAAGCTGAAGTTTATAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTT 1165

Db 772 GATGCCTGGAAGCTGAAGTTTATAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTT 713

QY 1166 TCCTTCATGCTCCTTACCCCTGCCAGCTGGGGAATCAAAAGGGCAAGAAACCAAAGA 1225

Db 712 TCCTTCATGCTCCTTACCCCTGCCAGCTGGGGAATCAAAAGGGCAAGAAACCAAAGA 653

QY 1226 AGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAG 1285

Db 652 AGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAG 593

QY 1286 TGCACCAAGAGAAATGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCTACC 1345

Db 592 TGCACCAAGAGAAATGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCTACC 533

QY 1346 TCCAAAGCTTCCCACGGCCTTTCAGCCTGGCTATGTCCTAATAATATCCCACCTGGGAGA 1405

Db 532 TCCAAAGCTTCCCACGGCCTTTCAGCCTGGCTATGTCCTAATAATATCCCACCTGGGAGA 473

QY 1406 AAGGAGTTTGCAAAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGG 1465

Db 472 AAGGAGTTTGCAAAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGG 413

QY 1466 CCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTT 1525

Db 412 CCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTT 353

QY 1526 TCTCTACTGATTCCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCC 1585

Db 352 TCTCTACTGATTCCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCC 293

QY 1586 ACCTGACATGTCTTCTGAGCCCCGGTAAGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCT 1645

Db 292 KCCTGACATGTCTTCTGAGCCCCGGTAAGAGCAAAAGAATGGKGGDARRGTTTAGCCCCCK 233

QY 1646 GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAA 1705

Db 232 GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAA 173

QY 1706 TAGAACAAAGGCTGAGGATACGACAGTACACTGTTCAGCAGGACTGTAAACACAGACAGGG 1765

Db 172 TAGAACAAAGGCTGAGGATACGACAGTACACTGTTCAGCAGGACTGTAAACACAGACAGGG 113

QY 1766 TCAAAGTGTTTCTCTGAACACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTAC 1825

Db 112 TCAAAGTGTTTCTCTGAACACACATTGAGTTGGAATCACTGTTTAGCACACACACACTTAC 53

QY 1826 TTTTCTCTGGTCTCTACCACTGCTGATATTTTCT 1858

Db 52 TTTYTCTGGTCTCTACCACTGCTGATTTTCTCT 20

RESULT 13

AL550279

LOCUS

DEFINITION

AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI039YJ06 5-PRIME, mRNA sequence.

ACCESSION

AL550279

VERSION

AL550279.3 GI:45750655

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1091)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31272096.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI039DE03QPI&c=5952.r.

FEATURES
source
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/clone="CS0DI039YJ06"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.0%; Score 1043.8; DB 1; Length 1091;
Best Local Similarity 98.9%; Pred. No..6.5e-248;
Matches 1057; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 102 CTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCTCGCTCTGAAGGGTAGGCACGAT 161
Db 1 CTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCTCGCTCTGAAGGGTAGGCACGAT 60
QY 162 GGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGT 221
Db 61 GGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGT 120
QY 222 CCAAGGCTCTTTCGGTGCAGAAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGGAT 281
Db 121 CCAAGGCTCTTTCGGTGCAGAAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGGAT 180
QY 282 CACCCCTGTGAGCAAAAAGCGAACACAGCAGTGAATTTTCACAGAAGCTTAAGGAGGCCTG 341
Db 181 CACCCCTGTGAGCAAAAAGCGAACACAGCAGTGAATTTTCACAGAAGCTTAAGGAGGCCTG 240
QY 342 TAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 401
Db 241 TAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 300
QY 402 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAG 461
Db 301 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAG 360
QY 462 CCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGTCTCTGATTTTGGAAAGTTCCAGTGAG 521
Db 361 CCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGTCTCTGATTTTGGAAAGTTCCAGTGAG 420
QY 522 CCGACAGTTTGCAGCCTATTGTTACAACCTCACTCTGATCTTGGACTAATCGTGCATTCC 581
Db 421 CCGACAGTTTGCAGCCTATTGTTACAACCTCACTCTGATCTTGGACTAATCGTGCATTCC 480
QY 582 AGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACACAGA 641
Db 481 AGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACACAGA 540
QY 642 ATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCC 701

Db 541 ATTTATTGTCACTGACAGTACCTACTCGTGGCATCCCCTTACTCTACAATACCTGCCCC 600
QY 702 TACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATGATTG 761
Db 601 TACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATGATTG 660
QY 762 TGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGA 821
Db 661 TGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGA 720
QY 822 AAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGCTCTGCT 881
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QY 882 AGTCTTGTCTCTCTCTTCTTTGGTGTCTGACGTGGTCTTGGATTTTGGTATGTCAAAAG 941
Db 781 AGTCTTGTCTCTCTCTTCTTTGGTGTCTGACGTGGTCTTGGATTTTGGTATGTCAAAAG 840
QY 942 GTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAA 1001
Db 841 GTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAA 900
QY 1002 AGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGA 1061
Db 901 AGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGA 960
QY 1062 TAAAAACCCGAAAGAGTCCAAGAGTCCAAGCAAAAAACTACCGTGCATGCTGGAAGCTGA 1121
Db 961 TAAAAACCCGAAAGAGTCCAAGAGTCCAAGCAAAAAACTACCGTGCATGCTGGAAGCTGA 1020
QY 1122 AGTTTAGATGACACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTT 1170
Db 1021 AGTTTAGATGAGAMAGAAATRAG--AGAMACACTGAGGCTGGTTCTTY 1067

RESULT 14
AL541927
LOCUS
DEFINITION
AL541927 Homo sapiens PLACENTA Homo sapiens cDNA clone EST 24-MAR-2004
5-PRIME, mRNA sequence.
ACCESSION
AL541927
VERSION
AL541927.3 GI:45717503
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1101)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30546572.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE007CC09QPI&c=5952.r.

FEATURES
Location/Qualifiers
1. .1101
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/clone="CS0DE007YF17"
/tissue_type="PLACENTA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match		42.2%;	Score 1000;	DB 1;	Length 1101;
Best Local Similarity		98.1%;	Pred. No. 5e-237;		
Matches 1026;		Conservative 6;	Mismatches 11;	Indels 3;	Gaps 2;
Qy	1260	CTCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAA	1319		
Db	19	CCCCGGATTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAA	78		
Qy	1320	CCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTA	1379		
Db	79	CCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTA	138		
Qy	1380	TGTCCTAATAATATCCCACCTGGGAGAAAAGGAGTTTTCGAAAAGTGCAGGACCTAAAAACAT	1439		
Db	139	TGTCCTAATAATATCCCACCTGGGAGAAAAGGAGTTTTCGAAAAGTGCAGGACCTAAAAACAT	198		
Qy	1440	CTCATCAGTATCCAGTGGTGTAAAAAGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAG	1499		
Db	199	CTCATCAGTATCCAGTGGTGTAAAAAGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAG	258		
Qy	1500	CCAAGGAGTCACTGAGACCAAGGCTTTCCTACTGATTCGCGAGCTCAGACCCCTTCTTC	1559		
Db	259	CCAAGGAGTCACTGAGACCAAGGCTTTCCTACTGATTCGCGAGCTCAGACCCCTTCTTC	318		
Qy	1560	AGCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTCCCTCTGAGCCCGTAAGAGCAA	1619		
Db	319	AGCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTCCCTCTGAGCCCGTAAGAGCAA	378		
Qy	1620	AAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTA	1679		
Db	379	AAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTA	438		
Qy	1680	ATCTCTGTAAGCTTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTC	1739		
Db	439	ATCTCTGTAAGCTTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTC	498		
Qy	1740	AGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAAACACATTGAGTTGGAA	1799		
Db	499	AGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAAACACATTGAGTTGGAA	558		
Qy	1800	TCACTGTTTAGAACACACACACTTACTTTTCTTGGTCTCTACCACTGCTGATATTTTCTC	1859		
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Qy	1860	TAGGAAATATACTTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATC	1919		
Db	619	TAGGAAATATACTTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATC	678		
Qy	1920	TGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTTGTTTAAAAAGTAATAA	1979		
Db	679	TGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTTGTTTAAAAAGTAATAA	738		
Qy	1980	ATTCAACAAACATTTGCTGTAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACT	2039		
Db	739	ATTCAACAAACATTTGCTGTAATAGCTACTATATGTCAAGTCTGTGCAAGGTATTACACT	798		
Qy	2040	CTGTAATTGAATATTATTCCTCAAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTA	2099		
Db	799	CTGTAATTGAATATTATTCCTCAAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTA	858		
Qy	2100	TTTTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAAACTAATTTTATTTTTGTCTG	2159		
Db	859	TTTTTTTTCAGTTTGTATATTCTAGCTTATCTACTTCCAAACTAATTTTATTTTTGTCTG	918		
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Qy	2220	CATACCTAAGAAAGTACATTGTTACCTCTATATATACCAAGCACATTTTAAAAAGTGCCATTA	2279	
Db	979	CATACCTAAG-AGKACATTGTTACCTCTATATATACCAAGMCM--TTTAAAAAGTGCMTTA	1035	
Qy	2280	ACAAATGTATCACTAGCCCTCCTTTT	2305	
Db	1036	ACAAATGTATCACTAGCCCTYCTTTT	1061	
RESULT 15				
AL550621				
LOCUS				
DEFINITION	AL550621	Homo sapiens	PLACENTA COT 25-NORMALIZED	linear EST 25-MAR-2004
		clone CS0DI058YN14	5-PRIME, mRNA sequence.	
ACCESSION	AL550621			
VERSION	AL550621.3	GI:45750987		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 1045)		
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31272438.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
	end enriched, double-strand cDNA was digested with Not I and cloned			
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
	was normalized. Library was constructed by Life Technologies, a			
	division of Invitrogen. This sequence belongs to sequence cluster			
	5952.r			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/cdna?s=CS0DI058DG07QP1&c=5952.r.			
FEATURES				
source	Location/Qualifiers			
	1. .1045			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
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ORIGIN				
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OM nucleic - nucleic search, using sw model

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 (without alignments)
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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C 276	387.6	16.3	820	15	US-10-079-111-5	Sequence 5, Appli
C 277	334	14.1	339	15	US-10-291-634-11	Sequence 11, Appl
C 278	328.6	13.9	559	15	US-10-079-111-3	Sequence 3, Appli
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C 286	239	10.1	241	13	US-10-007-805-324	Sequence 324, App
C 287	239	10.1	241	14	US-10-076-622-324	Sequence 324, App
C 288	239	10.1	241	16	US-10-124-805-324	Sequence 324, App
C 289	238	10.0	308	9	US-09-880-107-1687	Sequence 1687, Ap
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C 294	238	10.0	308	21	US-10-843-641A-2134	Sequence 2134, Ap
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c 298	237	10.0	241	10	US-09-551-621-323	Sequence 323, App	440	50	2.1	50	22	US-10-797-366-205	Sequence 205, App
c 299	237	10.0	241	13	US-10-007-805-323	Sequence 323, App	441	50	2.1	50	22	US-10-970-823-205	Sequence 205, App
c 300	237	10.0	241	14	US-10-076-622-323	Sequence 323, App	c 442	50	2.1	37515	19	US-10-433-793-28	Sequence 28, Appl
c 301	237	10.0	241	16	US-10-124-805-323	Sequence 323, App	c 443	49.6	2.1	7137	21	US-10-956-157-562	Sequence 562, App
c 302	226.2	9.5	239	9	US-09-954-456-913	Sequence 913, App	444	49.6	2.1	7137	22	US-10-287-436A-235	Sequence 235, App
c 303	226.2	9.5	239	9	US-09-954-456-1513	Sequence 1513, Ap	c 445	49.4	2.1	8305	15	US-10-311-455-1542	Sequence 1542, Ap
c 304	226.2	9.5	239	9	US-09-880-107-725	Sequence 725, App	446	49.4	2.1	47841	18	US-10-433-580-3	Sequence 3, Appli
c 305	226.2	9.5	239	9	US-09-954-531-875	Sequence 875, App	c 447	49.4	2.1	73334	15	US-10-311-455-2098	Sequence 2098, Ap
c 306	226.2	9.5	239	9	US-09-954-531-1285	Sequence 1285, Ap	c 448	49.4	2.1	73334	18	US-10-240-589C-128	Sequence 128, App
c 307	226.2	9.5	239	15	US-10-291-634-14	Sequence 14, Appl	c 449	49.2	2.1	7461	15	US-10-311-455-1757	Sequence 1757, Ap
c 308	226.2	9.5	239	21	US-10-843-641A-1942	Sequence 1942, Ap	c 450	49.2	2.1	21354	18	US-10-221-714A-512	Sequence 512, App
c 309	226.2	9.5	239	21	US-10-843-641A-2352	Sequence 2352, Ap	c 451	49.2	2.1	302250	9	US-09-962-832-154	Sequence 154, App
c 310	226.2	9.5	239	21	US-10-843-641A-3940	Sequence 3940, Ap	c 452	49.2	2.1	302250	21	US-10-843-641A-6040	Sequence 6040, Ap
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312	212.2	8.9	279	15	US-10-079-111-4	Sequence 4, Appli	454	49	2.1	6106	15	US-10-311-455-1445	Sequence 1445, Ap
313	191.4	8.1	466	15	US-10-291-634-13	Sequence 13, Appl	455	49	2.1	6106	17	US-10-257-166-113	Sequence 113, App
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316	160	6.7	498	15	US-10-291-634-15	Sequence 15, Appl	458	49	2.1	15767	15	US-10-240-485-106	Sequence 106, App
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c 322	60	2.5	60	11	US-09-908-975-10869	Sequence 10869, A	c 464	48.8	2.1	27890	21	US-10-741-600-17751	Sequence 17751, A
c 323	58.2	2.5	641	10	US-09-969-034-389	Sequence 389, App	c 465	48.8	2.1	32392	21	US-10-706-635-27	Sequence 27, Appl
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c 325	56.8	2.4	8056	20	US-10-473-126-240	Sequence 240, App	467	48.8	2.1	126872	21	US-10-741-600-17885	Sequence 17885, A
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c 330	55	2.3	83391	19	US-10-433-793-123	Sequence 123, App	c 472	48.6	2.0	11172	15	US-10-311-455-2026	Sequence 2026, Ap
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c 333	53.4	2.3	3673778	16	US-10-312-841-1	Sequence 1, Appli	c 475	48.4	2.0	643	18	US-10-424-599-106363	Sequence 106363,
334	53.2	2.2	622	18	US-10-424-599-3380	Sequence 3380, Ap	c 476	48.4	2.0	6775	19	US-10-433-793-190	Sequence 190, App
c 335	53	2.2	6544	14	US-10-239-676-45	Sequence 45, Appl	477	48.4	2.0	640681	9	US-09-790-988-1	Sequence 1, Appli
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c 338	53	2.2	13574	15	US-10-311-455-1290	Sequence 1290, Ap	480	48.2	2.0	972	9	US-09-764-853-156	Sequence 156, App
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c 352	51.4	2.2	3673778	16	US-10-312-841-2	Sequence 2, Appli	c 494	48.2	2.0	2694	14	US-10-050-704-40	Sequence 40, Appl
353	51	2.2	20579	19	US-10-433-793-104	Sequence 104, App	c 495	48.2	2.0	2694	19	US-10-798-512-40	Sequence 40, Appl
c 354	50.8	2.1	5407	15	US-10-311-455-2063	Sequence 2063, Ap	496	48.2	2.0	2730	10	US-09-759-130B-329	Sequence 329, App
c 355	50.6	2.1	392	9	US-09-960-352-4808	Sequence 4808, Ap	497	48.2	2.0	2730	14	US-10-189-123-59	Sequence 59, Appl
c 356	50.6	2.1	5504	17	US-10-221-613-270	Sequence 270, App	498	48.2	2.0	2730	16	US-10-188-495-59	Sequence 59, Appl
357	50.4	2.1	8056	20	US-10-473-126-240	Sequence 240, App	499	48.2	2.0	2730	19	US-10-741-790-329	Sequence 329, App
c 358	50.4	2.1	12237	15	US-10-311-455-2331	Sequence 2331, Ap	500	48.2	2.0	2878	17	US-10-453-420-7	Sequence 7, Appli
361	50	2.1	50	9	US-09-905-291A-205	Sequence 205, App	501	48.2	2.0	2878	17	US-10-295-027-259	Sequence 259, App
429	50	2.1	50	16	US-10-299-976-205	Sequence 205, App	502	48.2	2.0	3438	18	US-10-312-352-60	Sequence 60, Appl
430	50	2.1	50	16	US-10-299-937-205	Sequence 205, App	511	48.2	2.0	3476	14	US-10-237-535-51	Sequence 51, Appl
431	50	2.1	50	17	US-10-298-993-205	Sequence 205, App	520	48.2	2.0	3476	14	US-10-239-196-51	Sequence 51, Appl
432	50	2.1	50	17	US-10-448-923-205	Sequence 205, App	611	48.2	2.0	3476	21	US-10-936-626-11	Sequence 11, Appl
433	50	2.1	50	17	US-10-449-656-205	Sequence 205, App	612	48.2	2.0	3476	21	US-10-938-061-11	Sequence 11, Appl
434	50	2.1	50	17	US-10-448-713-205	Sequence 205, App	c 613	48.2	2.0	5430	14	US-10-091-438-279	Sequence 279, App
435	50	2.1	50	17	US-10-425-447-205	Sequence 205, App	c 614	48.2	2.0	6106	15	US-10-311-455-1445	Sequence 1445, Ap
436	50	2.1	50	19	US-10-215-371-205	Sequence 205, App	c 615	48.2	2.0	6106	17	US-10-257-166-113	Sequence 113, App
437	50	2.1	50	19	US-10-711-187-205	Sequence 205, App	c 616	48.2	2.0	6106	18	US-10-221-714A-151	Sequence 151, App
438	50	2.1	50	21	US-10-963-467-205	Sequence 205, App	617	48.2	2.0	9646	17	US-10-462-261-1	Sequence 1, Appli

618	48.2	2.0	143239	20	US-10-723-860-546	Sequence 546, App	C 691	46.2	1.9	5880	15	US-10-240-453-51	Sequence 51, Appl
619	48.2	2.0	143239	22	US-10-756-149-566	Sequence 566, App	C 692	46.2	1.9	5880	18	US-10-221-714A-53	Sequence 53, Appl
C 620	48	2.0	5362	15	US-10-240-453-288	Sequence 288, App	C 693	46.2	1.9	5981	15	US-10-311-455-1736	Sequence 1736, Ap
C 621	47.8	2.0	650	13	US-10-027-632-231715	Sequence 231715,	C 694	46.2	1.9	6831	15	US-10-311-455-1460	Sequence 1460, Ap
C 622	47.8	2.0	650	13	US-10-027-632-231716	Sequence 231716,	C 695	46.2	1.9	12507	15	US-10-311-455-272	Sequence 272, App
C 623	47.8	2.0	650	13	US-10-027-632-231717	Sequence 231717,	C 696	46.2	1.9	15743	15	US-10-240-453-270	Sequence 270, App
C 624	47.8	2.0	650	17	US-10-027-632-231715	Sequence 231715,	C 697	46.2	1.9	19380	17	US-10-221-613-390	Sequence 390, App
C 625	47.8	2.0	650	17	US-10-027-632-231716	Sequence 231716,	C 698	46.2	1.9	29993	21	US-10-482-823-5	Sequence 5, Appli
C 626	47.8	2.0	650	17	US-10-027-632-231717	Sequence 231717,	C 699	46.2	1.9	50000	21	US-10-706-635-23	Sequence 23, Appl
C 627	47.6	2.0	9965	15	US-10-311-455-1500	Sequence 1500, Ap	C 700	46.2	1.9	115218	21	US-10-278-698-255	Sequence 255, App
628	47.6	2.0	12578	18	US-10-221-714A-382	Sequence 382, App	C 701	46.2	1.9	115218	21	US-10-278-698-769	Sequence 769, App
629	47.6	2.0	12781	18	US-10-221-714A-107	Sequence 107, App	C 702	46.2	1.9	119036	21	US-10-741-600-1721	Sequence 17721, A
630	47.6	2.0	12781	18	US-10-240-589C-37	Sequence 37, Appl	C 703	46.2	1.9	337344	19	US-10-388-838-58	Sequence 58, Appl
631	47.6	2.0	32392	21	US-10-706-635-27	Sequence 27, Appl	C 704	46	1.9	3057	16	US-10-349-680-148	Sequence 148, App
632	47.4	2.0	40862	15	US-10-311-455-2046	Sequence 2046, Ap	C 705	46	1.9	4661	19	US-10-433-793-51	Sequence 51, Appl
633	47.4	2.0	161671	15	US-10-017-117-1	Sequence 1, Appli	C 706	46	1.9	6113	15	US-10-311-455-403	Sequence 403, App
C 634	47.2	2.0	960	14	US-10-198-846-6381	Sequence 6381, Ap	C 707	46	1.9	6113	18	US-10-240-589C-13	Sequence 13, Appl
635	47.2	2.0	5413	18	US-10-221-714A-418	Sequence 418, App	C 708	46	1.9	9095	19	US-10-433-793-92	Sequence 92, Appl
636	47.2	2.0	6074	15	US-10-240-453-248	Sequence 248, App	C 709	46	1.9	9524	15	US-10-311-455-812	Sequence 812, App
C 637	47.2	2.0	6174	18	US-10-221-714A-155	Sequence 155, App	C 710	46	1.9	9524	17	US-10-257-166-76	Sequence 76, Appl
638	47.2	2.0	6191	15	US-10-311-455-1189	Sequence 1189, Ap	C 711	46	1.9	14316	17	US-10-221-613-408	Sequence 408, App
C 639	47.2	2.0	7669	15	US-10-311-455-601	Sequence 601, App	C 712	46	1.9	15587	17	US-10-221-613-198	Sequence 198, App
C 640	47.2	2.0	17137	15	US-10-311-455-164	Sequence 164, App	C 713	46	1.9	16217	15	US-10-311-455-598	Sequence 598, App
641	47.2	2.0	17144	18	US-10-221-714A-387	Sequence 387, App	C 714	46	1.9	21537	15	US-10-311-455-1971	Sequence 1971, Ap
C 642	47.2	2.0	38678	22	US-10-893-315-136	Sequence 136, App	C 715	45.8	1.9	546	22	US-10-893-315-1192	Sequence 1192, Ap
C 643	47.2	2.0	38684	22	US-10-893-315-154	Sequence 154, App	C 716	45.8	1.9	548	22	US-10-893-315-1191	Sequence 1191, Ap
644	47.2	2.0	513509	10	US-09-754-853A-4	Sequence 4, Appli	C 717	45.8	1.9	1132	20	US-10-653-047-5452	Sequence 5452, Ap
C 645	47	2.0	4045	18	US-10-221-714A-466	Sequence 466, App	C 718	45.8	1.9	1533	20	US-10-723-860-7968	Sequence 7968, Ap
646	47	2.0	5006	9	US-09-837-751-7	Sequence 7, Appli	C 719	45.8	1.9	5520	15	US-10-311-455-1491	Sequence 1491, Ap
C 647	47	2.0	7057	15	US-10-311-455-1821	Sequence 1821, Ap	C 720	45.8	1.9	5659	15	US-10-172-086-31	Sequence 31, Appl
C 648	47	2.0	7057	15	US-10-240-485-147	Sequence 147, App	C 721	45.8	1.9	5659	15	US-10-311-455-347	Sequence 347, App
C 649	47	2.0	7057	17	US-10-221-613-317	Sequence 317, App	C 722	45.8	1.9	5659	15	US-10-240-485-39	Sequence 39, Appl
C 650	47	2.0	7057	18	US-10-221-714A-323	Sequence 323, App	C 723	45.8	1.9	5659	19	US-10-311-507-13	Sequence 13, Appl
C 651	47	2.0	11964	19	US-10-433-793-55	Sequence 55, Appl	C 724	45.8	1.9	5659	20	US-10-480-846-31	Sequence 31, Appl
C 652	47	2.0	16258	17	US-10-257-166-120	Sequence 120, App	C 725	45.8	1.9	6065	15	US-10-311-455-478	Sequence 478, App
C 653	47	2.0	172569	13	US-10-087-192-1366	Sequence 1366, Ap	C 726	45.8	1.9	6072	15	US-10-311-455-3	Sequence 3, Appli
654	46.8	2.0	319	10	US-09-814-353-6115	Sequence 6115, Ap	C 727	45.8	1.9	6120	15	US-10-311-455-466	Sequence 466, App
655	46.8	2.0	319	10	US-09-814-353-12394	Sequence 12394, A	C 728	45.8	1.9	6361	15	US-10-311-455-1113	Sequence 1113, Ap
656	46.8	2.0	3153	10	US-09-759-130B-343	Sequence 343, App	C 729	45.8	1.9	7498	15	US-10-311-455-230	Sequence 230, App
657	46.8	2.0	3153	14	US-10-189-123-73	Sequence 73, Appl	C 730	45.8	1.9	8093	20	US-10-473-126-317	Sequence 317, App
658	46.8	2.0	3153	16	US-10-188-495-73	Sequence 73, Appl	C 731	45.8	1.9	18218	15	US-10-311-455-1922	Sequence 1922, Ap
659	46.8	2.0	3153	19	US-10-741-790-343	Sequence 343, App	C 732	45.8	1.9	319608	17	US-10-147-603-1	GENERAL INFORMATI
C 660	46.8	2.0	5987	15	US-10-311-455-1536	Sequence 1536, Ap	C 733	45.6	1.9	6265	9	US-09-129-112-3	Sequence 3, Appli
C 661	46.8	2.0	5987	19	US-10-433-793-132	Sequence 132, App	C 734	45.6	1.9	11155	15	US-10-311-455-577	Sequence 577, App
C 662	46.8	2.0	6301	15	US-10-311-455-25	Sequence 25, Appl	C 735	45.6	1.9	176096	22	US-10-981-277-34	Sequence 34, Appl
663	46.8	2.0	9760	17	US-10-221-613-114	Sequence 114, App	C 736	45.4	1.9	343	18	US-10-424-599-89995	Sequence 89995, A
C 664	46.8	2.0	12968	14	US-10-239-676-202	Sequence 202, App	C 737	45.4	1.9	628	13	US-10-027-632-113152	Sequence 113152,
C 665	46.8	2.0	12968	15	US-10-311-455-2058	Sequence 2058, Ap	C 738	45.4	1.9	628	17	US-10-027-632-113152	Sequence 113152,
C 666	46.8	2.0	12968	15	US-10-240-453-298	Sequence 298, App	C 739	45.4	1.9	6265	9	US-09-129-112-3	Sequence 3, Appli
C 667	46.8	2.0	12968	18	US-10-221-714A-506	Sequence 506, App	C 740	45.4	1.9	7498	15	US-10-311-455-230	Sequence 230, App
668	46.8	2.0	50000	21	US-10-706-635-26	Sequence 26, Appl	C 741	45.4	1.9	9881	16	US-10-240-452-54	Sequence 54, Appl
669	46.8	2.0	168198	19	US-10-322-696-88	Sequence 88, Appl	C 742	45.4	1.9	10279	15	US-10-311-455-1564	Sequence 1564, Ap
C 670	46.8	2.0	394468	21	US-10-741-600-17952	Sequence 17952, A	C 743	45.4	1.9	10279	18	US-10-240-589C-86	Sequence 86, Appl
671	46.6	2.0	960	14	US-10-198-846-6381	Sequence 6381, Ap	C 744	45.4	1.9	11260	14	US-10-239-676-20	Sequence 20, Appl
672	46.6	2.0	2747	9	US-09-917-800A-1588	Sequence 1588, Ap	C 745	45.4	1.9	11260	15	US-10-240-453-28	Sequence 28, Appl
673	46.6	2.0	2747	22	US-10-024-607-7	Sequence 7, Appli	C 746	45.4	1.9	11996	15	US-10-240-485-46	Sequence 46, Appl
674	46.6	2.0	5163	15	US-10-311-455-1221	Sequence 1221, Ap	C 747	45.4	1.9	13420	15	US-10-311-455-890	Sequence 890, App
675	46.6	2.0	7676	15	US-10-240-485-151	Sequence 151, App	C 748	45.4	1.9	40324	19	US-10-433-793-179	Sequence 179, App
C 676	46.6	2.0	9180	15	US-10-311-455-1937	Sequence 1937, Ap	C 749	45.2	1.9	1109	18	US-10-424-599-134182	Sequence 134182,
C 677	46.6	2.0	10891	15	US-10-311-455-438	Sequence 438, App	C 750	45.2	1.9	2432	14	US-10-198-846-12893	Sequence 12893, A
C 678	46.6	2.0	11092	15	US-10-311-455-1485	Sequence 1485, Ap	C 751	45.2	1.9	5267	19	US-10-433-793-73	Sequence 73, Appl
679	46.6	2.0	12507	15	US-10-311-455-271	Sequence 271, App	C 752	45.2	1.9	6816	20	US-10-723-860-7676	Sequence 7676, Ap
680	46.6	2.0	15548	15	US-10-311-455-2128	Sequence 2128, Ap	C 753	45.2	1.9	8876	15	US-10-311-455-2049	Sequence 2049, Ap
681	46.6	2.0	38678	22	US-10-893-315-136	Sequence 136, App	C 754	45.2	1.9	17183	15	US-10-311-455-460	Sequence 460, App
682	46.6	2.0	38684	22	US-10-893-315-154	Sequence 154, App	C 755	45.2	1.9	17419	14	US-10-239-676-100	Sequence 100, App
C 683	46.6	2.0	40862	15	US-10-311-455-2046	Sequence 2046, Ap	C 756	45.2	1.9	17419	15	US-10-311-455-1268	Sequence 1268, Ap
684	46.6	2.0	50000	21	US-10-706-635-23	Sequence 23, Appl	C 757	45.2	1.9	17419	15	US-10-240-453-112	Sequence 112, App
C 685	46.4	2.0	4172	15	US-10-311-455-687	Sequence 687, App	C 758	45	1.9	535	19	US-10-021-323-1934	Sequence 1934, Ap
686	46.4	2.0	6040	18	US-10-240-589C-110	Sequence 110, App	C 759	45	1.9	6816	20	US-10-723-860-7676	Sequence 7676, Ap
687	46.4	2.0	16228	17	US-10-221-613-387	Sequence 387, App	C 760	45	1.9	12142	15	US-10-311-455-1646	Sequence 1646, Ap
C 688	46.4	2.0	17594	15	US-10-311-455-1999	Sequence 1999, App	C 761	45	1.9	14987	15	US-10-311-455-603	Sequence 603, App
C 689	46.4	2.0	19131	18	US-10-221-714A-442	Sequence 442, App	C 762	45	1.9	18133	15	US-10-311-455-914	Sequence 914, App
C 690	46.2	1.9	471	18	US-10-424-599-112213	Sequence 112213,	C 763	45	1.9	18133	17	US-10-257-166-100	Sequence 100, App

C 910	43.6	1.8	8866	14	US-10-239-676-139	Sequence 139, App	983	43.2	1.8	6286	18	US-10-221-714A-313	Sequence 313, App
C 911	43.6	1.8	8866	15	US-10-240-453-153	Sequence 153, App	C 984	43.2	1.8	6641	15	US-10-311-455-288	Sequence 288, App
C 912	43.6	1.8	10467	15	US-10-240-453-327	Sequence 327, App	C 985	43.2	1.8	6641	16	US-10-240-452-36	Sequence 36, Appl
913	43.6	1.8	12507	15	US-10-311-455-272	Sequence 272, App	C 986	43.2	1.8	6880	17	US-10-221-613-184	Sequence 184, App
914	43.6	1.8	13326	15	US-10-311-455-1685	Sequence 1685, Ap	C 987	43.2	1.8	10710	15	US-10-311-455-866	Sequence 866, App
C 915	43.6	1.8	13503	15	US-10-311-455-2043	Sequence 2043, Ap	C 988	43.2	1.8	11670	16	US-10-240-452-26	Sequence 26, Appl
916	43.6	1.8	14537	18	US-10-221-714A-78	Sequence 78, Appl	C 989	43.2	1.8	13712	15	US-10-311-455-1504	Sequence 1504, Ap
917	43.6	1.8	16173	15	US-10-240-485-22	Sequence 22, Appl	C 990	43.2	1.8	14307	15	US-10-311-455-702	Sequence 702, App
C 918	43.6	1.8	18624	15	US-10-311-455-1675	Sequence 1675, Ap	C 991	43.2	1.8	15373	15	US-10-311-455-440	Sequence 440, App
919	43.6	1.8	19734	15	US-10-311-455-1906	Sequence 1906, Ap	C 992	43.2	1.8	16217	15	US-10-311-455-598	Sequence 598, App
920	43.6	1.8	49979	19	US-10-741-601-5746	Sequence 5746, Ap	C 993	43.2	1.8	17594	15	US-10-311-455-2000	Sequence 2000, Ap
921	43.6	1.8	49979	21	US-10-741-600-17905	Sequence 17905, A	C 994	43.2	1.8	20674	17	US-10-170-097-651	Sequence 651, App
C 922	43.6	1.8	50000	21	US-10-706-635-24	Sequence 24, Appl	C 995	43.2	1.8	20674	21	US-10-926-684-651	Sequence 651, App
C 923	43.6	1.8	80032	21	US-10-741-600-17727	Sequence 17727, A	996	43.2	1.8	32341	22	US-10-737-082-13	Sequence 13, Appl
924	43.6	1.8	83391	19	US-10-433-793-123	Sequence 123, App	997	43.2	1.8	32341	22	US-10-765-790-13	Sequence 13, Appl
925	43.4	1.8	337	9	US-09-960-352-6976	Sequence 6976, Ap	998	43.2	1.8	74586	9	US-09-781-558-3	Sequence 3, Appli
926	43.4	1.8	547	20	US-10-363-345A-1577	Sequence 1577, Ap	999	43.2	1.8	74586	16	US-10-388-650-3	Sequence 3, Appli
C 927	43.4	1.8	547	20	US-10-363-345A-1578	Sequence 1578, Ap	1000	43.2	1.8	185458	20	US-10-719-993-6864	Sequence 6864, Ap
928	43.4	1.8	547	21	US-10-363-483A-1577	Sequence 1577, Ap	C1001	43	1.8	560	19	US-10-021-323-2253	Sequence 2253, Ap
C 929	43.4	1.8	547	21	US-10-363-483A-1578	Sequence 1578, Ap	1002	43	1.8	1132	9	US-09-938-842A-3452	Sequence 3452, Ap
930	43.4	1.8	830	17	US-10-012-697-609	Sequence 609, App	1003	43	1.8	1132	11	US-09-938-842A-3452	Sequence 3452, Ap
C 931	43.4	1.8	2196	21	US-10-764-420-1497	Sequence 1497, Ap	1004	43	1.8	1883	18	US-10-425-114-6422	Sequence 6422, Ap
932	43.4	1.8	2354	20	US-10-602-494-101	Sequence 101, App	1005	43	1.8	1925	18	US-10-424-599-71247	Sequence 71247, A
933	43.4	1.8	2354	20	US-10-602-494-243	Sequence 243, App	1006	43	1.8	2053	13	US-10-027-632-97533	Sequence 97533, A
C 934	43.4	1.8	5376	15	US-10-311-455-2123	Sequence 2123, Ap	1007	43	1.8	2053	17	US-10-027-632-97533	Sequence 97533, A
935	43.4	1.8	6106	15	US-10-311-455-1446	Sequence 1446, Ap	C1008	43	1.8	5218	15	US-10-311-455-1239	Sequence 1239, Ap
936	43.4	1.8	6106	17	US-10-257-166-114	Sequence 114, App	1009	43	1.8	5942	15	US-10-172-086-16	Sequence 16, Appl
937	43.4	1.8	6106	18	US-10-221-714A-152	Sequence 152, App	1010	43	1.8	5942	17	US-10-221-613-92	Sequence 92, Appl
C 938	43.4	1.8	6317	15	US-10-311-455-381	Sequence 381, App	1011	43	1.8	5942	19	US-10-311-507-28	Sequence 28, Appl
C 939	43.4	1.8	6585	15	US-10-311-455-805	Sequence 805, App	1012	43	1.8	5942	20	US-10-480-846-16	Sequence 16, Appl
C 940	43.4	1.8	6585	17	US-10-221-613-141	Sequence 141, App	1013	43	1.8	5942	20	US-10-473-126-142	Sequence 142, App
C 941	43.4	1.8	6590	15	US-10-311-455-1449	Sequence 1449, Ap	1014	43	1.8	5942	20	US-10-473-126-228	Sequence 228, App
942	43.4	1.8	6942	15	US-10-311-455-1708	Sequence 1708, Ap	1015	43	1.8	5942	20	US-10-473-126-288	Sequence 288, App
943	43.4	1.8	7903	14	US-10-239-676-110	Sequence 110, App	1016	43	1.8	5942	20	US-10-473-126-374	Sequence 374, App
944	43.4	1.8	7903	15	US-10-311-455-1336	Sequence 1336, Ap	C1017	43	1.8	6077	15	US-10-311-455-1219	Sequence 1219, Ap
945	43.4	1.8	7903	15	US-10-240-453-122	Sequence 122, App	C1018	43	1.8	6126	15	US-10-311-455-1803	Sequence 1803, Ap
946	43.4	1.8	8222	21	US-10-486-319A-43	Sequence 43, Appl	C1019	43	1.8	6126	18	US-10-221-714A-295	Sequence 295, App
947	43.4	1.8	8222	21	US-10-486-319A-65	Sequence 65, Appl	1020	43	1.8	6233	18	US-10-221-714A-220	Sequence 220, App
948	43.4	1.8	9021	15	US-10-172-086-53	Sequence 53, Appl	C1021	43	1.8	6317	15	US-10-311-455-382	Sequence 382, App
949	43.4	1.8	9021	15	US-10-311-455-2205	Sequence 2205, Ap	1022	43	1.8	7441	17	US-10-257-166-139	Sequence 139, App
950	43.4	1.8	9021	17	US-10-257-166-157	Sequence 157, App	1023	43	1.8	7479	18	US-10-240-454-39	Sequence 39, Appl
951	43.4	1.8	9021	19	US-10-311-507-73	Sequence 73, Appl	C1024	43	1.8	7900	18	US-10-221-714A-486	Sequence 486, App
952	43.4	1.8	9021	20	US-10-480-846-53	Sequence 53, Appl	C1025	43	1.8	8592	15	US-10-311-455-1956	Sequence 1956, Ap
C 953	43.4	1.8	11422	15	US-10-311-455-192	Sequence 192, App	C1026	43	1.8	9810	15	US-10-311-455-400	Sequence 400, App
C 954	43.4	1.8	11422	17	US-10-257-166-18	Sequence 18, Appl	C1027	43	1.8	11787	18	US-10-240-589C-52	Sequence 52, Appl
C 955	43.4	1.8	13427	15	US-10-311-455-1900	Sequence 1900, Ap	C1028	43	1.8	13574	15	US-10-311-455-1289	Sequence 1289, Ap
C 956	43.4	1.8	17137	15	US-10-311-455-163	Sequence 163, App	C1029	43	1.8	16228	17	US-10-221-613-387	Sequence 387, App
C 957	43.4	1.8	34722	19	US-10-322-281-700	Sequence 700, App	1030	43	1.8	19082	15	US-10-311-455-600	Sequence 600, App
958	43.4	1.8	35680	13	US-10-087-192-1186	Sequence 1186, Ap	C1031	43	1.8	19082	15	US-10-311-455-600	Sequence 600, App
C 959	43.4	1.8	40324	19	US-10-433-793-180	Sequence 180, App	C1032	43	1.8	20933	19	US-10-433-793-154	Sequence 154, App
C 960	43.4	1.8	90541	9	US-09-759-359A-3	Sequence 3, Appli	C1033	43	1.8	29993	21	US-10-482-823-3	Sequence 3, Appli
C 961	43.4	1.8	90541	16	US-10-207-973-3	Sequence 3, Appli	C1034	43	1.8	37184	19	US-10-433-793-108	Sequence 108, App
C 962	43.4	1.8	90541	19	US-10-799-676-3	Sequence 3, Appli	C1035	43	1.8	38342	18	US-10-221-714A-472	Sequence 472, App
C 963	43.4	1.8	158001	17	US-10-211-179-11	GENERAL INFORMATI	C1036	43	1.8	50000	21	US-10-706-635-26	Sequence 26, Appl
C 964	43.2	1.8	469	20	US-10-357-930-56657	Sequence 56657, A	C1037	42.8	1.8	608	13	US-10-027-632-200495	Sequence 200495,
C 965	43.2	1.8	499	19	US-10-021-323-10189	Sequence 10189, A	C1038	42.8	1.8	608	17	US-10-027-632-200495	Sequence 200495,
C 966	43.2	1.8	1982	18	US-10-678-521-13	Sequence 13, Appl	1039	42.8	1.8	643	18	US-10-424-599-138175	Sequence 138175,
967	43.2	1.8	1982	18	US-10-678-521-15	Sequence 15, Appl	C1040	42.8	1.8	2000	9	US-09-938-842A-3876	Sequence 3876, Ap
C 968	43.2	1.8	2144	18	US-10-678-521-57	Sequence 57, Appl	C1041	42.8	1.8	2000	11	US-09-938-842A-3876	Sequence 3876, Ap
969	43.2	1.8	2144	18	US-10-678-521-59	Sequence 59, Appl	1042	42.8	1.8	5204	15	US-10-311-455-872	Sequence 872, App
970	43.2	1.8	2652	14	US-10-195-970-4	Sequence 4, Appli	C1043	42.8	1.8	5611	19	US-10-433-793-99	Sequence 99, Appl
971	43.2	1.8	2652	14	US-10-195-970-5	Sequence 5, Appli	C1044	42.8	1.8	5928	15	US-10-311-455-2059	Sequence 2059, Ap
972	43.2	1.8	2652	17	US-10-453-420-4	Sequence 4, Appli	C1045	42.8	1.8	6208	15	US-10-311-455-167	Sequence 167, App
973	43.2	1.8	2652	17	US-10-453-420-5	Sequence 5, Appli	C1046	42.8	1.8	6237	15	US-10-311-455-332	Sequence 332, App
C 974	43.2	1.8	4597	16	US-10-176-149-4	Sequence 4, Appli	1047	42.8	1.8	6815	14	US-10-239-676-49	Sequence 49, Appl
C 975	43.2	1.8	4597	17	US-10-465-800-4	Sequence 4, Appli	1048	42.8	1.8	6815	15	US-10-311-455-643	Sequence 643, App
C 976	43.2	1.8	5294	15	US-10-311-455-1043	Sequence 1043, Ap	1049	42.8	1.8	6815	15	US-10-240-453-49	Sequence 49, Appl
977	43.2	1.8	6095	15	US-10-311-455-334	Sequence 334, App	C1050	42.8	1.8	7008	18	US-10-221-714A-254	Sequence 254, App
978	43.2	1.8	6095	15	US-10-240-485-28	Sequence 28, Appl	C1051	42.8	1.8	7346	15	US-10-311-455-318	Sequence 318, App
979	43.2	1.8	6095	18	US-10-221-714A-32	Sequence 32, Appl	C1052	42.8	1.8	7450	15	US-10-240-453-5	Sequence 5, Appli
C 980	43.2	1.8	6220	16	US-10-176-149-3	Sequence 3, Appli	C1053	42.8	1.8	7851	15	US-10-311-455-1734	Sequence 1734, Ap
C 981	43.2	1.8	6220	17	US-10-465-800-3	Sequence 3, Appli	C1054	42.8	1.8	8246	15	US-10-311-455-176	Sequence 176, App
C 982	43.2	1.8	6285	15	US-10-311-455-1469	Sequence 1469, Ap	C1055	42.8	1.8	8588	14	US-10-239-676-177	Sequence 177, App

c1056	42.8	1.8	8588	15	US-10-240-453-199	Sequence 199, App	1129	42.4	1.8	638	13	US-10-027-632-14078	Sequence 14078, A
c1057	42.8	1.8	9888	15	US-10-311-455-1214	Sequence 1214, Ap	1130	42.4	1.8	638	17	US-10-027-632-14078	Sequence 14078, A
1058	42.8	1.8	11691	15	US-10-311-455-2214	Sequence 2214, Ap	c1131	42.4	1.8	1139	13	US-10-027-632-117477	Sequence 117477,
1059	42.8	1.8	11745	15	US-10-240-453-206	Sequence 206, App	c1132	42.4	1.8	1139	13	US-10-027-632-117478	Sequence 117478,
1060	42.8	1.8	13376	15	US-10-311-455-556	Sequence 556, App	c1133	42.4	1.8	1139	13	US-10-027-632-117479	Sequence 117479,
c1061	42.8	1.8	14649	14	US-10-239-676-122	Sequence 122, App	c1134	42.4	1.8	1139	17	US-10-027-632-117477	Sequence 117477,
c1062	42.8	1.8	14649	15	US-10-240-453-142	Sequence 142, App	c1135	42.4	1.8	1139	17	US-10-027-632-117478	Sequence 117478,
c1063	42.8	1.8	17293	17	US-10-221-613-13	Sequence 13, Appl	c1136	42.4	1.8	1139	17	US-10-027-632-117479	Sequence 117479,
c1064	42.8	1.8	61177	19	US-10-741-601-5694	Sequence 5694, Ap	1137	42.4	1.8	1158	20	US-10-425-115-139364	Sequence 139364,
c1065	42.8	1.8	61177	21	US-10-741-600-17768	Sequence 17768, A	1138	42.4	1.8	4377	24	US-11-097-143-29425	Sequence 29425, A
1066	42.8	1.8	99116	17	US-10-298-122-1	Sequence 1, Appli	c1139	42.4	1.8	4537	13	US-10-044-090-337	Sequence 337, App
1067	42.8	1.8	154902	19	US-10-450-826-105	Sequence 105, App	1140	42.4	1.8	6079	15	US-10-311-455-231	Sequence 231, App
c1068	42.8	1.8	640681	9	US-09-790-988-1	Sequence 1, Appli	c1141	42.4	1.8	6104	15	US-10-311-455-1339	Sequence 1339, Ap
1069	42.6	1.8	513	13	US-10-027-632-65502	Sequence 65502, A	1142	42.4	1.8	6179	18	US-10-221-714A-66	Sequence 66, Appl
1070	42.6	1.8	513	13	US-10-027-632-65503	Sequence 65503, A	c1143	42.4	1.8	6233	18	US-10-221-714A-220	Sequence 220, App
1071	42.6	1.8	513	13	US-10-027-632-65504	Sequence 65504, A	c1144	42.4	1.8	6283	15	US-10-311-455-62	Sequence 62, Appl
1072	42.6	1.8	513	13	US-10-027-632-65505	Sequence 65505, A	c1145	42.4	1.8	6286	18	US-10-221-714A-313	Sequence 313, App
1073	42.6	1.8	513	13	US-10-027-632-65506	Sequence 65506, A	c1146	42.4	1.8	6292	18	US-10-221-714A-461	Sequence 461, App
1074	42.6	1.8	513	17	US-10-027-632-65502	Sequence 65502, A	c1147	42.4	1.8	7108	17	US-10-257-166-78	Sequence 78, Appl
1075	42.6	1.8	513	17	US-10-027-632-65503	Sequence 65503, A	c1148	42.4	1.8	8238	15	US-10-311-455-1962	Sequence 1962, Ap
1076	42.6	1.8	513	17	US-10-027-632-65504	Sequence 65504, A	c1149	42.4	1.8	8238	18	US-10-240-454-44	Sequence 44, Appl
1077	42.6	1.8	513	17	US-10-027-632-65505	Sequence 65505, A	c1150	42.4	1.8	9760	17	US-10-221-613-114	Sequence 114, App
1078	42.6	1.8	513	17	US-10-027-632-65506	Sequence 65506, A	c1151	42.4	1.8	12393	15	US-10-311-455-1236	Sequence 1236, Ap
c1079	42.6	1.8	535	20	US-10-357-930-46425	Sequence 46425, A	1152	42.4	1.8	16258	17	US-10-257-166-120	Sequence 120, App
c1080	42.6	1.8	587	18	US-10-424-599-50833	Sequence 50833, A	c1153	42.4	1.8	16373	15	US-10-311-455-592	Sequence 592, App
1081	42.6	1.8	1111	8	US-08-781-986A-756	Sequence 756, App	c1154	42.4	1.8	18598	15	US-10-311-455-360	Sequence 360, App
1082	42.6	1.8	1111	18	US-10-329-624-756	Sequence 756, App	c1155	42.4	1.8	18817	15	US-10-240-485-48	Sequence 48, Appl
c1083	42.6	1.8	2580	15	US-10-172-086-67	Sequence 67, Appl	1156	42.4	1.8	34688	19	US-10-433-793-89	Sequence 89, Appl
c1084	42.6	1.8	2580	19	US-10-311-507-29	Sequence 29, Appl	1157	42.4	1.8	37515	19	US-10-433-793-28	Sequence 28, Appl
c1085	42.6	1.8	2580	20	US-10-480-846-67	Sequence 67, Appl	1158	42.4	1.8	42027	20	US-10-417-375-58	Sequence 58, Appl
c1086	42.6	1.8	3287	20	US-10-473-126-331	Sequence 331, App	1159	42.4	1.8	113515	15	US-10-311-455-2148	Sequence 2148, Ap
1087	42.6	1.8	5107	15	US-10-311-455-1039	Sequence 1039, Ap	1160	42.2	1.8	294	10	US-09-814-353-5106	Sequence 5106, Ap
1088	42.6	1.8	5145	15	US-10-311-455-321	Sequence 321, App	1161	42.2	1.8	294	10	US-09-814-353-11398	Sequence 11398, A
1089	42.6	1.8	5145	15	US-10-240-485-17	Sequence 17, Appl	c1162	42.2	1.8	536	22	US-10-893-315-1193	Sequence 1193, Ap
c1090	42.6	1.8	5542	15	US-10-311-455-1994	Sequence 1994, Ap	1163	42.2	1.8	537	19	US-10-021-323-8120	Sequence 8120, Ap
1091	42.6	1.8	5925	15	US-10-311-455-1550	Sequence 1550, Ap	1164	42.2	1.8	560	19	US-10-021-323-2253	Sequence 2253, Ap
c1092	42.6	1.8	5929	15	US-10-311-455-681	Sequence 681, App	c1165	42.2	1.8	649	13	US-10-027-632-191432	Sequence 191432,
c1093	42.6	1.8	6063	18	US-10-221-714A-59	Sequence 59, Appl	c1166	42.2	1.8	649	17	US-10-027-632-191432	Sequence 191432,
c1094	42.6	1.8	6075	17	US-10-221-613-277	Sequence 277, App	1167	42.2	1.8	839	14	US-10-198-846-5829	Sequence 5829, Ap
c1095	42.6	1.8	6129	17	US-10-221-613-262	Sequence 262, App	1168	42.2	1.8	5070	15	US-10-311-455-774	Sequence 774, App
c1096	42.6	1.8	6175	15	US-10-311-455-1280	Sequence 1280, Ap	1169	42.2	1.8	6013	17	US-10-221-613-226	Sequence 226, App
1097	42.6	1.8	6494	15	US-10-311-455-1366	Sequence 1366, Ap	c1170	42.2	1.8	6014	17	US-10-221-613-368	Sequence 368, App
1098	42.6	1.8	6533	15	US-10-311-455-1682	Sequence 1682, Ap	1171	42.2	1.8	6079	15	US-10-311-455-394	Sequence 394, App
c1099	42.6	1.8	7312	15	US-10-311-455-1788	Sequence 1788, Ap	c1172	42.2	1.8	6337	15	US-10-311-455-1283	Sequence 1283, Ap
c1100	42.6	1.8	7312	17	US-10-221-613-312	Sequence 312, App	c1173	42.2	1.8	6337	18	US-10-221-714A-171	Sequence 171, App
1101	42.6	1.8	8093	15	US-10-172-086-26	Sequence 26, Appl	c1174	42.2	1.8	7348	18	US-10-221-714A-58	Sequence 58, Appl
1102	42.6	1.8	8093	18	US-10-221-714A-158	Sequence 158, App	1175	42.2	1.8	11260	14	US-10-239-676-20	Sequence 20, Appl
1103	42.6	1.8	8093	18	US-10-240-589C-46	Sequence 46, Appl	1176	42.2	1.8	11260	15	US-10-240-453-28	Sequence 28, Appl
1104	42.6	1.8	8093	19	US-10-311-507-58	Sequence 58, Appl	c1177	42.2	1.8	12138	15	US-10-311-455-1916	Sequence 1916, Ap
1105	42.6	1.8	8093	20	US-10-480-846-26	Sequence 26, Appl	c1178	42.2	1.8	12138	15	US-10-240-453-210	Sequence 210, App
1106	42.6	1.8	8093	20	US-10-473-126-172	Sequence 172, App	1179	42.2	1.8	12409	18	US-10-240-454-7	Sequence 7, Appli
c1107	42.6	1.8	8392	15	US-10-311-455-1464	Sequence 1464, Ap	c1180	42.2	1.8	12507	15	US-10-311-455-271	Sequence 271, App
c1108	42.6	1.8	9731	15	US-10-311-455-963	Sequence 963, App	1181	42.2	1.8	15161	17	US-10-221-613-386	Sequence 386, App
c1109	42.6	1.8	11694	18	US-10-221-714A-422	Sequence 422, App	c1183	42.2	1.8	15373	15	US-10-311-455-439	Sequence 439, App
1110	42.6	1.8	11996	15	US-10-240-485-46	Sequence 46, Appl	c1184	42.2	1.8	17538	15	US-10-311-455-1130	Sequence 1130, Ap
c1111	42.6	1.8	12405	14	US-10-239-676-36	Sequence 36, Appl	c1185	42.2	1.8	18997	15	US-10-172-086-18	Sequence 18, Appl
c1112	42.6	1.8	12405	15	US-10-240-453-44	Sequence 44, Appl	c1186	42.2	1.8	18997	15	US-10-311-455-544	Sequence 544, Appl
c1113	42.6	1.8	12405	17	US-10-221-613-102	Sequence 102, App	c1187	42.2	1.8	18997	19	US-10-311-507-32	Sequence 32, Appl
c1114	42.6	1.8	17144	18	US-10-221-714A-387	Sequence 387, App	c1187	42.2	1.8	18997	20	US-10-480-846-18	Sequence 18, Appl
c1115	42.6	1.8	42348	19	US-10-715-066-2	Sequence 2, Appli	c1188	42.2	1.8	19787	15	US-10-311-455-1424	Sequence 1424, Ap
c1116	42.6	1.8	53332	9	US-09-801-861-3	Sequence 3, Appli	1189	42.2	1.8	29993	21	US-10-482-823-3	Sequence 3, Appli
c1117	42.6	1.8	53332	14	US-10-224-562-3	Sequence 3, Appli	1190	42.2	1.8	38342	18	US-10-221-714A-472	Sequence 472, App
c1118	42.6	1.8	53332	24	US-11-108-869-3	Sequence 3, Appli	1191	42.2	1.8	69081	13	US-10-087-192-1192	Sequence 1192, Ap
1119	42.6	1.8	71553	20	US-10-719-993-7039	Sequence 7039, Ap	1192	42.2	1.8	89567	19	US-10-322-281-838	Sequence 838, App
1120	42.6	1.8	71553	21	US-10-741-600-17960	Sequence 17960, A	c1193	42.2	1.8	177380	21	US-10-484-577-683	Sequence 683, App
c1121	42.6	1.8	127197	10	US-09-754-853A-1	Sequence 1, Appli	c1194	42.2	1.8	206739	22	US-10-981-277-49	Sequence 49, Appl
c1122	42.6	1.8	1980090	20	US-10-719-993-6815	Sequence 6815, Ap	c1195	42.2	1.8	580073	16	US-10-205-220-1	Sequence 1, Appli
c1123	42.6	1.8	1980090	21	US-10-741-600-17676	Sequence 17676, A	c1196	42	1.8	411	13	US-10-027-632-302856	Sequence 302856,
c1124	42.4	1.8	275	18	US-10-621-901-2242	Sequence 2242, Ap	c1197	42	1.8	411	17	US-10-027-632-302856	Sequence 302856,
c1125	42.4	1.8	308	18	US-10-424-599-75198	Sequence 75198, A	c1198	42	1.8	433	20	US-10-425-115-73890	Sequence 73890, A
1126	42.4	1.8	549	18	US-10-621-901-2116	Sequence 2116, Ap	1199	42	1.8	492	20	US-10-425-115-64219	Sequence 64219, A
c1127	42.4	1.8	552	19	US-10-021-323-93	Sequence 93, Appl	c1200	42	1.8	502	18	US-10-424-599-65625	Sequence 65625, A
c1128	42.4	1.8	612	20	US-10-425-115-104533	Sequence 104533,	c1201	42	1.8	601	22	US-10-893-315-1190	Sequence 1190, Ap

1202	42	1.8	612	13	US-10-027-632-193818	Sequence 193818,	c1275	41.8	1.8	6894	15	US-10-311-455-1212	Sequence 1212, Ap
1203	42	1.8	612	13	US-10-027-632-193819	Sequence 193819,	c1276	41.8	1.8	6894	19	US-10-311-507-54	Sequence 54, Appl
1204	42	1.8	612	17	US-10-027-632-193818	Sequence 193818,	c1277	41.8	1.8	6894	20	US-10-480-846-30	Sequence 30, Appl
1205	42	1.8	612	17	US-10-027-632-193819	Sequence 193819,	1278	41.8	1.8	6963	15	US-10-311-455-952	Sequence 952, App
1206	42	1.8	683	9	US-09-984-245-17	Sequence 17, Appl	1279	41.8	1.8	7058	17	US-10-257-166-133	Sequence 133, App
1207	42	1.8	683	10	US-09-966-262-17	Sequence 17, Appl	c1280	41.8	1.8	7135	18	US-10-221-714A-145	Sequence 145, App
1208	42	1.8	683	10	US-09-983-966-17	Sequence 17, Appl	c1281	41.8	1.8	8033	17	US-10-221-613-74	Sequence 74, Appl
1209	42	1.8	683	14	US-10-059-395-17	Sequence 17, Appl	c1282	41.8	1.8	8033	18	US-10-221-714A-30	Sequence 30, Appl
1210	42	1.8	683	14	US-10-143-090-17	Sequence 17, Appl	c1283	41.8	1.8	8197	15	US-10-240-485-67	Sequence 67, Appl
1211	42	1.8	683	21	US-10-960-251-17	Sequence 17, Appl	c1284	41.8	1.8	8776	17	US-10-257-166-150	Sequence 150, App
1212	42	1.8	971	19	US-10-437-963-6452	Sequence 6452, Ap	1285	41.8	1.8	8801	14	US-10-239-676-144	Sequence 144, App
c1213	42	1.8	1398	20	US-10-425-115-81395	Sequence 81395, A	1286	41.8	1.8	8801	15	US-10-311-455-1714	Sequence 1714, Ap
c1214	42	1.8	1431	9	US-09-774-414-2	Sequence 2, Appli	1287	41.8	1.8	8801	15	US-10-240-453-160	Sequence 160, App
c1215	42	1.8	2032	18	US-10-424-599-128236	Sequence 128236,	c1288	41.8	1.8	9848	15	US-10-311-455-1772	Sequence 1772, Ap
1216	42	1.8	5467	15	US-10-311-455-2082	Sequence 2082, Ap	c1289	41.8	1.8	10039	15	US-10-311-455-2016	Sequence 2016, Ap
1217	42	1.8	5666	15	US-10-311-455-1746	Sequence 1746, Ap	c1290	41.8	1.8	11944	15	US-10-311-455-2160	Sequence 2160, Ap
c1218	42	1.8	5666	17	US-10-221-613-145	Sequence 145, App	c1291	41.8	1.8	17131	15	US-10-311-455-1025	Sequence 1025, Ap
c1219	42	1.8	5881	15	US-10-172-086-82	Sequence 82, Appl	1292	41.8	1.8	26000	20	US-10-476-022-10	Sequence 10, Appl
c1220	42	1.8	5881	20	US-10-480-846-82	Sequence 82, Appl	1293	41.8	1.8	34200	13	US-10-087-192-1507	Sequence 1507, Ap
1221	42	1.8	6127	15	US-10-311-455-1587	Sequence 1587, Ap	c1294	41.8	1.8	34337	9	US-09-741-149-3	Sequence 3, Appli
1222	42	1.8	6131	15	US-10-311-455-864	Sequence 864, App	c1295	41.8	1.8	34337	16	US-10-385-614-3	Sequence 3, Appli
1223	42	1.8	6261	17	US-10-221-613-2	Sequence 2, Appli	c1296	41.8	1.8	83391	19	US-10-433-793-124	Sequence 124, App
1224	42	1.8	6261	18	US-10-221-714A-366	Sequence 366, App	1297	41.8	1.8	1980090	20	US-10-719-993-6815	Sequence 6815, Ap
1225	42	1.8	6270	15	US-10-311-455-1845	Sequence 1845, Ap	1298	41.8	1.8	1980090	21	US-10-741-600-17676	Sequence 17676, A
c1226	42	1.8	6509	17	US-10-221-613-41	Sequence 41, Appl	1299	41.6	1.8	299	10	US-09-814-353-4844	Sequence 4844, Ap
c1227	42	1.8	6650	15	US-10-311-455-612	Sequence 612, App	1300	41.6	1.8	299	10	US-09-814-353-11141	Sequence 11141, A
1228	42	1.8	6681	15	US-10-311-455-128	Sequence 128, App	c1301	41.6	1.8	411	19	US-10-021-323-7694	Sequence 7694, Ap
c1229	42	1.8	6681	15	US-10-311-455-128	Sequence 128, App	1302	41.6	1.8	469	19	US-10-021-323-16830	Sequence 16830, A
1230	42	1.8	6681	16	US-10-240-452-4	Sequence 4, Appli	c1303	41.6	1.8	539	10	US-09-814-353-17862	Sequence 17862, A
c1231	42	1.8	6681	16	US-10-240-452-4	Sequence 4, Appli	1304	41.6	1.8	1569	15	US-10-128-714-2043	Sequence 2043, Ap
1232	42	1.8	6980	15	US-10-311-455-426	Sequence 426, App	1305	41.6	1.8	1569	15	US-10-128-714-7043	Sequence 7043, Ap
1233	42	1.8	7131	17	US-10-221-613-324	Sequence 324, App	1306	41.6	1.8	1689	15	US-10-128-714-6043	Sequence 6043, Ap
1234	42	1.8	7384	15	US-10-311-455-719	Sequence 719, App	1307	41.6	1.8	1714	15	US-10-128-714-1043	Sequence 1043, Ap
c1235	42	1.8	7657	14	US-10-239-676-185	Sequence 185, App	c1308	41.6	1.8	2115	9	US-09-117-860-23	Sequence 23, Appl
c1236	42	1.8	7657	15	US-10-311-455-1995	Sequence 1995, Ap	c1309	41.6	1.8	2115	16	US-10-393-590-82	Sequence 82, Appl
c1237	42	1.8	7823	14	US-10-239-676-197	Sequence 197, App	c1310	41.6	1.8	2115	16	US-10-393-567-82	Sequence 82, Appl
c1238	42	1.8	7823	15	US-10-311-455-2033	Sequence 2033, Ap	c1311	41.6	1.8	2115	16	US-10-394-087-82	Sequence 82, Appl
c1239	42	1.8	7823	15	US-10-240-453-291	Sequence 291, App	c1312	41.6	1.8	2115	17	US-10-172-118-1392	Sequence 1392, Ap
1240	42	1.8	8166	15	US-10-311-455-1766	Sequence 1766, Ap	c1313	41.6	1.8	2115	18	US-10-342-887-1392	Sequence 1392, Ap
1241	42	1.8	8305	15	US-10-311-455-1542	Sequence 1542, Ap	c1314	41.6	1.8	2115	21	US-10-848-755A-157	Sequence 157, App
1242	42	1.8	8310	21	US-10-861-875-9	Sequence 9, Appli	c1315	41.6	1.8	2115	22	US-10-500-240-98	Sequence 98, Appl
c1243	42	1.8	8576	15	US-10-311-455-2202	Sequence 2202, Ap	c1316	41.6	1.8	2339	18	US-10-181-108-44	Sequence 44, Appl
c1244	42	1.8	9238	15	US-10-240-453-240	Sequence 240, App	c1317	41.6	1.8	2339	24	US-11-079-743-44	Sequence 44, Appl
c1245	42	1.8	10189	15	US-10-311-455-2134	Sequence 2134, Ap	1318	41.6	1.8	3689	15	US-10-128-714-5043	Sequence 5043, Ap
c1246	42	1.8	10609	18	US-10-221-714A-82	Sequence 82, Appl	1319	41.6	1.8	3714	15	US-10-128-714-43	Sequence 43, Appl
1247	42	1.8	11155	15	US-10-311-455-578	Sequence 578, App	1320	41.6	1.8	5379	15	US-10-311-455-1649	Sequence 1649, Ap
1248	42	1.8	13123	16	US-10-240-452-63	Sequence 63, Appl	1321	41.6	1.8	5379	15	US-10-240-485-129	Sequence 129, App
c1249	42	1.8	15698	15	US-10-311-455-2114	Sequence 2114, Ap	1322	41.6	1.8	5507	20	US-10-473-126-344	Sequence 344, App
c1250	42	1.8	18011	15	US-10-311-455-8	Sequence 8, Appli	1323	41.6	1.8	5641	15	US-10-311-455-1369	Sequence 1369, Ap
c1251	42	1.8	34688	19	US-10-433-793-89	Sequence 89, Appl	c1324	41.6	1.8	5660	20	US-10-473-126-284	Sequence 284, App
1252	42	1.8	74665	20	US-10-719-993-6854	Sequence 6854, Ap	c1325	41.6	1.8	5663	15	US-10-311-455-670	Sequence 670, App
1253	42	1.8	96588	11	US-09-997-722-292	Sequence 292, App	c1326	41.6	1.8	5663	18	US-10-240-589C-32	Sequence 32, Appl
1254	42	1.8	117750	19	US-10-367-094-169	Sequence 169, App	c1327	41.6	1.8	5666	21	US-10-486-319A-61	Sequence 61, Appl
1255	42	1.8	271990	15	US-10-195-144-87	Sequence 87, Appl	1328	41.6	1.8	5798	15	US-10-311-455-1640	Sequence 1640, Ap
1256	42	1.8	271990	17	US-10-345-072-87	Sequence 87, Appl	c1329	41.6	1.8	5887	17	US-10-221-613-379	Sequence 379, App
1257	41.8	1.8	375	10	US-09-814-353-5244	Sequence 5244, Ap	c1330	41.6	1.8	6013	17	US-10-221-613-226	Sequence 226, App
1258	41.8	1.8	375	10	US-09-814-353-11531	Sequence 11531, A	1331	41.6	1.8	6156	18	US-10-240-589C-97	Sequence 97, Appl
c1259	41.8	1.8	552	20	US-10-425-115-42027	Sequence 42027, A	c1332	41.6	1.8	6167	15	US-10-240-453-243	Sequence 243, App
c1260	41.8	1.8	606	19	US-10-437-963-54715	Sequence 54715, A	c1333	41.6	1.8	6233	18	US-10-221-714A-219	Sequence 219, App
1261	41.8	1.8	903	13	US-10-027-632-121072	Sequence 121072,	c1334	41.6	1.8	6327	14	US-10-239-676-152	Sequence 152, App
1262	41.8	1.8	903	13	US-10-027-632-121073	Sequence 121073,	c1335	41.6	1.8	6327	15	US-10-240-453-168	Sequence 168, App
1263	41.8	1.8	903	17	US-10-027-632-121072	Sequence 121072,	1336	41.6	1.8	6641	15	US-10-311-455-288	Sequence 288, App
1264	41.8	1.8	903	17	US-10-027-632-121073	Sequence 121073,	1337	41.6	1.8	6641	16	US-10-240-452-36	Sequence 36, Appl
1265	41.8	1.8	1300	13	US-10-027-632-206926	Sequence 206926,	1338	41.6	1.8	6899	15	US-10-311-455-1867	Sequence 1867, Ap
1266	41.8	1.8	1300	17	US-10-027-632-206926	Sequence 206926,	c1339	41.6	1.8	8260	15	US-10-240-453-216	Sequence 216, App
1267	41.8	1.8	2478	16	US-10-349-680-145	Sequence 145, App	1340	41.6	1.8	9118	19	US-10-433-793-20	Sequence 20, Appl
c1268	41.8	1.8	5033	20	US-10-473-126-140	Sequence 140, App	c1341	41.6	1.8	9382	22	US-10-964-838-2	Sequence 2, Appli
c1269	41.8	1.8	5033	20	US-10-473-126-286	Sequence 286, App	1342	41.6	1.8	9741	15	US-10-311-455-1296	Sequence 1296, Ap
c1270	41.8	1.8	5107	15	US-10-311-455-1039	Sequence 1039, Ap	c1343	41.6	1.8	10710	15	US-10-311-455-865	Sequence 865, App
c1271	41.8	1.8	6156	18	US-10-240-589C-98	Sequence 98, Appl	c1344	41.6	1.8	10996	15	US-10-240-453-339	Sequence 339, App
c1272	41.8	1.8	6195	15	US-10-311-455-564	Sequence 564, App	c1345	41.6	1.8	10996	18	US-10-221-714A-531	Sequence 531, App
c1273	41.8	1.8	6823	15	US-10-311-455-1118	Sequence 1118, Ap	c1346	41.6	1.8	11029	18	US-10-221-714A-136	Sequence 136, App
c1274	41.8	1.8	6894	15	US-10-172-086-30	Sequence 30, Appl	1347	41.6	1.8	11047	14	US-10-239-676-187	Sequence 187, App

1348	41.6	1.8	11047	15	US-10-311-455-1957	Sequence 1957, Ap	1421	41.2	1.7	5445	18	US-10-221-714A-317	Sequence 317, App
1349	41.6	1.8	11047	15	US-10-240-453-275	Sequence 275, App	1422	41.2	1.7	5884	15	US-10-311-455-2138	Sequence 2138, Ap
1350	41.6	1.8	11422	15	US-10-311-455-192	Sequence 192, App	cl1423	41.2	1.7	6113	15	US-10-311-455-404	Sequence 404, App
1351	41.6	1.8	11422	17	US-10-257-166-18	Sequence 18, Appl	cl1424	41.2	1.7	6113	18	US-10-240-589C-14	Sequence 14, Appl
1352	41.6	1.8	12356	18	US-10-221-714A-231	Sequence 231, App	cl1425	41.2	1.7	6264	16	US-10-240-452-68	Sequence 68, Appl
1353	41.6	1.8	14316	17	US-10-221-613-407	Sequence 407, App	cl1426	41.2	1.7	6264	18	US-10-221-714A-334	Sequence 334, App
1354	41.6	1.8	15732	14	US-10-239-676-96	Sequence 96, Appl	1427	41.2	1.7	6343	20	US-10-473-126-187	Sequence 187, App
1355	41.6	1.8	15732	15	US-10-240-453-108	Sequence 108, App	cl1428	41.2	1.7	6365	15	US-10-311-455-97	Sequence 97, Appl
1356	41.6	1.8	16173	15	US-10-240-485-21	Sequence 21, Appl	1429	41.2	1.7	6394	17	US-10-221-613-240	Sequence 240, App
1357	41.6	1.8	16287	15	US-10-311-455-645	Sequence 645, App	cl1430	41.2	1.7	6636	15	US-10-311-455-763	Sequence 763, App
1358	41.6	1.8	16811	15	US-10-311-455-1919	Sequence 1919, Ap	cl1431	41.2	1.7	6863	18	US-10-221-714A-340	Sequence 340, App
1359	41.6	1.8	17294	15	US-10-311-455-960	Sequence 960, App	cl1432	41.2	1.7	7255	15	US-10-311-455-1251	Sequence 1251, Ap
1360	41.6	1.8	19576	17	US-10-221-613-220	Sequence 220, App	cl1433	41.2	1.7	9110	18	US-10-221-714A-116	Sequence 116, App
1361	41.6	1.8	40324	19	US-10-433-793-179	Sequence 179, App	1434	41.2	1.7	9243	15	US-10-240-453-127	Sequence 127, App
1362	41.6	1.8	48509	19	US-10-322-281-510	Sequence 510, App	1435	41.2	1.7	11143	24	US-11-097-143-16492	Sequence 16492, A
1363	41.6	1.8	158001	17	US-10-211-179-11	GENERAL INFORMATI	cl1436	41.2	1.7	13511	15	US-10-311-455-254	Sequence 254, App
1364	41.6	1.8	176096	22	US-10-981-277-34	Sequence 34, Appl	1437	41.2	1.7	13573	15	US-10-311-455-1841	Sequence 1841, Ap
1365	41.4	1.7	628	13	US-10-027-632-28987	Sequence 28987, A	cl1438	41.2	1.7	15046	15	US-10-311-455-2074	Sequence 2074, Ap
1366	41.4	1.7	628	17	US-10-027-632-28987	Sequence 28987, A	1439	41.2	1.7	15951	15	US-10-311-455-1653	Sequence 1653, Ap
1367	41.4	1.7	679	10	US-09-814-353-5129	Sequence 5129, Ap	1440	41.2	1.7	15951	15	US-10-240-485-133	Sequence 133, App
1368	41.4	1.7	679	10	US-09-814-353-11420	Sequence 11420, A	cl1441	41.2	1.7	16217	15	US-10-311-455-597	Sequence 597, App
1369	41.4	1.7	712	15	US-10-106-698-1404	Sequence 1404, Ap	cl1442	41.2	1.7	17211	15	US-10-311-455-628	Sequence 628, App
1370	41.4	1.7	1599	21	US-10-706-635-58	Sequence 58, Appl	cl1443	41.2	1.7	19087	15	US-10-311-455-766	Sequence 766, App
1371	41.4	1.7	2562	24	US-11-097-143-30379	Sequence 30379, A	cl1444	41.2	1.7	73334	15	US-10-311-455-2097	Sequence 2097, Ap
1372	41.4	1.7	3197	22	US-10-499-554-3	Sequence 3, Appli	cl1445	41.2	1.7	73334	18	US-10-240-589C-127	Sequence 127, App
1373	41.4	1.7	5277	14	US-10-213-509-1	Sequence 1, Appli	1446	41.2	1.7	119036	21	US-10-741-600-17721	Sequence 17721, A
1374	41.4	1.7	5312	15	US-10-311-455-815	Sequence 815, App	1447	41.2	1.7	133787	19	US-10-322-281-858	Sequence 858, App
1375	41.4	1.7	5312	17	US-10-257-166-79	Sequence 79, Appl	1448	41.2	1.7	198522	13	US-10-087-192-244	Sequence 244, App
1376	41.4	1.7	6022	18	US-10-221-714A-384	Sequence 384, App	1449	41.2	1.7	247461	19	US-10-322-281-131	Sequence 131, App
1377	41.4	1.7	6118	15	US-10-311-455-1004	Sequence 1004, Ap	1450	41	1.7	502	10	US-09-814-353-17272	Sequence 17272, A
1378	41.4	1.7	6132	15	US-10-311-455-836	Sequence 836, App	cl1451	41	1.7	996	18	US-10-424-599-54364	Sequence 54364, A
1379	41.4	1.7	6179	18	US-10-221-714A-65	Sequence 65, Appl	cl1452	41	1.7	1117	18	US-10-424-599-46014	Sequence 46014, A
1380	41.4	1.7	6242	15	US-10-311-455-2121	Sequence 2121, Ap	cl1453	41	1.7	2427	20	US-10-602-494-300	Sequence 300, App
1381	41.4	1.7	6271	15	US-10-172-086-36	Sequence 36, Appl	1454	41	1.7	2919	24	US-11-097-143-42274	Sequence 42274, A
1382	41.4	1.7	6271	15	US-10-311-455-1310	Sequence 1310, Ap	1455	41	1.7	3891	17	US-10-282-122A-35508	Sequence 35508, A
1383	41.4	1.7	6271	18	US-10-221-714A-178	Sequence 178, App	1456	41	1.7	4902	24	US-11-097-143-40636	Sequence 40636, A
1384	41.4	1.7	6271	19	US-10-311-507-62	Sequence 62, Appl	cl1457	41	1.7	5236	15	US-10-311-455-323	Sequence 323, App
1385	41.4	1.7	6271	20	US-10-480-846-36	Sequence 36, Appl	cl1458	41	1.7	5397	15	US-10-311-455-2178	Sequence 2178, Ap
1386	41.4	1.7	6298	14	US-10-239-676-64	Sequence 64, Appl	1459	41	1.7	5455	24	US-11-097-143-23071	Sequence 23071, A
1387	41.4	1.7	6298	15	US-10-240-453-68	Sequence 68, Appl	1460	41	1.7	5660	20	US-10-473-126-138	Sequence 138, App
1388	41.4	1.7	6303	19	US-10-433-793-116	Sequence 116, App	1461	41	1.7	5660	20	US-10-473-126-284	Sequence 284, App
1389	41.4	1.7	7046	15	US-10-311-455-2089	Sequence 2089, Ap	1462	41	1.7	5666	21	US-10-486-319A-39	Sequence 39, Appl
1390	41.4	1.7	8461	24	US-11-097-143-42007	Sequence 42007, A	1463	41	1.7	5666	21	US-10-486-319A-61	Sequence 61, Appl
1391	41.4	1.7	8805	15	US-10-311-455-485	Sequence 485, App	1464	41	1.7	5891	17	US-10-221-613-44	Sequence 44, Appl
1392	41.4	1.7	9817	15	US-10-311-455-1341	Sequence 1341, Ap	cl1465	41	1.7	6127	15	US-10-311-455-1587	Sequence 1587, Ap
1393	41.4	1.7	10254	15	US-10-311-455-1048	Sequence 1048, Ap	cl1466	41	1.7	6270	15	US-10-311-455-1846	Sequence 1846, Ap
1394	41.4	1.7	11892	24	US-11-097-143-40924	Sequence 40924, A	cl1467	41	1.7	6373	15	US-10-311-455-1939	Sequence 1939, Ap
1395	41.4	1.7	13712	15	US-10-311-455-1503	Sequence 1503, Ap	cl1468	41	1.7	6503	15	US-10-311-455-743	Sequence 743, App
1396	41.4	1.7	15548	15	US-10-311-455-2128	Sequence 2128, Ap	cl1469	41	1.7	6522	15	US-10-311-455-1776	Sequence 1776, Ap
1397	41.4	1.7	16173	15	US-10-240-485-22	Sequence 22, Appl	1470	41	1.7	6641	15	US-10-311-455-287	Sequence 287, App
1398	41.4	1.7	16373	15	US-10-311-455-591	Sequence 591, App	1471	41	1.7	6641	16	US-10-240-452-35	Sequence 35, Appl
1399	41.4	1.7	17738	15	US-10-311-455-1512	Sequence 1512, Ap	cl1472	41	1.7	6713	15	US-10-311-455-1054	Sequence 1054, Ap
1400	41.4	1.7	17918	17	US-10-221-613-382	Sequence 382, App	cl1473	41	1.7	6815	14	US-10-240-485-80	Sequence 80, Appl
1401	41.4	1.7	19659	15	US-10-311-455-740	Sequence 740, App	cl1474	41	1.7	6815	15	US-10-239-676-49	Sequence 49, Appl
1402	41.4	1.7	50000	21	US-10-706-635-25	Sequence 25, Appl	cl1475	41	1.7	6815	15	US-10-311-455-643	Sequence 643, App
1403	41.4	1.7	118356	21	US-10-741-600-17643	Sequence 17643, A	cl1476	41	1.7	6815	15	US-10-240-453-49	Sequence 49, Appl
1404	41.2	1.7	393	9	US-09-960-352-4582	Sequence 4582, Ap	cl1477	41	1.7	6881	15	US-10-311-455-1354	Sequence 1354, Ap
1405	41.2	1.7	553	20	US-10-363-345A-22741	Sequence 22741, A	cl1478	41	1.7	6881	15	US-10-240-453-124	Sequence 124, App
1406	41.2	1.7	553	20	US-10-363-345A-22742	Sequence 22742, A	cl1479	41	1.7	7072	17	US-10-221-613-348	Sequence 348, App
1407	41.2	1.7	553	21	US-10-363-483A-22741	Sequence 22741, A	cl1480	41	1.7	7238	15	US-10-311-455-421	Sequence 421, App
1408	41.2	1.7	553	21	US-10-363-483A-22742	Sequence 22742, A	1481	41	1.7	8346	15	US-10-240-453-202	Sequence 202, App
1409	41.2	1.7	574	19	US-10-021-323-11147	Sequence 11147, A	1482	41	1.7	8666	15	US-10-311-455-370	Sequence 370, App
1410	41.2	1.7	631	10	US-09-814-353-5993	Sequence 5993, Ap	1483	41	1.7	8666	18	US-10-221-714A-28	Sequence 28, Appl
1411	41.2	1.7	631	10	US-09-814-353-12272	Sequence 12272, A	1484	41	1.7	8666	19	US-10-311-507-96	Sequence 96, Appl
1412	41.2	1.7	1013	19	US-10-437-963-47635	Sequence 47635, A	1485	41	1.7	9524	15	US-10-433-793-208	Sequence 208, App
1413	41.2	1.7	2000	9	US-09-938-842A-3655	Sequence 3655, Ap	cl1486	41	1.7	9524	17	US-10-257-166-75	Sequence 75, Appl
1414	41.2	1.7	2000	11	US-09-938-842A-3655	Sequence 3655, Ap	cl1487	41	1.7	9524	17	US-10-221-613-212	Sequence 212, App
1415	41.2	1.7	2501	16	US-10-190-312A-68	Sequence 68, Appl	cl1488	41	1.7	10048	17	US-10-221-613-212	Sequence 212, App
1416	41.2	1.7	2501	24	US-11-013-031A-68	Sequence 68, Appl	cl1489	41	1.7	11691	15	US-10-311-455-2214	Sequence 2214, Ap
1417	41.2	1.7	2501	24	US-11-012-546-68	Sequence 68, Appl	1490	41	1.7	12138	15	US-10-311-455-1602	Sequence 1602, Ap
1418	41.2	1.7	2825	10	US-09-919-039-325	Sequence 325, App	1491	41	1.7	12138	17	US-10-257-166-116	Sequence 116, App
1419	41.2	1.7	2825	16	US-10-252-157-51	Sequence 51, Appl	1492	41	1.7	12356	18	US-10-221-714A-232	Sequence 232, App
1420	41.2	1.7	5427	15	US-10-311-455-686	Sequence 686, App	1493	41	1.7	13131	18	US-10-240-589C-58	Sequence 58, Appl

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21	239	10.1	241	4	US-09-834-759-324
22	239	10.1	241	4	US-09-590-751A-324
23	239	10.1	241	4	US-09-551-621-324
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39	52.8	2.2	266293	4	US-09-949-016-11934	Sequence 11934, A
40	51.4	2.2	187169	4	US-09-949-016-12776	Sequence 12776, A
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42	51.2	2.2	724	3	US-08-998-416-683	Sequence 683, Appl
43	51	2.2	1141	4	US-09-806-708B-22	Sequence 22, Appl
44	50.6	2.1	18773	4	US-09-949-016-14164	Sequence 14164, A
54	49.4	2.1	1055	4	US-09-806-708B-23	Sequence 23, Appl
55	49.2	2.1	663	3	US-08-998-416-191	Sequence 191, Appl
56	49.2	2.1	732	3	US-08-998-416-1036	Sequence 1036, Ap
57	49.2	2.1	854	3	US-08-998-416-534	Sequence 534, Appl
58	49.2	2.1	387902	4	US-09-949-016-14543	Sequence 14543, A
59	49.2	2.1	421883	4	US-09-949-016-12557	Sequence 12557, A
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62	48.2	2.0	1587	4	US-09-010-147B-19	Sequence 19, Appl
63	48.2	2.0	1720	4	US-09-148-545-53	Sequence 53, Appl
64	48	2.0	601	4	US-09-949-016-168196	Sequence 168196,
65	48	2.0	19438	4	US-09-949-016-12699	Sequence 12699, A
66	47.8	2.0	4529	4	US-09-949-016-14004	Sequence 14004, A
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68	47.4	2.0	67755	4	US-09-949-016-13703	Sequence 13703, A
69	46.8	2.0	129415	4	US-09-949-016-16997	Sequence 16997, A
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75	46.6	2.0	231129	4	US-09-949-016-16110	Sequence 16110, A
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78	46.4	2.0	4092	4	US-09-710-279-4263	Sequence 4263, Ap
79	46.4	2.0	55886	4	US-09-949-016-15129	Sequence 15129, A
80	46.4	2.0	59519	4	US-09-949-016-13504	Sequence 13504, A
81	46.4	2.0	263693	4	US-09-949-016-12386	Sequence 12386, A
82	46.4	2.0	263694	4	US-09-949-016-16915	Sequence 16915, A
83	46.2	1.9	119153	4	US-09-949-016-12378	Sequence 12378, A
84	46	1.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
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86	45.8	1.9	319608	4	US-09-539-333D-1	Sequence 1, Appli
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92	45.4	1.9	95255	4	US-09-949-016-17067	Sequence 17067, A
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94	45.4	1.9	201529	4	US-09-949-016-12740	Sequence 12740, A
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96	45	1.9	96922	4	US-09-949-016-17061	Sequence 17061, A
97	45	1.9	113966	4	US-09-949-016-12277	Sequence 12277, A
98	45	1.9	113967	4	US-09-949-016-17051	Sequence 17051, A
99	44.6	1.9	711	3	US-08-998-416-786	Sequence 786, Appl
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114	43.2	1.8	1520	1	US-08-225-477B-1	Sequence 1, Appli
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c 122	43.2	1.8	2144	3	US-08-747-221B-57	Sequence 57, Appl
c 123	43.2	1.8	2144	3	US-08-747-221B-59	Sequence 59, Appl
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c 130	43.2	1.8	134987	4	US-09-949-016-15348	Sequence 15348, A
c 131	43.2	1.8	134987	4	US-09-949-016-15349	Sequence 15349, A
c 132	43.2	1.8	134987	4	US-09-949-016-15350	Sequence 15350, A
c 133	43.2	1.8	134987	4	US-09-949-016-15507	Sequence 15507, A
c 134	43.2	1.8	134987	4	US-09-949-016-15508	Sequence 15508, A
c 135	43.2	1.8	134987	4	US-09-949-016-15509	Sequence 15509, A
c 136	43	1.8	601	4	US-09-949-016-155350	Sequence 155350, A
c 137	43	1.8	60489	4	US-09-949-016-16287	Sequence 16287, A
c 138	43	1.8	237241	4	US-09-949-016-16101	Sequence 16101, A
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c 140	42.8	1.8	28129	4	US-09-949-016-17169	Sequence 17169, A
c 141	42.8	1.8	34011	4	US-09-949-016-12485	Sequence 12485, A
c 142	42.8	1.8	48536	4	US-09-949-016-11867	Sequence 11867, A
c 143	42.8	1.8	48536	4	US-09-949-016-17167	Sequence 17167, A
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c 146	42.6	1.8	601	4	US-09-949-016-30531	Sequence 30531, A
c 147	42.6	1.8	601	4	US-09-949-016-37149	Sequence 37149, A
c 148	42.6	1.8	601	4	US-09-949-016-37150	Sequence 37150, A
c 149	42.6	1.8	601	4	US-09-949-016-37163	Sequence 37163, A
c 150	42.6	1.8	601	4	US-09-949-016-37164	Sequence 37164, A
c 151	42.6	1.8	601	4	US-09-949-016-145867	Sequence 145867, A
c 152	42.6	1.8	601	4	US-09-949-016-145868	Sequence 145868, A
c 153	42.6	1.8	601	4	US-09-949-016-146135	Sequence 146135, A
c 154	42.6	1.8	601	4	US-09-949-016-146136	Sequence 146136, A
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c 156	42.6	1.8	601	4	US-09-949-016-146404	Sequence 146404, A
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c 158	42.6	1.8	1111	4	US-08-781-986A-756	Sequence 756, App
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c 161	42.6	1.8	53332	4	US-10-224-562-3	Sequence 3, Appli
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c 168	42.6	1.8	223471	4	US-09-949-016-12725	Sequence 12725, A
c 169	42.6	1.8	298336	4	US-09-949-016-16600	Sequence 16600, A
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c 173	42.2	1.8	601	4	US-09-949-016-185650	Sequence 185650, A
c 174	42.2	1.8	1603	3	US-09-009-443-11	Sequence 11, Appl
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c 182	42.2	1.8	134987	4	US-09-949-016-15508	Sequence 15508, A
c 183	42.2	1.8	134987	4	US-09-949-016-15509	Sequence 15509, A
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c 185	42	1.8	636	3	US-08-998-416-1137	Sequence 1137, Ap
c 186	42	1.8	1431	3	US-09-316-083-2	Sequence 2, Appli
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c 193	42	1.8	317366	4	US-09-949-016-16001	Sequence 16001, A
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c 195	41.8	1.8	2478	4	US-09-601-198-52	Sequence 52, Appl
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c 197	41.8	1.8	26000	4	US-09-843-376-10	Sequence 10, Appl
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c 203	41.6	1.8	47781	4	US-09-949-016-16492	Sequence 16492, A
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c 206	41.6	1.8	50383	4	US-09-949-016-17600	Sequence 17600, A
c 207	41.6	1.8	60589	4	US-09-949-016-17070	Sequence 17070, A
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c 209	41.4	1.7	601	4	US-09-949-016-37271	Sequence 37271, A
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c 211	41.4	1.7	601	4	US-09-949-016-195068	Sequence 195068, A
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c 214	41.4	1.7	94847	4	US-09-949-016-16336	Sequence 16336, A
c 215	41.2	1.7	601	4	US-09-949-016-185649	Sequence 185649, A
c 216	41.2	1.7	2825	4	US-09-919-039-325	Sequence 325, App
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c 218	41.2	1.7	47781	4	US-09-949-016-16492	Sequence 16492, A
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c 226	41.2	1.7	818128	4	US-09-949-016-14547	Sequence 14547, A
c 227	41.2	1.7	818128	4	US-09-949-016-14548	Sequence 14548, A
c 228	41.2	1.7	818128	4	US-09-949-016-14549	Sequence 14549, A
c 229	41.2	1.7	818128	4	US-09-949-016-14550	Sequence 14550, A
c 230	41.2	1.7	818128	4	US-09-949-016-14551	Sequence 14551, A
c 231	41.2	1.7	818128	4	US-09-949-016-14552	Sequence 14552, A
c 232	41.2	1.7	818128	4	US-09-949-016-14553	Sequence 14553, A
c 233	41.2	1.7	818128	4	US-09-949-016-14554	Sequence 14554, A
c 234	41.2	1.7	818128	4	US-09-949-016-14555	Sequence 14555, A
c 235	41.2	1.7	818128	4	US-09-949-016-14556	Sequence 14556, A
c 236	41.2	1.7	818128	4	US-09-949-016-14557	Sequence 14557, A
c 237	41.2	1.7	818128	4	US-09-949-016-14558	Sequence 14558, A
c 238	41.2	1.7	818128	4	US-09-949-016-14559	Sequence 14559, A
c 239	41.2	1.7	818128	4	US-09-949-016-14560	Sequence 14560, A
c 240	41.2	1.7	818128	4	US-09-949-016-14561	Sequence 14561, A
c 241	41.2	1.7	818128	4	US-09-949-016-14562	Sequence 14562, A
c 242	41.2	1.7	818128	4	US-09-949-016-14564	Sequence 14564, A
c 243	41.2	1.7	818128	4	US-09-949-016-14565	Sequence 14565, A
c 244	41.2	1.7	818128	4	US-09-949-016-14566	Sequence 14566, A
c 245	41.2	1.7	818128	4	US-09-949-016-14567	Sequence 14567, A
c 246	41	1.7	601	4	US-09-949-016-30532	Sequence 30532, A
c 247	41	1.7	601	4	US-09-949-016-30532	Sequence 30532, A
c 248	41	1.7	601	4	US-09-949-016-37151	Sequence 37151, A
c 249	41	1.7	601	4	US-09-949-016-37151	Sequence 37151, A
c 250	41	1.7	601	4	US-09-949-016-37165	Sequence 37165, A
c 251	41	1.7	601	4	US-09-949-016-37165	Sequence 37165, A
c 252	41	1.7	601	4	US-09-949-016-145869	Sequence 145869, A
c 253	41	1.7	601	4	US-09-949-016-145869	Sequence 145869, A
c 254	41	1.7	601	4	US-09-949-016-146137	Sequence 146137, A
c 255	41	1.7	601	4	US-09-949-016-146137	Sequence 146137, A
c 256	41	1.7	601	4	US-09-949-016-146405	Sequence 146405, A
c 257	41	1.7	601	4	US-09-949-016-146405	Sequence 146405, A
c 258	41	1.7	3259	5	PCT-US95-03747-1	Sequence 1, Appli
c 259	41	1.7	5432	4	US-09-949-016-15178	Sequence 15178, A
c 260	41	1.7	5852	1	US-07-867-106-2	Sequence 2, Appli
c 261	41	1.7	19124	2	US-08-487-828B-13	Sequence 13, Appl
c 262	41	1.7	55264	4	US-09-949-016-15014	Sequence 15014, A
c 263	41	1.7	87323	4	US-09-949-016-13828	Sequence 13828, A
c 264	41	1.7	94755	4	US-09-949-016-11839	Sequence 11839, A
c 265	41	1.7	205044	4	US-09-949-016-15851	Sequence 15851, A

266	41	1.7	205044	4	US-09-949-016-15852	Sequence 15852, A	C 339	40	1.7	74962	4	US-09-685-853A-3	Sequence 3, Appli
267	41	1.7	205044	4	US-09-949-016-15853	Sequence 15853, A	C 340	40	1.7	99748	4	US-09-949-016-11990	Sequence 11990, A
268	41	1.7	223471	4	US-09-949-016-12387	Sequence 12387, A	C 341	40	1.7	99749	4	US-09-949-016-16518	Sequence 16518, A
269	41	1.7	223471	4	US-09-949-016-12724	Sequence 12724, A	342	40	1.7	251672	4	US-09-949-016-17296	Sequence 17296, A
270	41	1.7	223471	4	US-09-949-016-12725	Sequence 12725, A	343	40	1.7	251682	4	US-09-949-016-11973	Sequence 11973, A
C 271	41	1.7	451924	4	US-09-949-016-12896	Sequence 12896, A	C 344	39.8	1.7	601	4	US-09-949-016-133300	Sequence 133300, A
C 272	41	1.7	451925	4	US-09-949-016-17305	Sequence 17305, A	C 345	39.8	1.7	7234	4	US-09-949-016-12159	Sequence 12159, A
273	40.8	1.7	601	4	US-09-949-016-39876	Sequence 39876, A	C 346	39.8	1.7	7235	4	US-09-949-016-16479	Sequence 16479, A
274	40.8	1.7	601	4	US-09-949-016-185199	Sequence 185199, A	C 347	39.8	1.7	17082	4	US-09-949-016-14893	Sequence 14893, A
275	40.8	1.7	1851	4	US-09-601-198-51	Sequence 51, Appl	348	39.8	1.7	19124	2	US-08-487-826B-13	Sequence 13, Appl
C 276	40.8	1.7	17616	4	US-09-949-016-13170	Sequence 13170, A	349	39.8	1.7	38983	4	US-09-949-016-15700	Sequence 15700, A
C 277	40.8	1.7	70262	4	US-09-949-016-13375	Sequence 13375, A	C 350	39.8	1.7	118143	4	US-09-949-016-17196	Sequence 17196, A
C 278	40.8	1.7	70263	4	US-09-949-016-12748	Sequence 12748, A	C 351	39.8	1.7	392000	4	US-10-027-983-11	Sequence 11, Appl
279	40.8	1.7	101128	4	US-09-949-016-14293	Sequence 14293, A	352	39.6	1.7	601	4	US-09-949-016-39877	Sequence 39877, A
280	40.8	1.7	165841	4	US-09-949-016-16192	Sequence 16192, A	353	39.6	1.7	601	4	US-09-949-016-39878	Sequence 39878, A
281	40.6	1.7	149	4	US-09-513-999C-25254	Sequence 25254, A	354	39.6	1.7	601	4	US-09-949-016-169759	Sequence 169759, A
282	40.6	1.7	762	4	US-09-543-681A-3870	Sequence 3870, Ap	C 355	39.6	1.7	601	4	US-09-949-016-173637	Sequence 173637, A
283	40.6	1.7	1689	1	US-07-991-867B-41	Sequence 41, Appl	C 356	39.6	1.7	601	4	US-09-949-016-179439	Sequence 179439, A
284	40.6	1.7	1689	2	US-08-544-332-41	Sequence 41, Appl	357	39.6	1.7	601	4	US-09-949-016-185200	Sequence 185200, A
285	40.6	1.7	1689	3	US-09-370-861A-41	Sequence 41, Appl	358	39.6	1.7	601	4	US-09-949-016-185201	Sequence 185201, A
286	40.6	1.7	1947	3	US-09-370-861A-74	Sequence 74, Appl	359	39.6	1.7	51101	4	US-09-949-016-12859	Sequence 12859, A
C 287	40.6	1.7	5796	4	US-09-366-715-4	Sequence 4, Appli	360	39.6	1.7	51101	4	US-09-949-016-17036	Sequence 17036, A
288	40.6	1.7	8457	1	US-07-991-867B-1	Sequence 1, Appli	361	39.6	1.7	100863	4	US-09-949-016-17031	Sequence 17031, A
289	40.6	1.7	8457	2	US-08-544-332-1	Sequence 1, Appli	C 362	39.6	1.7	263693	4	US-09-949-016-12386	Sequence 12386, A
290	40.6	1.7	8457	3	US-09-370-861A-1	Sequence 1, Appli	C 363	39.6	1.7	263694	4	US-09-949-016-16915	Sequence 16915, A
C 291	40.6	1.7	34011	4	US-09-949-016-12485	Sequence 12485, A	364	39.4	1.7	601	4	US-09-949-016-170363	Sequence 170363, A
C 292	40.6	1.7	40936	4	US-09-949-016-16607	Sequence 16607, A	C 365	39.4	1.7	1683	3	US-09-347-803-11	Sequence 11, Appl
C 293	40.6	1.7	40936	4	US-09-949-016-16608	Sequence 16608, A	C 366	39.4	1.7	1785	4	US-09-601-198-156	Sequence 156, App
C 294	40.6	1.7	54452	4	US-09-949-016-12642	Sequence 12642, A	C 367	39.4	1.7	94142	4	US-09-949-016-16553	Sequence 16553, A
C 295	40.6	1.7	54452	4	US-09-949-016-13003	Sequence 13003, A	368	39.4	1.7	114139	4	US-09-949-016-16536	Sequence 16536, A
C 296	40.4	1.7	601	4	US-09-949-016-54117	Sequence 54117, A	369	39.4	1.7	134890	4	US-09-949-016-15602	Sequence 15602, A
297	40.4	1.7	601	4	US-09-949-016-204629	Sequence 204629, A	C 370	39.4	1.7	189560	4	US-09-949-016-17202	Sequence 17202, A
298	40.4	1.7	662	3	US-08-998-416-185	Sequence 185, App	371	39.2	1.7	601	4	US-09-949-016-39879	Sequence 39879, A
299	40.4	1.7	665	3	US-08-998-416-937	Sequence 937, App	372	39.2	1.7	601	4	US-09-949-016-39879	Sequence 39879, A
300	40.4	1.7	701	3	US-08-998-416-701	Sequence 701, App	373	39.2	1.7	601	4	US-09-949-016-74721	Sequence 74721, A
301	40.4	1.7	767	3	US-08-998-416-472	Sequence 472, App	374	39.2	1.7	601	4	US-09-949-016-74722	Sequence 74722, A
302	40.4	1.7	827	3	US-08-998-416-535	Sequence 535, App	375	39.2	1.7	601	4	US-09-949-016-74920	Sequence 74920, A
303	40.4	1.7	834	3	US-08-998-416-305	Sequence 305, App	376	39.2	1.7	601	4	US-09-949-016-74921	Sequence 74921, A
304	40.4	1.7	1297	4	US-09-023-655-876	Sequence 876, App	377	39.2	1.7	601	4	US-09-949-016-75119	Sequence 75119, A
305	40.4	1.7	1928	3	US-08-675-816-4	Sequence 4, Appli	378	39.2	1.7	601	4	US-09-949-016-75318	Sequence 75318, A
C 306	40.4	1.7	30820	4	US-09-949-016-17145	Sequence 17145, A	379	39.2	1.7	601	4	US-09-949-016-75319	Sequence 75319, A
307	40.4	1.7	32573	4	US-09-949-016-13359	Sequence 13359, A	380	39.2	1.7	601	4	US-09-949-016-75517	Sequence 75517, A
C 308	40.4	1.7	64593	4	US-09-949-016-16554	Sequence 16654, A	381	39.2	1.7	601	4	US-09-949-016-75518	Sequence 75518, A
C 309	40.4	1.7	64593	4	US-09-949-016-16655	Sequence 16655, A	382	39.2	1.7	601	4	US-09-949-016-106075	Sequence 106075, A
C 310	40.4	1.7	64593	4	US-09-949-016-16656	Sequence 16656, A	383	39.2	1.7	601	4	US-09-949-016-106076	Sequence 106076, A
C 311	40.4	1.7	67755	4	US-09-949-016-13703	Sequence 13703, A	384	39.2	1.7	601	4	US-09-949-016-106274	Sequence 106274, A
312	40.4	1.7	95255	4	US-09-949-016-17067	Sequence 17067, A	385	39.2	1.7	601	4	US-09-949-016-106275	Sequence 106275, A
C 313	40.4	1.7	99498	4	US-09-949-016-12621	Sequence 12621, A	386	39.2	1.7	601	4	US-09-949-016-106473	Sequence 106473, A
314	40.4	1.7	120213	4	US-09-949-016-13304	Sequence 13304, A	387	39.2	1.7	601	4	US-09-949-016-106474	Sequence 106474, A
315	40.4	1.7	120217	4	US-09-949-016-12260	Sequence 12260, A	388	39.2	1.7	601	4	US-09-949-016-106672	Sequence 106672, A
C 316	40.4	1.7	122626	4	US-09-949-016-17524	Sequence 17524, A	389	39.2	1.7	601	4	US-09-949-016-106673	Sequence 106673, A
C 317	40.4	1.7	146428	4	US-09-949-016-12620	Sequence 12620, A	390	39.2	1.7	601	4	US-09-949-016-106871	Sequence 106871, A
C 318	40.4	1.7	146438	4	US-09-949-016-12081	Sequence 12081, A	391	39.2	1.7	601	4	US-09-949-016-106872	Sequence 106872, A
C 319	40.4	1.7	165841	4	US-09-949-016-16192	Sequence 16192, A	392	39.2	1.7	601	4	US-09-949-016-185202	Sequence 185202, A
C 320	40.2	1.7	658	3	US-08-998-416-595	Sequence 595, App	C 393	39.2	1.7	601	4	US-09-949-016-186365	Sequence 186365, A
321	40.2	1.7	863	3	US-08-998-416-498	Sequence 498, App	394	39.2	1.7	1055	4	US-09-806-708B-23	Sequence 23, Appl
C 322	40.2	1.7	2142	4	US-09-107-532A-905	Sequence 905, App	C 395	39.2	1.7	2949	4	US-09-236-995D-1	Sequence 1, Appli
C 323	40.2	1.7	6152	3	US-08-973-462-1	Sequence 1, Appli	C 396	39.2	1.7	3211	4	US-09-118-276-1	Sequence 1, Appli
324	40.2	1.7	160759	4	US-09-949-016-16514	Sequence 16514, A	C 397	39.2	1.7	3212	4	US-09-118-276-10	Sequence 10, Appl
325	40.2	1.7	168104	4	US-09-949-016-12026	Sequence 12026, A	398	39.2	1.7	3361	4	US-09-710-279-4125	Sequence 4125, Ap
326	40.2	1.7	168105	4	US-09-949-016-16554	Sequence 16554, A	399	39.2	1.7	6124	3	US-08-213-419B-3	Sequence 3, Appli
327	40	1.7	601	4	US-09-949-016-169758	Sequence 169758, A	C 400	39.2	1.7	12658	4	US-08-956-171E-127	Sequence 127, App
328	40	1.7	601	4	US-09-949-016-169760	Sequence 169760, A	C 401	39.2	1.7	12658	4	US-08-781-986A-127	Sequence 127, App
329	40	1.7	1025	3	US-08-480-640A-224	Sequence 224, App	402	39.2	1.7	20674	3	US-09-641-638-651	Sequence 651, App
330	40	1.7	1025	3	US-08-686-968C-224	Sequence 224, App	403	39.2	1.7	20674	4	US-10-170-097-651	Sequence 651, App
331	40	1.7	1025	3	US-08-488-237A-224	Sequence 224, App	404	39.2	1.7	55886	4	US-09-949-016-15129	Sequence 15129, A
332	40	1.7	1025	4	US-08-472-679H-224	Sequence 224, App	C 405	39.2	1.7	152331	3	US-09-128-155-16	Sequence 16, Appl
C 333	40	1.7	3164	3	US-08-686-968C-1	Sequence 1, Appli	C 406	39.2	1.7	176373	3	US-09-128-155-17	Sequence 17, Appl
334	40	1.7	8920	2	US-08-446-855A-1	Sequence 1, Appli	C 407	39.2	1.7	181429	4	US-09-949-016-12372	Sequence 12372, A
335	40	1.7	8920	3	US-09-150-741-1	Sequence 1, Appli	C 408	39.2	1.7	181430	4	US-09-949-016-15772	Sequence 15772, A
C 336	40	1.7	10640	4	US-09-417-485D-5	Sequence 5, Appli	409	39.2	1.7	278866	4	US-09-949-016-13922	Sequence 13922, A
337	40	1.7	53332	4	US-09-801-861-3	Sequence 3, Appli	410	39.2	1.7	278866	4	US-09-949-016-13923	Sequence 13923, A
338	40	1.7	53332	4	US-10-224-562-3	Sequence 3, Appli	411	39.2	1.7	278866	4	US-09-949-016-13924	Sequence 13924, A

412	39.2	1.7	278866	4	US-09-949-016-13925	Sequence 13925, A
413	39.2	1.7	278866	4	US-09-949-016-13926	Sequence 13926, A
414	39.2	1.7	278866	4	US-09-949-016-14699	Sequence 14699, A
415	39.2	1.7	278866	4	US-09-949-016-14700	Sequence 14700, A
416	39.2	1.7	278866	4	US-09-949-016-14701	Sequence 14701, A
417	39.2	1.7	278866	4	US-09-949-016-14702	Sequence 14702, A
418	39.2	1.7	278866	4	US-09-949-016-14703	Sequence 14703, A
419	39	1.6	472	3	US-09-020-956-95	Sequence 95, Appl
420	39	1.6	472	3	US-09-030-607-95	Sequence 95, Appl
421	39	1.6	472	3	US-09-439-313-95	Sequence 95, Appl
422	39	1.6	472	3	US-09-352-616A-95	Sequence 95, Appl
423	39	1.6	472	3	US-09-232-149A-95	Sequence 95, Appl
424	39	1.6	472	4	US-09-159-812-95	Sequence 95, Appl
425	39	1.6	472	4	US-09-636-215-95	Sequence 95, Appl
426	39	1.6	472	4	US-09-685-166A-95	Sequence 95, Appl
427	39	1.6	472	4	US-09-115-453-95	Sequence 95, Appl
428	39	1.6	472	4	US-09-688-489-95	Sequence 95, Appl
429	39	1.6	472	4	US-09-679-426-95	Sequence 95, Appl
430	39	1.6	472	4	US-09-759-143-95	Sequence 95, Appl
431	39	1.6	472	4	US-09-651-236-95	Sequence 95, Appl
432	39	1.6	601	4	US-09-949-016-196382	Sequence 196382,
433	39	1.6	3787	4	US-09-976-594-716	Sequence 716, App
434	39	1.6	18989	4	US-09-949-016-13435	Sequence 13435, A
435	39	1.6	21885	4	US-09-949-016-12600	Sequence 12600, A
436	39	1.6	96690	4	US-09-949-016-17103	Sequence 17103, A
437	39	1.6	152655	4	US-09-949-016-16246	Sequence 16246, A
438	39	1.6	238815	4	US-09-949-016-16274	Sequence 16274, A
439	38.8	1.6	285	2	US-08-250-346-18	Sequence 18, Appl
440	38.8	1.6	601	4	US-09-949-016-18855	Sequence 18855, A
441	38.8	1.6	601	4	US-09-949-016-56720	Sequence 56720, A
442	38.8	1.6	2216	4	US-09-426-783-5	Sequence 5, Appli
443	38.8	1.6	2621	2	US-08-553-619B-8	Sequence 8, Appli
444	38.8	1.6	3095	6	5231168-1	Patent No. 5231168
445	38.8	1.6	3095	6	5231168-1	Patent No. 5231168
446	38.8	1.6	4004	4	US-09-710-279-3534	Sequence 3534, Ap
447	38.8	1.6	27250	4	US-09-949-016-15537	Sequence 15537, A
448	38.8	1.6	37580	4	US-09-949-016-16658	Sequence 16658, A
449	38.8	1.6	43463	4	US-09-949-016-16341	Sequence 16341, A
450	38.8	1.6	59977	4	US-09-949-016-12259	Sequence 12259, A
451	38.8	1.6	59978	4	US-09-949-016-15397	Sequence 15397, A
452	38.8	1.6	86213	4	US-09-949-016-17240	Sequence 17240, A
453	38.8	1.6	86213	4	US-09-949-016-17241	Sequence 17241, A
454	38.8	1.6	86213	4	US-09-949-016-17242	Sequence 17242, A
455	38.8	1.6	86213	4	US-09-949-016-17243	Sequence 17243, A
456	38.6	1.6	601	4	US-09-949-016-103833	Sequence 103833,
457	38.6	1.6	601	4	US-09-949-016-103877	Sequence 103877,
458	38.6	1.6	601	4	US-09-949-016-121245	Sequence 121245,
459	38.6	1.6	601	4	US-09-949-016-160244	Sequence 160244,
460	38.6	1.6	601	4	US-09-949-016-160288	Sequence 160288,
461	38.6	1.6	1590	4	US-09-799-451-647	Sequence 647, App
462	38.6	1.6	2099	4	US-09-949-016-2191	Sequence 2191, Ap
463	38.6	1.6	2384	1	US-07-814-964-10	Sequence 10, Appl
464	38.6	1.6	2384	1	US-08-258-442-10	Sequence 10, Appl
465	38.6	1.6	2384	1	US-08-328-809-5	Sequence 5, Appli
466	38.6	1.6	2384	4	US-08-866-840-5	Sequence 5, Appli
467	38.6	1.6	2384	5	PCT-US92-11107-10	Sequence 10, Appl
468	38.6	1.6	4507	2	US-08-568-459A-3	Sequence 3, Appli
469	38.6	1.6	4507	2	US-08-487-826B-3	Sequence 3, Appli
470	38.6	1.6	4507	3	US-09-210-288-3	Sequence 3, Appli
471	38.6	1.6	19438	4	US-09-949-016-12699	Sequence 12699, A
472	38.6	1.6	27968	4	US-09-949-016-15191	Sequence 15191, A
473	38.6	1.6	27968	4	US-09-949-016-15192	Sequence 15192, A
474	38.6	1.6	28315	4	US-09-949-016-16916	Sequence 16916, A
475	38.6	1.6	30032	4	US-09-949-016-13933	Sequence 13933, A
476	38.6	1.6	78649	4	US-09-949-016-14619	Sequence 14619, A
477	38.6	1.6	78649	4	US-09-949-016-14620	Sequence 14620, A
478	38.6	1.6	78649	4	US-09-949-016-16227	Sequence 16227, A
479	38.6	1.6	78649	4	US-09-949-016-16228	Sequence 16228, A
480	38.6	1.6	80632	4	US-09-949-016-12951	Sequence 12951, A
481	38.6	1.6	84870	4	US-09-949-016-17547	Sequence 17547, A
482	38.6	1.6	111235	4	US-09-949-016-15328	Sequence 15328, A
483	38.6	1.6	183770	4	US-09-949-016-15494	Sequence 15494, A
484	38.6	1.6	421491	4	US-09-949-016-12805	Sequence 12805, A

485	38.6	1.6	421494	4	US-09-949-016-14060	Sequence 14060, A
486	38.4	1.6	601	4	US-09-949-016-130489	Sequence 130489,
487	38.4	1.6	601	4	US-09-949-016-153399	Sequence 153399,
488	38.4	1.6	601	4	US-09-949-016-153400	Sequence 153400,
489	38.4	1.6	601	4	US-09-949-016-153401	Sequence 153401,
490	38.4	1.6	601	4	US-09-949-016-153402	Sequence 153402,
491	38.4	1.6	1017	4	US-09-248-796A-929	Sequence 929, App
492	38.4	1.6	1962	4	US-09-148-545-111	Sequence 111, App
493	38.4	1.6	5046	4	US-09-725-735A-13	Sequence 13, Appl
494	38.4	1.6	18591	4	US-09-949-016-14719	Sequence 14719, A
495	38.4	1.6	40465	4	US-09-949-016-12561	Sequence 12561, A
496	38.4	1.6	57267	4	US-09-949-016-11899	Sequence 11899, A
497	38.4	1.6	66524	4	US-09-949-001-32	Sequence 32, Appl
498	38.4	1.6	66525	4	US-09-949-001-38	Sequence 38, Appl
499	38.4	1.6	91933	4	US-09-949-016-11855	Sequence 11855, A
500	38.4	1.6	91933	4	US-09-949-016-14628	Sequence 14628, A
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502	38.4	1.6	108310	4	US-09-949-016-16366	Sequence 16366, A
503	38.4	1.6	130563	4	US-09-949-016-12273	Sequence 12273, A
504	38.4	1.6	131379	4	US-09-949-016-16050	Sequence 16050, A
505	38.4	1.6	298336	4	US-09-949-016-16600	Sequence 16600, A
506	38.4	1.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
507	38.4	1.6	1664976	4	US-09-692-570-1	Sequence 104, App
508	38.2	1.6	591	4	US-09-495-050A-104	Sequence 80518, A
509	38.2	1.6	601	4	US-09-949-016-80518	Sequence 972, App
510	38.2	1.6	688	3	US-08-998-416-972	Sequence 288, App
511	38.2	1.6	837	3	US-08-998-416-288	Sequence 2262, Ap
512	38.2	1.6	924	4	US-09-248-796A-2262	Sequence 4484, Ap
513	38.2	1.6	957	4	US-09-270-767-4484	Sequence 19766, A
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515	38.2	1.6	1519	1	US-08-225-477B-2	Sequence 2, Appli
516	38.2	1.6	1519	5	PCT-US95-04353-2	Sequence 2, Appli
517	38.2	1.6	2323	3	US-09-149-476-24	Sequence 24, Appl
518	38.2	1.6	3867	4	US-09-366-715-5	Sequence 5, Appli
519	38.2	1.6	6671	1	US-08-280-443-1	Sequence 1, Appli
520	38.2	1.6	6671	1	US-08-457-459-1	Sequence 1, Appli
521	38.2	1.6	6671	1	US-08-555-678-1	Sequence 1, Appli
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523	38.2	1.6	10825	3	US-08-652-265-1	Sequence 1, Appli
524	38.2	1.6	10825	3	US-08-652-265-3	Sequence 3, Appli
525	38.2	1.6	10825	3	US-08-652-265-5	Sequence 5, Appli
526	38.2	1.6	10825	3	US-08-652-265-7	Sequence 7, Appli
527	38.2	1.6	10825	3	US-08-834-497A-1	Sequence 1, Appli
528	38.2	1.6	10825	3	US-08-834-497A-3	Sequence 3, Appli
529	38.2	1.6	10825	3	US-08-834-497A-5	Sequence 5, Appli
530	38.2	1.6	10825	3	US-08-834-497A-7	Sequence 7, Appli
531	38.2	1.6	10825	3	US-09-503-444A-1	Sequence 1, Appli
532	38.2	1.6	10825	3	US-09-503-444A-3	Sequence 3, Appli
533	38.2	1.6	10825	3	US-09-503-444A-5	Sequence 5, Appli
534	38.2	1.6	10825	3	US-09-503-444A-7	Sequence 7, Appli
535	38.2	1.6	12146	3	US-09-277-457-27	Sequence 27, Appl
536	38.2	1.6	12146	4	US-09-679-729-27	Sequence 27, Appl
537	38.2	1.6	12313	4	US-09-949-016-13248	Sequence 13248, A
538	38.2	1.6	13607	4	US-09-949-016-11806	Sequence 11806, A
539	38.2	1.6	13609	4	US-09-949-016-12922	Sequence 12922, A
540	38.2	1.6	123513	4	US-09-949-016-15794	Sequence 15794, A
541	38.2	1.6	134890	4	US-09-949-016-15602	Sequence 15602, A
542	38.2	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
543	38.2	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
544	38.2	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
545	38.2	1.6	247299	4	US-09-949-016-17590	Sequence 17590, A
546	38.2	1.6	269223	4	US-09-596-002-41	Sequence 41, Appl
547	38.2	1.6	314798	4	US-09-949-016-13539	Sequence 13539, A
548	38	1.6	399	4	US-09-621-976-8976	Sequence 8976, Ap
549	38	1.6	549	1	US-07-991-867B-28	Sequence 28, Appl
550	38	1.6	549	1	US-08-107-755A-28	Sequence 28, Appl
551	38	1.6	549	2	US-08-544-332-28	Sequence 28, Appl
552	38	1.6	549	3	US-09-370-861A-28	Sequence 28, Appl
553	38	1.6	601	4	US-09-949-016-48158	Sequence 48158, A
554	38	1.6	601	4	US-09-949-016-48160	Sequence 48160, A
555	38	1.6	601	4	US-09-949-016-96127	Sequence 96127, A
556	38	1.6	601	4	US-09-949-016-171662	Sequence 171662,
557	38	1.6	1276	2	US-08-463-911-1	Sequence 1, Appli

558	38	1.6	1276	4	US-09-776-976-3	Sequence 3, Appli	C 631	37.6	1.6	6804	4	US-09-949-016-16082	Sequence 16082, A
559	38	1.6	1276	4	US-09-909-547-3	Sequence 3, Appli	C 632	37.6	1.6	6804	4	US-09-949-016-16083	Sequence 16083, A
560	38	1.6	1309	6	5221624-4	Patent No. 5221624	C 633	37.6	1.6	25067	4	US-09-949-016-11794	Sequence 11794, A
561	38	1.6	1309	6	5221624-4	Patent No. 5221624	634	37.6	1.6	25441	4	US-09-949-016-14232	Sequence 14232, A
562	38	1.6	1511	1	US-07-991-867B-8	Sequence 8, Appli	C 635	37.6	1.6	25992	4	US-09-949-016-17308	Sequence 17308, A
563	38	1.6	1511	1	US-08-107-755A-8	Sequence 8, Appli	636	37.6	1.6	27377	4	US-09-816-248-18	Sequence 18, Appl
564	38	1.6	1511	2	US-08-544-332-8	Sequence 8, Appli	637	37.6	1.6	33155	4	US-09-949-016-12704	Sequence 12704, A
565	38	1.6	1511	3	US-09-370-861A-8	Sequence 8, Appli	638	37.6	1.6	33157	4	US-09-949-016-15756	Sequence 15756, A
566	38	1.6	2215	2	US-08-980-329C-1	Sequence 1, Appli	639	37.6	1.6	43896	4	US-09-949-016-14942	Sequence 14942, A
567	38	1.6	2966	4	US-09-569-098A-103	Sequence 103, App	640	37.6	1.6	54161	4	US-09-949-016-11905	Sequence 11905, A
568	38	1.6	4526	1	US-07-855-412B-4	Sequence 4, Appli	C 641	37.6	1.6	91559	4	US-09-949-016-12581	Sequence 12581, A
569	38	1.6	4526	2	US-08-308-887A-4	Sequence 4, Appli	C 642	37.6	1.6	91559	4	US-09-949-016-13701	Sequence 13701, A
570	38	1.6	4526	3	US-08-881-094-4	Sequence 4, Appli	643	37.6	1.6	126176	4	US-09-949-016-16137	Sequence 16137, A
571	38	1.6	4810	3	US-08-852-629-11	Sequence 11, Appl	644	37.6	1.6	126176	4	US-09-949-016-16138	Sequence 16138, A
572	38	1.6	4838	3	US-08-852-629-15	Sequence 15, Appl	C 645	37.6	1.6	167708	4	US-09-949-016-16423	Sequence 16423, A
573	38	1.6	7859	1	US-07-854-596B-4	Sequence 4, Appli	646	37.6	1.6	211049	4	US-09-949-016-15770	Sequence 15770, A
574	38	1.6	7859	2	US-08-450-905B-15	Sequence 15, Appl	C 647	37.6	1.6	636591	4	US-09-949-016-11808	Sequence 11808, A
575	38	1.6	7859	3	US-07-982-759F-15	Sequence 15, Appl	C 648	37.6	1.6	636591	4	US-09-949-016-13388	Sequence 13388, A
576	38	1.6	15016	4	US-09-601-198-60	Sequence 60, Appl	649	37.4	1.6	370	3	US-09-376-113-1	Sequence 1, Appli
577	38	1.6	79824	4	US-09-949-016-13919	Sequence 13919, A	C 650	37.4	1.6	419	4	US-09-513-999C-32705	Sequence 32705, A
578	38	1.6	98962	4	US-09-949-016-14133	Sequence 14133, A	C 651	37.4	1.6	601	4	US-09-949-016-30533	Sequence 30533, A
579	38	1.6	102884	4	US-09-949-016-17100	Sequence 17100, A	C 652	37.4	1.6	601	4	US-09-949-016-30534	Sequence 30534, A
C 580	38	1.6	140224	4	US-09-949-016-17002	Sequence 17002, A	C 653	37.4	1.6	601	4	US-09-949-016-37152	Sequence 37152, A
C 581	38	1.6	177797	4	US-09-949-016-14125	Sequence 14125, A	C 654	37.4	1.6	601	4	US-09-949-016-37153	Sequence 37153, A
C 582	38	1.6	212139	4	US-09-949-016-16065	Sequence 16065, A	C 655	37.4	1.6	601	4	US-09-949-016-37166	Sequence 37166, A
C 583	38	1.6	227979	4	US-09-949-016-11842	Sequence 11842, A	C 656	37.4	1.6	601	4	US-09-949-016-37167	Sequence 37167, A
C 584	38	1.6	346112	4	US-09-949-016-13165	Sequence 13165, A	C 657	37.4	1.6	601	4	US-09-949-016-145870	Sequence 145870, A
585	37.8	1.6	192	3	US-09-157-177-115	Sequence 115, App	C 658	37.4	1.6	601	4	US-09-949-016-145871	Sequence 145871, A
586	37.8	1.6	192	4	US-09-541-210-115	Sequence 115, App	C 659	37.4	1.6	601	4	US-09-949-016-146138	Sequence 146138, A
587	37.8	1.6	400	4	US-08-956-171E-1040	Sequence 1040, Ap	C 660	37.4	1.6	601	4	US-09-949-016-146139	Sequence 146139, A
588	37.8	1.6	400	4	US-08-781-986A-1040	Sequence 1040, Ap	C 661	37.4	1.6	601	4	US-09-949-016-146406	Sequence 146406, A
C 589	37.8	1.6	601	4	US-09-949-016-30530	Sequence 30530, A	C 662	37.4	1.6	601	4	US-09-949-016-146407	Sequence 146407, A
C 590	37.8	1.6	601	4	US-09-949-016-30531	Sequence 30531, A	C 663	37.4	1.6	601	4	US-09-949-016-171662	Sequence 171662, A
C 591	37.8	1.6	601	4	US-09-949-016-37149	Sequence 37149, A	664	37.4	1.6	690	4	US-09-248-798A-5743	Sequence 5743, App
C 592	37.8	1.6	601	4	US-09-949-016-37150	Sequence 37150, A	C 665	37.4	1.6	837	3	US-08-998-416-288	Sequence 288, App
C 593	37.8	1.6	601	4	US-09-949-016-37163	Sequence 37163, A	666	37.4	1.6	854	3	US-08-998-416-534	Sequence 534, App
C 594	37.8	1.6	601	4	US-09-949-016-37164	Sequence 37164, A	667	37.4	1.6	860	3	US-08-998-416-287	Sequence 287, App
C 595	37.8	1.6	601	4	US-09-949-016-47329	Sequence 47329, A	668	37.4	1.6	1027	4	US-09-270-767-5517	Sequence 5517, Ap
C 596	37.8	1.6	601	4	US-09-949-016-145081	Sequence 145081, A	669	37.4	1.6	1027	4	US-09-270-767-20799	Sequence 20799, A
C 597	37.8	1.6	601	4	US-09-949-016-145867	Sequence 145867, A	670	37.4	1.6	1794	3	US-09-213-719-1	Sequence 1, Appli
C 598	37.8	1.6	601	4	US-09-949-016-145868	Sequence 145868, A	671	37.4	1.6	1794	4	US-09-949-016-97	Sequence 97, Appl
C 599	37.8	1.6	601	4	US-09-949-016-146135	Sequence 146135, A	672	37.4	1.6	1883	4	US-09-799-451-559	Sequence 559, App
C 600	37.8	1.6	601	4	US-09-949-016-146136	Sequence 146136, A	673	37.4	1.6	4675	4	US-09-566-921-97	Sequence 97, Appl
C 601	37.8	1.6	601	4	US-09-949-016-146403	Sequence 146403, A	674	37.4	1.6	7244	3	US-08-378-313-26	Sequence 26, Appl
C 602	37.8	1.6	601	4	US-09-949-016-146404	Sequence 146404, A	C 675	37.4	1.6	11613	4	US-09-949-016-16905	Sequence 16905, A
603	37.8	1.6	601	4	US-09-949-016-155213	Sequence 155213, A	676	37.4	1.6	21438	4	US-09-949-016-14198	Sequence 14198, A
604	37.8	1.6	601	4	US-09-949-016-196383	Sequence 196383, A	C 677	37.4	1.6	31842	4	US-09-949-016-15123	Sequence 15123, A
605	37.8	1.6	615	3	US-08-998-416-186	Sequence 186, App	678	37.4	1.6	32244	4	US-09-949-016-16806	Sequence 16806, A
606	37.8	1.6	663	3	US-08-998-416-191	Sequence 191, App	C 679	37.4	1.6	35262	4	US-09-949-016-12797	Sequence 12797, A
C 607	37.8	1.6	720	1	US-08-117-083-23	Sequence 23, Appl	C 680	37.4	1.6	35263	4	US-09-949-016-16399	Sequence 16399, A
C 608	37.8	1.6	1500	1	US-08-117-083-67	Sequence 67, Appl	681	37.4	1.6	36532	4	US-09-949-016-16585	Sequence 16585, A
609	37.8	1.6	1537	6	5504194-1	Patent No. 5504194	C 682	37.4	1.6	67156	4	US-09-949-016-12284	Sequence 12284, A
610	37.8	1.6	1537	6	5504194-1	Patent No. 5504194	C 683	37.4	1.6	67157	4	US-09-949-016-16558	Sequence 16558, A
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612	37.8	1.6	6152	3	US-08-973-462-1	Sequence 1, Appli	C 685	37.4	1.6	140725	4	US-09-949-016-17074	Sequence 17074, A
613	37.8	1.6	10640	4	US-09-417-485D-5	Sequence 5, Appli	686	37.4	1.6	140844	4	US-09-949-016-14199	Sequence 14199, A
614	37.8	1.6	11585	4	US-09-949-016-14453	Sequence 14453, A	C 687	37.4	1.6	152070	4	US-09-949-016-15402	Sequence 15402, A
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616	37.8	1.6	132456	4	US-09-949-016-13750	Sequence 13750, A	C 689	37.4	1.6	194537	4	US-09-949-016-12928	Sequence 12928, A
617	37.8	1.6	152070	4	US-09-949-016-15402	Sequence 15402, A	C 690	37.4	1.6	201529	4	US-09-949-016-12740	Sequence 12740, A
C 618	37.8	1.6	175265	4	US-09-949-016-16089	Sequence 16089, A	C 691	37.4	1.6	317366	4	US-09-949-016-16001	Sequence 16001, A
C 619	37.8	1.6	192302	4	US-09-949-016-15270	Sequence 15270, A	692	37.4	1.6	1664376	4	US-08-916-421B-1	Sequence 1, Appli
C 620	37.8	1.6	285478	4	US-09-949-016-13362	Sequence 13362, A	693	37.4	1.6	1664376	4	US-09-692-570-1	Sequence 1, Appli
C 621	37.8	1.6	321022	4	US-09-949-016-11852	Sequence 11852, A	C 694	37.2	1.6	601	4	US-09-949-016-26256	Sequence 26256, A
C 622	37.8	1.6	321022	4	US-09-949-016-14166	Sequence 14166, A	C 695	37.2	1.6	601	4	US-09-949-016-107476	Sequence 107476, A
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624	37.8	1.6	451925	4	US-09-949-016-17305	Sequence 17305, A	C 697	37.2	1.6	601	4	US-09-949-016-156901	Sequence 156901, A
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626	37.6	1.6	601	4	US-09-949-016-48159	Sequence 48159, A	C 699	37.2	1.6	601	4	US-09-949-016-185650	Sequence 185650, A
C 627	37.6	1.6	601	4	US-09-949-016-166398	Sequence 166398, A	C 700	37.2	1.6	782	3	US-08-998-416-224	Sequence 224, App
628	37.6	1.6	688	3	US-08-998-416-972	Sequence 972, App	701	37.2	1.6	1497	4	US-09-220-132-94	Sequence 94, Appl
629	37.6	1.6	1137	4	US-09-949-016-3272	Sequence 3272, Ap	702	37.2	1.6	1645	4	US-09-270-767-9219	Sequence 9219, Ap
C 630	37.6	1.6	3616	4	US-09-710-279-3666	Sequence 3666, Ap	703	37.2	1.6	1645	4	US-09-270-767-24501	Sequence 24501, A

859	36.6	1.5	222697	4	US-09-949-016-15842	Sequence 15842, A	932	36.2	1.5	601	4	US-09-949-016-133631	Sequence 133631,
860	36.6	1.5	314798	4	US-09-949-016-13539	Sequence 13539, A	C 933	36.2	1.5	601	4	US-09-949-016-135610	Sequence 135610,
C 861	36.6	1.5	784019	4	US-09-949-016-14033	Sequence 14033, A	C 934	36.2	1.5	601	4	US-09-949-016-135611	Sequence 135611,
C 862	36.6	1.5	828152	4	US-09-949-016-12777	Sequence 12777, A	C 935	36.2	1.5	601	4	US-09-949-016-145080	Sequence 145080,
C 863	36.4	1.5	474	4	US-09-621-976-18033	Sequence 18033, A	936	36.2	1.5	601	4	US-09-949-016-185733	Sequence 185733,
864	36.4	1.5	583	3	US-08-991-789A-36	Sequence 36, Appl	C 937	36.2	1.5	601	4	US-09-949-016-186364	Sequence 186364,
865	36.4	1.5	583	3	US-09-062-451-36	Sequence 36, Appl	938	36.2	1.5	601	4	US-09-949-016-195404	Sequence 195404,
866	36.4	1.5	583	3	US-09-598-326-36	Sequence 36, Appl	939	36.2	1.5	601	4	US-09-949-016-195405	Sequence 195405,
867	36.4	1.5	583	4	US-09-289-198-36	Sequence 36, Appl	C 940	36.2	1.5	816	4	US-09-248-796A-835	Sequence 835, App
868	36.4	1.5	583	4	US-09-429-755-36	Sequence 36, Appl	C 941	36.2	1.5	921	4	US-09-248-796A-9583	Sequence 9583, Ap
869	36.4	1.5	583	4	US-09-699-295-36	Sequence 36, Appl	942	36.2	1.5	1244	4	US-09-710-279-3653	Sequence 3653, Ap
870	36.4	1.5	601	4	US-09-949-016-92273	Sequence 92273, A	C 943	36.2	1.5	1428	4	US-09-248-796A-1072	Sequence 1072, Ap
871	36.4	1.5	601	4	US-09-949-016-92274	Sequence 92274, A	C 944	36.2	1.5	1641	1	US-08-300-903A-8	Sequence 8, Appli
872	36.4	1.5	601	4	US-09-949-016-92275	Sequence 92275, A	C 945	36.2	1.5	1641	4	US-08-988-197-8	Sequence 8, Appli
873	36.4	1.5	601	4	US-09-949-016-94458	Sequence 94458, A	C 946	36.2	1.5	1641	4	US-10-385-072-8	Sequence 8, Appli
874	36.4	1.5	601	4	US-09-949-016-128979	Sequence 128979,	947	36.2	1.5	1848	3	US-09-134-001C-447	Sequence 447, App
875	36.4	1.5	601	4	US-09-949-016-128980	Sequence 128980,	C 948	36.2	1.5	2683	4	US-09-710-279-3709	Sequence 3709, Ap
876	36.4	1.5	601	4	US-09-949-016-128981	Sequence 128981,	C	36.2	1.5	3008	4	US-09-710-279-3513	Sequence 3513, Ap
C 877	36.4	1.5	601	4	US-09-949-016-150219	Sequence 150219,	950	36.2	1.5	3150	4	US-08-956-171E-343	Sequence 343, App
C 878	36.4	1.5	601	4	US-09-949-016-168341	Sequence 168341,	951	36.2	1.5	3150	4	US-08-781-986A-343	Sequence 343, App
879	36.4	1.5	601	4	US-09-949-016-168342	Sequence 168342,	952	36.2	1.5	3167	4	US-09-710-279-4117	Sequence 4117, Ap
C 880	36.4	1.5	601	4	US-09-949-016-179399	Sequence 179399,	953	36.2	1.5	3241	4	US-09-710-279-4276	Sequence 4276, Ap
C 881	36.4	1.5	767	4	US-09-270-767-28477	Sequence 28477, A	954	36.2	1.5	5163	3	US-08-700-651-1	Sequence 1, Appli
882	36.4	1.5	885	3	US-08-952-089A-2	Sequence 2, Appli	955	36.2	1.5	5163	3	US-08-928-361B-4	Sequence 4, Appli
883	36.4	1.5	885	4	US-09-690-885-2	Sequence 2, Appli	956	36.2	1.5	5163	4	US-09-588-995A-4	Sequence 4, Appli
C 884	36.4	1.5	923	4	US-08-956-171E-850	Sequence 850, App	957	36.2	1.5	5318	3	US-08-700-651-2	Sequence 2, Appli
C 885	36.4	1.5	923	4	US-08-781-986A-850	Sequence 850, App	958	36.2	1.5	5318	3	US-08-928-361B-3	Sequence 3, Appli
C 886	36.4	1.5	1107	4	US-09-248-796A-11324	Sequence 11324, A	959	36.2	1.5	5318	4	US-09-588-995A-3	Sequence 3, Appli
C 887	36.4	1.5	1404	4	US-09-270-767-12670	Sequence 12670, A	C 960	36.2	1.5	5939	4	US-09-949-016-17300	Sequence 17300, A
889	36.4	1.5	1588	4	US-09-690-885-26	Sequence 26, Appl	C 961	36.2	1.5	5941	4	US-09-949-016-12512	Sequence 12512, A
890	36.4	1.5	1822	4	US-09-356-806-43	Sequence 43, Appl	962	36.2	1.5	6136	4	US-08-956-171E-307	Sequence 307, App
891	36.4	1.5	1881	4	US-09-270-767-5997	Sequence 5997, Ap	963	36.2	1.5	6136	4	US-08-781-986A-307	Sequence 307, App
892	36.4	1.5	1881	4	US-09-270-767-21279	Sequence 21279, A	964	36.2	1.5	6623	4	US-09-949-016-12157	Sequence 12157, A
C 893	36.4	1.5	2132	3	US-08-844-188-39	Sequence 39, Appl	965	36.2	1.5	10396	1	US-08-245-809-5	Sequence 5, Appli
C 894	36.4	1.5	2132	3	US-09-378-088A-39	Sequence 39, Appl	966	36.2	1.5	10965	1	US-08-107-748-4	Sequence 4, Appli
C 895	36.4	1.5	2132	4	US-09-548-334A-39	Sequence 39, Appl	C 967	36.2	1.5	10965	5	PCT-US92-01385-4	Sequence 4, Appli
C 896	36.4	1.5	2132	4	US-09-547-621-39	Sequence 39, Appl	C 968	36.2	1.5	27543	4	US-09-949-016-17455	Sequence 17455, A
C 897	36.4	1.5	2132	4	US-09-643-596B-39	Sequence 39, Appl	969	36.2	1.5	28696	4	US-09-949-016-17054	Sequence 17054, A
C 898	36.4	1.5	2946	4	US-09-710-279-3738	Sequence 3738, Ap	970	36.2	1.5	28780	4	US-09-949-016-12335	Sequence 12335, A
899	36.4	1.5	4146	3	US-08-952-089A-29	Sequence 29, Appl	C 971	36.2	1.5	47064	4	US-09-949-016-13380	Sequence 13380, A
900	36.4	1.5	4146	4	US-09-690-885-29	Sequence 29, Appl	972	36.2	1.5	59479	4	US-09-949-016-16910	Sequence 16910, A
C 901	36.4	1.5	4235	1	US-08-021-601-3	Sequence 3, Appli	973	36.2	1.5	77851	4	US-09-949-016-12508	Sequence 12508, A
C 902	36.4	1.5	4235	1	US-08-082-849B-3	Sequence 3, Appli	974	36.2	1.5	77867	4	US-09-949-016-13211	Sequence 13211, A
C 903	36.4	1.5	4235	5	PCT-US94-01624-3	Sequence 3, Appli	975	36.2	1.5	77867	4	US-09-949-016-13212	Sequence 13212, A
C 904	36.4	1.5	6124	3	US-08-213-419B-3	Sequence 3, Appli	976	36.2	1.5	77940	4	US-09-949-016-12509	Sequence 12509, A
C 905	36.4	1.5	13938	4	US-09-949-016-16019	Sequence 16019, A	C 977	36.2	1.5	106924	4	US-09-949-016-13834	Sequence 13834, A
C 906	36.4	1.5	13938	4	US-09-949-016-16020	Sequence 16020, A	C 978	36.2	1.5	112114	4	US-09-949-016-17292	Sequence 17292, A
907	36.4	1.5	20441	4	US-09-949-016-14476	Sequence 14476, A	979	36.2	1.5	128516	4	US-09-949-016-13501	Sequence 13501, A
908	36.4	1.5	42975	4	US-09-949-016-11965	Sequence 11965, A	980	36.2	1.5	133157	4	US-09-949-016-12541	Sequence 12541, A
C 909	36.4	1.5	47363	4	US-09-949-016-13420	Sequence 13420, A	C 981	36.2	1.5	148794	4	US-09-949-016-12751	Sequence 12751, A
C 910	36.4	1.5	71251	4	US-09-949-016-15332	Sequence 15332, A	C 982	36.2	1.5	154605	4	US-09-949-016-11894	Sequence 11894, A
C 911	36.4	1.5	96048	4	US-09-949-016-15966	Sequence 15966, A	C 983	36.2	1.5	155617	4	US-09-949-016-16191	Sequence 16191, A
C 912	36.4	1.5	101835	4	US-09-949-016-14695	Sequence 14695, A	984	36.2	1.5	187595	4	US-09-949-016-15546	Sequence 15546, A
C 913	36.4	1.5	112219	4	US-09-949-016-12453	Sequence 12453, A	985	36.2	1.5	197875	4	US-09-949-016-15425	Sequence 15425, A
C 914	36.4	1.5	112222	4	US-09-949-016-14324	Sequence 14324, A	C 986	36.2	1.5	200663	4	US-09-949-016-12569	Sequence 12569, A
C 915	36.4	1.5	113186	4	US-09-949-016-17572	Sequence 17572, A	C 987	36.2	1.5	202111	4	US-09-949-016-13877	Sequence 13877, A
916	36.4	1.5	147840	4	US-09-949-016-15236	Sequence 15236, A	C 988	36.2	1.5	203093	4	US-09-949-016-14445	Sequence 14445, A
917	36.4	1.5	171700	4	US-09-949-016-12276	Sequence 12276, A	989	36.2	1.5	234884	4	US-09-949-016-16420	Sequence 16420, A
918	36.4	1.5	171701	4	US-09-949-016-15835	Sequence 15835, A	C 990	36.2	1.5	253345	4	US-09-949-016-12656	Sequence 12656, A
C 919	36.4	1.5	192506	4	US-09-949-016-15830	Sequence 15830, A	C 991	36.2	1.5	253364	4	US-09-949-016-13639	Sequence 13639, A
920	36.4	1.5	192956	4	US-09-949-016-14382	Sequence 14382, A	992	36.2	1.5	256287	4	US-09-949-016-14608	Sequence 14608, A
921	36.4	1.5	236341	4	US-09-949-016-13978	Sequence 13978, A	993	36.2	1.5	343352	4	US-09-949-016-13498	Sequence 13498, A
C 922	36.4	1.5	421118	4	US-09-949-016-16297	Sequence 16297, A	C 994	36.2	1.5	343352	4	US-09-949-016-13498	Sequence 13498, A
C 923	36.2	1.5	430	4	US-09-513-999C-21291	Sequence 21291, A	995	36	1.5	441	4	US-09-107-532A-2002	Sequence 2002, Ap
924	36.2	1.5	582	4	US-09-949-016-61868	Sequence 61868, A	C 996	36	1.5	469	4	US-09-270-767-14304	Sequence 14304, A
925	36.2	1.5	582	4	US-09-949-016-29459	Sequence 29459, A	997	36	1.5	533	4	US-09-270-767-6357	Sequence 6357, Ap
926	36.2	1.5	601	4	US-09-949-016-60326	Sequence 60326, A	C 998	36	1.5	533	4	US-09-270-767-21639	Sequence 21639, A
927	36.2	1.5	601	4	US-09-949-016-60327	Sequence 60327, A	C 999	36	1.5	601	4	US-09-949-016-18854	Sequence 18854, A
C 928	36.2	1.5	601	4	US-09-949-016-70762	Sequence 70762, A	C1000	36	1.5	601	4	US-09-949-016-56719	Sequence 56719, A
C 929	36.2	1.5	601	4	US-09-949-016-78633	Sequence 78633, A	C1001	36	1.5	601	4	US-09-949-016-60120	Sequence 60120, A
C 930	36.2	1.5	601	4	US-09-949-016-103570	Sequence 103570, A	C1002	36	1.5	601	4	US-09-949-016-117499	Sequence 117499,
C 931	36.2	1.5	601	4	US-09-949-016-130586	Sequence 130586,	C1003	36	1.5	601	4	US-09-949-016-117500	Sequence 117500,
							C1004	36	1.5	601	4	US-09-949-016-117501	Sequence 117501,

c1005	36	1.5	601	4	US-09-949-016-117502	Sequence 117502,	c1078	35.8	1.5	943	3	US-09-149-476-35	Sequence 35, Appl
c1006	36	1.5	601	4	US-09-949-016-117503	Sequence 117503,	c1079	35.8	1.5	1344	4	US-09-107-433-925	Sequence 925, App
c1007	36	1.5	601	4	US-09-949-016-117504	Sequence 117504,	c1080	35.8	1.5	1555	3	US-08-669-408B-9	Sequence 9, Appli
c1008	36	1.5	601	4	US-09-949-016-117505	Sequence 117505,	c1081	35.8	1.5	1738	4	US-09-918-909A-27	Sequence 27, Appl
c1009	36	1.5	601	4	US-09-949-016-117506	Sequence 117506,	c1082	35.8	1.5	3241	4	US-09-710-279-3628	Sequence 3628, Ap
c1010	36	1.5	601	4	US-09-949-016-117507	Sequence 117507,	1083	35.8	1.5	3451	4	US-09-710-279-3984	Sequence 3984, Ap
c1011	36	1.5	601	4	US-09-949-016-117508	Sequence 117508,	1084	35.8	1.5	3695	4	US-09-774-528-320	Sequence 320, App
c1012	36	1.5	601	4	US-09-949-016-117509	Sequence 117509,	c1085	35.8	1.5	4383	3	US-08-397-653B-2	Sequence 2, Appli
c1013	36	1.5	601	4	US-09-949-016-169756	Sequence 169756,	c1086	35.8	1.5	4383	6	5175095-4	Patent No.5175095
c1014	36	1.5	601	4	US-09-949-016-169757	Sequence 169757,	c1087	35.8	1.5	4383	6	5177307-1	Patent No. 5177307
1015	36	1.5	601	4	US-09-949-016-171125	Sequence 171125,	c1088	35.8	1.5	4383	6	5175095-4	Patent No.5175095
1016	36	1.5	601	4	US-09-949-016-171126	Sequence 171126,	c1089	35.8	1.5	4383	6	5177307-1	Patent No. 5177307
1017	36	1.5	601	4	US-09-949-016-171255	Sequence 171255,	1090	35.8	1.5	9728	4	US-09-949-016-12161	Sequence 12161, A
1018	36	1.5	601	4	US-09-949-016-171256	Sequence 171256,	1091	35.8	1.5	9729	4	US-09-949-016-13612	Sequence 13612, A
1019	36	1.5	601	4	US-09-949-016-171451	Sequence 171451,	1092	35.8	1.5	19157	4	US-09-949-016-13142	Sequence 13142, A
c1020	36	1.5	737	4	US-09-270-767-11417	Sequence 11417, A	1093	35.8	1.5	20303	1	US-08-370-975B-6	Sequence 6, Appli
1021	36	1.5	746	4	US-09-270-767-3259	Sequence 3259, Ap	c1094	35.8	1.5	24221	4	US-09-949-016-14964	Sequence 14964, A
1022	36	1.5	746	4	US-09-270-767-18541	Sequence 18541, A	c1095	35.8	1.5	25067	4	US-09-949-016-11794	Sequence 11794, A
c1023	36	1.5	893	2	US-08-394-152A-45	Sequence 45, Appl	c1096	35.8	1.5	25441	4	US-09-949-016-14232	Sequence 14232, A
c1024	36	1.5	1393	4	US-09-645-055-56	Sequence 56, Appl	1097	35.8	1.5	26764	1	US-08-370-975B-1	Sequence 1, Appli
c1025	36	1.5	1481	4	US-09-645-055-55	Sequence 55, Appl	c1098	35.8	1.5	28494	4	US-09-949-016-13200	Sequence 13200, A
1026	36	1.5	2796	4	US-09-949-016-5678	Sequence 5678, Ap	c1099	35.8	1.5	32244	4	US-09-949-016-16806	Sequence 16806, A
c1027	36	1.5	2839	3	US-09-160-496-3	Sequence 3, Appli	c1100	35.8	1.5	50263	4	US-09-949-016-13563	Sequence 13563, A
c1028	36	1.5	2839	4	US-08-945-826-5	Sequence 5, Appli	1101	35.8	1.5	63588	4	US-09-873-404-3	Sequence 3, Appli
c1029	36	1.5	2839	4	US-09-197-503-5	Sequence 5, Appli	1102	35.8	1.5	63588	4	US-10-243-735-3	Sequence 3, Appli
1030	36	1.5	3504	1	US-08-485-568A-5	Sequence 5, Appli	1103	35.8	1.5	66804	4	US-09-740-041-3	Sequence 3, Appli
1031	36	1.5	3504	1	US-08-620-717A-8	Sequence 8, Appli	1104	35.8	1.5	76985	4	US-09-949-016-12416	Sequence 12416, A
1032	36	1.5	3504	2	US-08-590-554A-5	Sequence 5, Appli	1105	35.8	1.5	76986	4	US-09-949-016-13120	Sequence 13120, A
1033	36	1.5	3504	2	US-09-184-223-5	Sequence 5, Appli	1106	35.8	1.5	77586	4	US-09-949-016-13220	Sequence 13220, A
c1034	36	1.5	3805	3	US-09-513-729B-10	Sequence 10, Appl	1107	35.8	1.5	77586	4	US-09-949-016-13221	Sequence 13221, A
c1035	36	1.5	3805	4	US-09-023-655-1443	Sequence 1443, Ap	1108	35.8	1.5	79350	4	US-09-949-016-12467	Sequence 12467, A
1036	36	1.5	5340	4	US-09-627-122-21	Sequence 21, Appl	1109	35.8	1.5	79351	4	US-09-949-016-16275	Sequence 16275, A
1037	36	1.5	16592	4	US-08-956-171E-53	Sequence 53, Appl	c1110	35.8	1.5	82178	4	US-09-949-016-13394	Sequence 13394, A
1038	36	1.5	16592	4	US-08-781-986A-53	Sequence 53, Appl	1111	35.8	1.5	93778	4	US-09-949-016-15096	Sequence 15096, A
c1039	36	1.5	23975	4	US-09-949-016-17126	Sequence 17126, A	c1112	35.8	1.5	101011	4	US-09-949-016-16933	Sequence 16933, A
c1040	36	1.5	31573	4	US-09-949-016-16327	Sequence 16327, A	c1113	35.8	1.5	137394	4	US-09-949-016-13872	Sequence 13872, A
1041	36	1.5	33411	4	US-09-949-016-15201	Sequence 15201, A	c1114	35.8	1.5	137743	4	US-09-949-016-12178	Sequence 12178, A
c1042	36	1.5	37940	4	US-09-949-016-15550	Sequence 15550, A	c1115	35.8	1.5	160018	4	US-09-949-016-12617	Sequence 12617, A
1043	36	1.5	42075	4	US-09-949-016-15550	Sequence 15550, A	c1116	35.8	1.5	160018	4	US-09-949-016-15994	Sequence 15994, A
1044	36	1.5	58407	4	US-08-916-421B-2	Sequence 14995, A	c1117	35.8	1.5	168104	4	US-09-949-016-12026	Sequence 12026, A
c1046	36	1.5	58407	4	US-09-692-570-2	Sequence 2, Appli	c1118	35.8	1.5	168105	4	US-09-949-016-16554	Sequence 16554, A
c1047	36	1.5	60141	4	US-09-949-016-15874	Sequence 15874, A	1119	35.8	1.5	176006	4	US-09-949-016-16804	Sequence 16804, A
c1048	36	1.5	92304	4	US-09-949-016-15943	Sequence 15943, A	c1120	35.8	1.5	193303	4	US-09-497-855A-37	Sequence 37, Appl
c1049	36	1.5	112507	4	US-09-949-016-12420	Sequence 12420, A	1121	35.8	1.5	193303	4	US-09-497-855A-44	Sequence 44, Appl
c1050	36	1.5	112508	4	US-09-949-016-16589	Sequence 16589, A	1122	35.8	1.5	200663	4	US-09-949-016-12569	Sequence 12569, A
c1051	36	1.5	112508	4	US-09-949-016-16590	Sequence 16590, A	1123	35.8	1.5	203093	4	US-09-949-016-14445	Sequence 14445, A
c1052	36	1.5	114842	4	US-09-949-016-14993	Sequence 14993, A	1124	35.8	1.5	205163	4	US-09-949-016-17009	Sequence 17009, A
c1053	36	1.5	126176	4	US-09-949-016-16137	Sequence 16137, A	1125	35.8	1.5	236474	4	US-09-949-016-13418	Sequence 13418, A
c1054	36	1.5	126176	4	US-09-949-016-16138	Sequence 16138, A	1126	35.8	1.5	253375	4	US-09-949-016-12849	Sequence 12849, A
1055	36	1.5	126982	4	US-09-949-016-16597	Sequence 16597, A	c1127	35.8	1.5	278866	4	US-09-949-016-13922	Sequence 13922, A
1056	36	1.5	145241	4	US-09-949-016-17394	Sequence 17394, A	c1128	35.8	1.5	278866	4	US-09-949-016-13923	Sequence 13923, A
1057	36	1.5	145241	4	US-09-949-016-17395	Sequence 17395, A	c1129	35.8	1.5	278866	4	US-09-949-016-13924	Sequence 13924, A
c1058	36	1.5	256171	4	US-09-949-016-12822	Sequence 12822, A	c1130	35.8	1.5	278866	4	US-09-949-016-13925	Sequence 13925, A
c1059	36	1.5	256176	4	US-09-949-016-15524	Sequence 15524, A	c1131	35.8	1.5	278866	4	US-09-949-016-13926	Sequence 13926, A
c1060	36	1.5	363032	4	US-09-949-016-12415	Sequence 12415, A	c1132	35.8	1.5	278866	4	US-09-949-016-14699	Sequence 14699, A
c1061	36	1.5	363033	4	US-09-949-016-15754	Sequence 15754, A	c1133	35.8	1.5	278866	4	US-09-949-016-14700	Sequence 14700, A
1062	36	1.5	1830121	4	US-09-557-884-1	Sequence 1, Appli	c1134	35.8	1.5	278866	4	US-09-949-016-14701	Sequence 14701, A
1063	36	1.5	1830121	4	US-09-643-990A-1	Sequence 1, Appli	c1135	35.8	1.5	278866	4	US-09-949-016-14702	Sequence 14702, A
c1064	35.8	1.5	601	4	US-09-949-016-35095	Sequence 35095, A	c1136	35.8	1.5	278866	4	US-09-949-016-14703	Sequence 14703, A
1065	35.8	1.5	601	4	US-09-949-016-50946	Sequence 50946, A	1137	35.8	1.5	670689	4	US-09-949-016-12505	Sequence 12505, A
1066	35.8	1.5	601	4	US-09-949-016-51000	Sequence 51000, A	1138	35.8	1.5	670690	4	US-09-949-016-14207	Sequence 14207, A
1067	35.8	1.5	601	4	US-09-949-016-57131	Sequence 57131, A	c1139	35.6	1.5	189	4	US-09-513-999C-21756	Sequence 21756, A
1068	35.8	1.5	601	4	US-09-949-016-72668	Sequence 72668, A	c1140	35.6	1.5	417	4	US-09-248-796A-2849	Sequence 2849, Ap
1069	35.8	1.5	601	4	US-09-949-016-103973	Sequence 103973,	1141	35.6	1.5	601	4	US-09-949-016-28524	Sequence 28524, A
1070	35.8	1.5	601	4	US-09-949-016-120884	Sequence 120884,	1142	35.6	1.5	601	4	US-09-949-016-60957	Sequence 60957, A
1071	35.8	1.5	601	4	US-09-949-016-120886	Sequence 120886,	1143	35.6	1.5	601	4	US-09-949-016-113260	Sequence 113260,
c1072	35.8	1.5	601	4	US-09-949-016-151246	Sequence 151246,	1144	35.6	1.5	601	4	US-09-949-016-133630	Sequence 133630,
1073	35.8	1.5	601	4	US-09-949-016-180548	Sequence 180548,	c1145	35.6	1.5	601	4	US-09-949-016-159300	Sequence 159300,
1074	35.8	1.5	601	4	US-09-949-016-195406	Sequence 195406,	1146	35.6	1.5	601	4	US-09-949-016-164036	Sequence 164036,
c1075	35.8	1.5	665	3	US-08-998-416-937	Sequence 937, App	1147	35.6	1.5	601	4	US-09-949-016-171504	Sequence 171504,
c1076	35.8	1.5	711	3	US-08-998-416-786	Sequence 786, App	1148	35.6	1.5	658	3	US-08-998-416-595	Sequence 595, App
c1077	35.8	1.5	840	4	US-09-248-796A-1930	Sequence 1930, Ap	1149	35.6	1.5	740	3	US-08-998-416-971	Sequence 971, App
							1150	35.6	1.5	966	4	US-09-248-796A-9577	Sequence 9577, Ap

c1151	35.6	1.5	1441	4	US-08-956-171E-1000	Sequence 1000, Ap
c1152	35.6	1.5	1441	4	US-08-781-986A-1000	Sequence 1000, Ap
1153	35.6	1.5	1485	4	US-09-248-796A-2443	Sequence 2443, Ap
1154	35.6	1.5	2349	4	US-09-601-198-46	Sequence 46, Appli
c1155	35.6	1.5	2481	2	US-08-630-118A-1	Sequence 1, Appli
c1156	35.6	1.5	2481	2	US-08-838-399-1	Sequence 1, Appli
c1157	35.6	1.5	2481	3	US-09-235-839-1	Sequence 1, Appli
c1158	35.6	1.5	2481	3	US-09-327-035-1	Sequence 1, Appli
c1159	35.6	1.5	2604	2	US-08-630-118A-3	Sequence 3, Appli
c1160	35.6	1.5	2604	2	US-08-838-399-3	Sequence 3, Appli
c1161	35.6	1.5	2604	3	US-09-235-839-3	Sequence 3, Appli
c1162	35.6	1.5	2604	3	US-09-327-035-3	Sequence 3, Appli
c1163	35.6	1.5	2960	3	US-08-913-842-3	Sequence 3, Appli
1164	35.6	1.5	3129	4	US-09-897-425-40	Sequence 40, Appl
c1165	35.6	1.5	3440	1	US-08-471-791-27	Sequence 27, Appl
c1166	35.6	1.5	3440	5	PCT-US91-01746-27	Sequence 48, Appl
1167	35.6	1.5	3787	4	US-09-897-425-48	Sequence 42, Appl
1168	35.6	1.5	3888	4	US-09-897-425-42	Sequence 45, Appl
1169	35.6	1.5	3888	4	US-09-897-425-45	Sequence 53, Appl
1170	35.6	1.5	4545	4	US-09-897-425-53	Sequence 50, Appl
1171	35.6	1.5	4546	4	US-09-897-425-50	Sequence 36, Appl
1172	35.6	1.5	4652	4	US-09-893-525-36	Sequence 1125, Ap
c1173	35.6	1.5	4910	4	US-09-023-655-1125	Sequence 75, Appl
c1174	35.6	1.5	4910	4	US-09-814-915A-75	Sequence 129, App
c1175	35.6	1.5	4910	4	US-09-949-016-129	Sequence 41, Appl
1176	35.6	1.5	5390	4	US-09-893-525-41	Sequence 38, Appl
1177	35.6	1.5	5418	4	US-09-893-525-38	Sequence 1, Appli
1178	35.6	1.5	6768	1	US-08-107-755A-1	Sequence 127, App
1179	35.6	1.5	12658	4	US-08-956-171E-127	Sequence 127, App
1180	35.6	1.5	12658	4	US-08-781-986A-127	Sequence 16199, A
1181	35.6	1.5	22205	4	US-09-949-016-16199	Sequence 16284, A
1182	35.6	1.5	29717	4	US-09-949-016-16284	Sequence 11871, A
c1183	35.6	1.5	29935	4	US-09-949-016-11871	Sequence 14443, A
c1184	35.6	1.5	29936	4	US-09-949-016-14443	Sequence 17171, A
1185	35.6	1.5	42250	4	US-09-949-016-17171	Sequence 15302, A
c1186	35.6	1.5	44353	4	US-09-949-016-15302	Sequence 17416, A
c1187	35.6	1.5	51161	4	US-09-949-016-17416	Sequence 12423, A
1188	35.6	1.5	60376	4	US-09-949-016-12423	Sequence 15595, A
c1189	35.6	1.5	82000	4	US-09-949-016-15595	Sequence 16823, A
c1190	35.6	1.5	82612	4	US-09-949-016-16823	Sequence 16356, A
1191	35.6	1.5	84171	4	US-09-949-016-16356	Sequence 12414, A
1192	35.6	1.5	94830	4	US-09-949-016-16336	Sequence 16336, A
1193	35.6	1.5	94847	4	US-09-949-016-13276	Sequence 13276, A
1194	35.6	1.5	100877	4	US-09-949-016-13276	Sequence 14773, A
1195	35.6	1.5	113060	4	US-09-949-016-14773	Sequence 14774, A
1196	35.6	1.5	113060	4	US-09-949-016-14774	Sequence 12427, A
1197	35.6	1.5	137046	4	US-09-949-016-12427	Sequence 13438, A
1198	35.6	1.5	137048	4	US-09-949-016-13438	Sequence 13693, A
c1199	35.6	1.5	142504	4	US-09-949-016-13693	Sequence 12474, A
c1200	35.6	1.5	142506	4	US-09-949-016-12474	Sequence 13530, A
c1201	35.6	1.5	145287	4	US-09-949-016-13530	Sequence 13531, A
c1202	35.6	1.5	145287	4	US-09-949-016-13531	Sequence 3, Appli
c1203	35.6	1.5	148567	4	US-09-801-876B-3	Sequence 3, Appli
c1204	35.6	1.5	148567	4	US-10-254-869-3	Sequence 3, Appli
c1205	35.6	1.5	148567	4	US-10-667-442-3	Sequence 15091, A
1206	35.6	1.5	193169	4	US-09-949-016-15091	Sequence 15497, A
1207	35.6	1.5	245286	4	US-09-949-016-15497	Sequence 14381, A
1208	35.6	1.5	254405	4	US-09-949-016-14381	Sequence 15974, A
1209	35.6	1.5	294836	4	US-09-949-016-15974	Sequence 16073, A
c1210	35.6	1.5	385136	4	US-09-949-016-16073	Sequence 12505, A
c1211	35.6	1.5	670689	4	US-09-949-016-12505	Sequence 14207, A
c1212	35.6	1.5	670690	4	US-09-949-016-14207	Sequence 65915, A
c1213	35.4	1.5	601	4	US-09-949-016-65915	Sequence 105996,
1214	35.4	1.5	601	4	US-09-949-016-105996	Sequence 145592,
1215	35.4	1.5	601	4	US-09-949-016-145592	Sequence 145593,
1216	35.4	1.5	601	4	US-09-949-016-145593	Sequence 157975,
1217	35.4	1.5	601	4	US-09-949-016-145594	Sequence 179398,
c1218	35.4	1.5	601	4	US-09-949-016-157975	Sequence 206449,
c1219	35.4	1.5	601	4	US-09-949-016-179398	Sequence 186, App
1220	35.4	1.5	601	4	US-09-949-016-206449	Sequence 683, App
c1221	35.4	1.5	615	3	US-08-998-416-186	Sequence 2, Appli
c1222	35.4	1.5	724	3	US-08-998-416-683	
1223	35.4	1.5	940	1	US-08-448-600-2	

c1224	35.4	1.5	1041	3	US-09-033-055A-4	Sequence 4, Appli
1225	35.4	1.5	1712	3	US-09-144-776B-5	Sequence 5, Appli
1226	35.4	1.5	1712	3	US-09-144-776B-7	Sequence 7, Appli
1227	35.4	1.5	1712	4	US-08-882-431B-5	Sequence 5, Appli
1228	35.4	1.5	1712	4	US-08-882-431B-7	Sequence 7, Appli
1229	35.4	1.5	2049	3	US-09-134-001C-2413	Sequence 2413, Ap
1230	35.4	1.5	2529	4	US-09-270-767-118	Sequence 118, App
1231	35.4	1.5	2529	4	US-09-270-767-15400	Sequence 15400, A
c1232	35.4	1.5	2646	1	US-08-539-304A-5	Sequence 5, Appli
1233	35.4	1.5	2998	4	US-09-710-279-3506	Sequence 3506, Ap
1234	35.4	1.5	3001	4	US-09-539-333D-188	Sequence 188, App
1235	35.4	1.5	3088	3	US-08-937-610-3	Sequence 3, Appli
1236	35.4	1.5	3173	4	US-09-710-279-3554	Sequence 3554, Ap
1237	35.4	1.5	3527	4	US-09-710-279-3890	Sequence 3890, Ap
1238	35.4	1.5	3941	4	US-09-710-279-3755	Sequence 3755, Ap
1239	35.4	1.5	4126	4	US-09-710-279-4154	Sequence 4154, Ap
c1240	35.4	1.5	4185	4	US-09-417-485D-7	Sequence 7, Appli
1241	35.4	1.5	4291	2	US-08-417-210A-80	Sequence 80, Appl
1242	35.4	1.5	4291	4	US-09-136-159A-80	Sequence 80, Appl
1243	35.4	1.5	4857	2	US-08-566-398-16	Sequence 16, Appl
c1244	35.4	1.5	6243	2	US-09-056-075-1	Sequence 1, Appli
1245	35.4	1.5	6628	3	US-08-815-809-3	Sequence 3, Appli
1246	35.4	1.5	6649	2	US-08-816-155B-5	Sequence 5, Appli
1247	35.4	1.5	6649	3	US-09-079-587-5	Sequence 5, Appli
1248	35.4	1.5	7091	3	US-08-658-665-40	Sequence 40, Appl
1249	35.4	1.5	7091	3	US-08-796-101-4	Sequence 4, Appli
1250	35.4	1.5	7091	3	US-09-085-273-40	Sequence 40, Appl
1251	35.4	1.5	7091	4	US-09-916-963-40	Sequence 40, Appl
1252	35.4	1.5	7351	1	US-08-224-391-83	Sequence 83, Appl
1253	35.4	1.5	7351	1	US-08-484-304-83	Sequence 83, Appl
1254	35.4	1.5	7351	2	US-08-184-009-127	Sequence 127, App
1255	35.4	1.5	7351	2	US-08-566-398-39	Sequence 39, Appl
1256	35.4	1.5	7351	2	US-08-458-356-127	Sequence 127, App
1257	35.4	1.5	7351	2	US-08-658-665-39	Sequence 39, Appl
1258	35.4	1.5	7351	3	US-08-796-101-3	Sequence 3, Appli
1259	35.4	1.5	7351	3	US-08-460-736-127	Sequence 127, App
1260	35.4	1.5	7351	3	US-09-085-273-39	Sequence 39, Appl
1261	35.4	1.5	7351	4	US-09-535-370-127	Sequence 127, App
1262	35.4	1.5	7351	4	US-09-916-963-39	Sequence 39, Appl
1263	35.4	1.5	7351	4	US-09-663-667-127	Sequence 127, App
c1264	35.4	1.5	9636	1	US-08-323-170B-1	Sequence 1, Appli
c1265	35.4	1.5	9636	3	US-08-954-441-1	Sequence 1, Appli
1266	35.4	1.5	27916	4	US-09-949-016-15202	Sequence 15202, A
1267	35.4	1.5	33529	4	US-09-949-016-12865	Sequence 12865, A
1268	35.4	1.5	33529	4	US-09-949-016-17364	Sequence 17364, A
c1269	35.4	1.5	36242	4	US-09-949-016-12996	Sequence 12996, A
c1270	35.4	1.5	36242	4	US-09-949-016-12997	Sequence 12997, A
c1271	35.4	1.5	36242	4	US-09-949-016-12998	Sequence 12998, A
c1272	35.4	1.5	36242	4	US-09-949-016-12999	Sequence 12999, A
c1273	35.4	1.5	36242	4	US-09-949-016-13000	Sequence 13000, A
c1274	35.4	1.5	38371	4	US-09-949-016-12061	Sequence 12061, A
c1275	35.4	1.5	38371	4	US-09-949-016-12488	Sequence 12488, A
c1276	35.4	1.5	38371	4	US-09-949-016-15596	Sequence 15596, A
c1277	35.4	1.5	38371	4	US-09-949-016-15597	Sequence 15597, A
c1278	35.4	1.5	39937	4	US-09-949-016-16147	Sequence 16147, A
c1279	35.4	1.5	44439	4	US-09-949-016-17102	Sequence 17102, A
1280	35.4	1.5	45840	4	US-09-949-016-13903	Sequence 13903, A
1281	35.4	1.5	45840	4	US-09-949-016-15042	Sequence 15042, A
1282	35.4	1.5	46559	4	US-09-949-016-15043	Sequence 15043, A
c1283	35.4	1.5	54245	4	US-09-949-016-13499	Sequence 13499, A
1284	35.4	1.5	60002	4	US-09-949-016-12464	Sequence 12464, A
1285	35.4	1.5	60003	4	US-09-949-016-13823	Sequence 13823, A
c1286	35.4	1.5	68490	4	US-09-949-016-15849	Sequence 15849, A
c1287	35.4	1.5	75212	4	US-09-949-016-13313	Sequence 13313, A
c1288	35.4	1.5	75212	4	US-09-949-016-13314	Sequence 13314, A
c1289	35.4	1.5	75212	4	US-09-949-016-13315	Sequence 13315, A
c1290	35.4	1.5	84571	4	US-09-949-016-17420	Sequence 17420, A
1291	35.4	1.5	85122	4	US-09-949-016-14693	Sequence 14693, A
c1292	35.4	1.5	87523	4	US-09-949-016-12670	Sequence 12670, A
c1293	35.4	1.5	87523	4	US-09-949-016-15047	Sequence 15047, A
c1294	35.4	1.5	87523	4	US-09-949-016-15048	Sequence 15048, A
c1295	35.4	1.5	87523	4	US-09-949-016-15049	Sequence 15049, A
c1296	35.4	1.5	87869	4	US-09-949-016-11744	Sequence 11744, A

c1297	35.4	1.5	87869	4	US-09-949-016-15044	Sequence 15044, A	c1370	35.2	1.5	18788	4	US-09-949-016-17090	Sequence 17090, A
c1298	35.4	1.5	87869	4	US-09-949-016-15045	Sequence 15045, A	c1371	35.2	1.5	20935	4	US-09-949-016-15383	Sequence 15383, A
c1299	35.4	1.5	87869	4	US-09-949-016-15046	Sequence 15046, A	1372	35.2	1.5	24508	4	US-09-949-016-16005	Sequence 16005, A
c1300	35.4	1.5	94879	4	US-09-949-016-12101	Sequence 12101, A	1373	35.2	1.5	24519	4	US-09-949-016-11864	Sequence 11864, A
c1301	35.4	1.5	94884	4	US-09-949-016-13393	Sequence 13393, A	c1374	35.2	1.5	25512	4	US-09-949-016-15886	Sequence 15886, A
1302	35.4	1.5	95890	4	US-09-949-016-16412	Sequence 16412, A	c1375	35.2	1.5	25512	4	US-09-949-016-15887	Sequence 15887, A
1303	35.4	1.5	100836	4	US-09-949-016-12871	Sequence 12871, A	c1376	35.2	1.5	35380	4	US-09-949-016-11994	Sequence 11994, A
1304	35.4	1.5	100837	4	US-09-949-016-17063	Sequence 17063, A	1377	35.2	1.5	38702	4	US-09-949-016-13788	Sequence 13788, A
1305	35.4	1.5	101894	4	US-09-949-016-12005	Sequence 12005, A	c1378	35.2	1.5	47883	4	US-09-949-016-11886	Sequence 11886, A
1306	35.4	1.5	103894	4	US-09-949-016-14450	Sequence 14450, A	c1379	35.2	1.5	47883	4	US-09-949-016-17213	Sequence 17213, A
1307	35.4	1.5	119214	4	US-09-949-016-12507	Sequence 12507, A	c1380	35.2	1.5	54161	4	US-09-949-016-11905	Sequence 11905, A
c1308	35.4	1.5	125192	4	US-09-949-016-14120	Sequence 14120, A	1381	35.2	1.5	57392	4	US-09-949-016-12070	Sequence 12070, A
c1309	35.4	1.5	126254	4	US-09-949-016-15341	Sequence 15341, A	1382	35.2	1.5	57402	4	US-09-949-016-13293	Sequence 13293, A
c1310	35.4	1.5	134434	4	US-09-949-016-17362	Sequence 17362, A	1383	35.2	1.5	59948	4	US-09-949-016-15594	Sequence 15594, A
1311	35.4	1.5	162450	3	US-09-345-882-1	Sequence 1, Appli	1384	35.2	1.5	67899	4	US-09-949-016-15432	Sequence 15432, A
1312	35.4	1.5	174493	4	US-09-804-471A-3	Sequence 3, Appli	1385	35.2	1.5	67902	4	US-09-949-016-11870	Sequence 11870, A
1313	35.4	1.5	174493	4	US-10-238-709-3	Sequence 3, Appli	1386	35.2	1.5	95318	4	US-09-949-016-11784	Sequence 11784, A
c1314	35.4	1.5	192956	4	US-09-949-016-14382	Sequence 14382, A	1387	35.2	1.5	95318	4	US-09-949-016-13998	Sequence 13998, A
c1315	35.4	1.5	235452	4	US-09-949-016-13675	Sequence 13675, A	1388	35.2	1.5	103447	4	US-09-949-016-16320	Sequence 16320, A
c1316	35.4	1.5	237241	4	US-09-949-016-16101	Sequence 16101, A	c1389	35.2	1.5	129415	4	US-09-949-016-16997	Sequence 16997, A
c1317	35.4	1.5	312957	4	US-09-949-001-31	Sequence 31, Appl	c1390	35.2	1.5	136917	4	US-09-949-016-16369	Sequence 16369, A
c1318	35.4	1.5	312972	4	US-09-949-001-34	Sequence 34, Appl	c1391	35.2	1.5	139049	4	US-09-949-016-17030	Sequence 17030, A
c1319	35.4	1.5	1830121	4	US-09-557-884-1	Sequence 1, Appli	1392	35.2	1.5	141560	4	US-09-949-016-16476	Sequence 16476, A
c1320	35.4	1.5	1830121	4	US-09-643-990A-1	Sequence 1, Appli	1393	35.2	1.5	142783	4	US-09-949-016-15127	Sequence 15127, A
c1321	35.2	1.5	504	4	US-09-248-796A-3317	Sequence 3317, Ap	c1394	35.2	1.5	145812	4	US-09-949-016-15698	Sequence 15698, A
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ALIGNMENTS

RESULT 1
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

Sequence 11, Appl
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Sequence 16, Appl
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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

RESULT 3

; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594

;
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
;
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
;
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
;
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
;
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
;
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
;
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
;
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
;
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
;
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
;
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
;
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 541 TGTTACAACTCATCTGACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAA 600
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Qy 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACCTT 2372

Db 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACCTT 2372

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
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; APPLICANT: Williams, P. Mickey
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches	2372;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	AGCAGGAAATCCGGATGTCTCGGTATATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60							
Db	1	AGCAGGAAATCCGGATGTCTCGGTATATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60							
Qy	61	GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120							
Db	61	GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120							
Qy	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCACGGTCTTCAGCCTG	180							
Db	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCACGGTCTTCAGCCTG	180							
Qy	181	GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTCGCTGCA	240							
Db	181	GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTCGCTGCA	240							
Qy	241	GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	300							
Db	241	GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	300							
Qy	301	GCGAACCAAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCTGTAGGCTGCTGGACTAAGT	360							
Db	301	GCGAACCAAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCTGTAGGCTGCTGGACTAAGT	360							
Qy	361	TTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420							
Db	361	TTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420							
Qy	421	GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAACCCCAAGTGTGGG	480							
Db	421	GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAACCCCAAGTGTGGG	480							
Qy	481	AAAAATGGGTGGGTGTCTGTGTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540							
Db	481	AAAAATGGGTGGGTGTCTGTGTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540							
Qy	541	TGTTACAACTCATCTGATACTTGGACTTAACTCGTGCATTCAGAAATATCACCACCAAA	600							
Db	541	TGTTACAACTCATCTGATACTTGGACTTAACTCGTGCATTCAGAAATATCACCACCAAA	600							
Qy	601	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTGAGTGACAGT	660							
Db	601	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTGAGTGACAGT	660							
Qy	661	ACCTACTCGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT	720							
Db	661	ACCTACTCGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT	720							
Qy	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTATG	780							
Db	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTATG	780							
Qy	781	GAAGCTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAAG	840							
Db	781	GAAGCTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAAG	840							
Qy	841	AATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCTGTAGTGTGCTCTCTCTTC	900							
Db	841	AATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCTGTAGTGTGCTCTCTCTTC	900							
Qy	901	TTTGGTGTGAGCTGGTCTTGGATTTTGCCTATGTCAAAAGGTATGGAAGGCTTCCCT	960							
Db	901	TTTGGTGTGAGCTGGTCTTGGATTTTGCCTATGTCAAAAGGTATGGAAGGCTTCCCT	960							
Qy	961	TTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACCAAACTAGTAAAGGAGGAAG	1020							
Db	961	TTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACCAAACTAGTAAAGGAGGAAG	1020							
Qy	1021	GCCATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAACCCAGAAAGTCC	1080							
Db	1021	GCCATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAACCCAGAAAGTCC	1080							

QY 1081 AAGAGTCCAAGCAAAACHTACCGTGGATGCCCTGGAAAGCTGAAGTTTAGATGACACAGAAA 1140
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1081 AAGAGTCCAAGCAAAACHTACCGTGGATGCCCTGGAAAGCTGAAGTTTAGATGACACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGGTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200
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1141 TGAGGAGACACACCTGAGGTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAAACAAAGAAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC 1260
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1201 ATCAAAAGGGCCAAAGAAACAAAGAAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC 1260
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAAC 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCCTTTCTAGCCTGGCTAT 1380
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1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCCTTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAAGTGCAAGGACCTAAACATC 1440
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1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAAGTGCAAGGACCTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAGAGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 TCATCAGTATCCAGTGGTAAAGAGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAATATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 TCTCTGTAAAGCTAAATATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCAGTGTGATTTTTCTCT 1860
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1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCAGTGTGATTTTTCTCT 1860
QY 1861 AGGAAATATACCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTATCT 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 AGGAAATATACCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
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1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2041 TGTAAATTGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTTTGATATTTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTGTCTGA 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 TTTTTCAGTTTTTGATATTTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTGTCTGA 2160

RESULT 6

; Sequence 200, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30


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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 60

QY     61  GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
Db     61  GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY    121  CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 180
Db    121  CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 180

QY    181  GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTTTTGC GTGA 240
Db    181  GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTTTTGC GTGA 240

QY    241  GAAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
Db    241  GAAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300

QY    301  GCGAACCCAGCAGCTGAATTTTACAGAAAGCTTAAGGAGGCCCTGTAGGCTCTGGGACTAAGT 360
Db    301  GCGAACCCAGCAGCTGAATTTTACAGAAAGCTTAAGGAGGCCCTGTAGGCTCTGGGACTAAGT 360

QY    361  TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTTGAAACTTGCAGCTAT 420
Db    361  TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTTGAAACTTGCAGCTAT 420

QY    421  GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCAAACCCCAAGTGTGGG 480
Db    421  GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCAAACCCCAAGTGTGGG 480

QY    481  AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
Db    481  AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY    541  TGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAATCCAGAAATTTATCACCACAAA 600
Db    541  TGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAATCCAGAAATTTATCACCACAAA 600

QY    601  GATCCCATATTTCAACACTCAAACCTGCAACACAAACAAACAGAAATTTATTGTCAGTGACAGT 660
Db    601  GATCCCATATTTCAACACTCAAACCTGCAACACAAACAAACAGAAATTTATTGTCAGTGACAGT 660

QY    661  ACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
Db    661  ACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720

QY    721  CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCAAGAAGTTTTTATG 780
Db    721  CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCAAGAAGTTTTTATG 780
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QY      781  GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGTGAAATAAAGCAGCATTCAAG 840
Db      781  GAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGTGAAATAAAGCAGCATTCAAG 840

QY     841  AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCCTCTTC 900
Db     841  AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCCTCTTC 900

QY     901  TTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960
Db     901  TTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960

QY     961  TTTTACAAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAAGTACTAAAGGAGGAAG 1020
Db     961  TTTTACAAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAAGTACTAAAGGAGGAAG 1020

QY    1021  GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAAACCCAGAAGTCC 1080
Db    1021  GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAAACCCAGAAGTCC 1080

QY    1081  AAGAGTCCAAGCAAAAACCTACCGTGCATGCCTTGGAAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db    1081  AAGAGTCCAAGCAAAAACCTACCGTGCATGCCTTGGAAAGCTGAAGTTTAGATGAGACAGAAA 1140

QY    1141  TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCCAGCTGGGGAA 1200
Db    1141  TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCCAGCTGGGGAA 1200

QY    1201  ATCAAAAAGGGCCAAAAGAACCAAAAGAAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC 1260
Db    1201  ATCAAAAAGGGCCAAAAGAACCAAAAGAAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC 1260

QY    1261  TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
Db    1261  TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

QY    1321  CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT 1380
Db    1321  CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT 1380

QY    1381  GTCCTAATAATATCCCACCTGGGAGAAAAGGAGTTTTTGCAAAAGTGCRAAGGACCTAAAAACATC 1440
Db    1381  GTCCTAATAATATCCCACCTGGGAGAAAAGGAGTTTTTGCAAAAGTGCRAAGGACCTAAAAACATC 1440

QY    1441  TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC 1500
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QY    1501  CAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db    1501  CAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

QY    1561  GCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTCCCTTCTGAGCCCGGTAAGAGCAAA 1620
Db    1561  GCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTCCCTTCTGAGCCCGGTAAGAGCAAA 1620

QY    1621  AGAATGGCAGAAAAGTTTAGCCCTGAAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680
Db    1621  AGAATGGCAGAAAAGTTTAGCCCTGAAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY    1681  TCTCTGTAAGCTAAAAATAAGAAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db    1681  TCTCTGTAAGCTAAAAATAAGAAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY    1741  GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800
Db    1741  GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800

QY    1801  CACTGTTTAGAAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT 1860
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QY	1861	AGGAAATATAC	TTTTACAA	GTAAACAAAA	AACTCTT	ATAAAATTT	CTATTTT	TATCT	1920					
DB	1861	AGGAAATATAC	TTTTACAA	GTAAACAAAA	AACTCTT	ATAAAATTT	CTATTTT	TATCT	1920					
QY	1921	GAGTTACAG	AAATGATT	ACTAAG	GAAGATT	ACTCAG	TAAATTT	GTTTAAAA	AGTAATAAAA	1980				
DB	1921	GAGTTACAG	AAATGATT	ACTAAG	GAAGATT	ACTCAG	TAAATTT	GTTTAAAA	AGTAATAAAA	1980				
QY	1981	TTCAACAA	ACATTT	TGCTG	NAATAG	CTACTAT	ATGTCA	AGTGCT	GTGCA	AGGTATTACACTC	2040			
DB	1981	TTCAACAA	ACATTT	TGCTG	NAATAG	CTACTAT	ATGTCA	AGTGCT	GTGCA	AGGTATTACACTC	2040			
QY	2041	TGTAATTG	AATATT	ATTCCT	CAAAAA	AATTGC	ACATAG	TAGAAC	CGCTAT	CTGGGA	AGCTAT	2100		
DB	2041	TGTAATTG	AATATT	ATTCCT	CAAAAA	AATTGC	ACATAG	TAGAAC	CGCTAT	CTGGGA	AGCTAT	2100		
QY	2101	TTTTTTT	CAGTTT	TGATAT	TTCTAG	CTTAT	CTACTT	CCAAAA	CTAATTT	TTTATTT	TGCTGA	2160		
DB	2101	TTTTTTT	CAGTTT	TGATAT	TTCTAG	CTTAT	CTACTT	CCAAAA	CTAATTT	TTTATTT	TGCTGA	2160		
QY	2161	GACTAAT	CTTAT	TCTCT	CTAAT	TATGG	CAACCA	TATATA	ACCTTA	ATTTAT	TATTAAC	2220		
DB	2161	GACTAAT	CTTAT	TCTCT	CTAAT	TATGG	CAACCA	TATATA	ACCTTA	ATTTAT	TATTAAC	2220		
QY	2221	ATACCTA	AGAGT	ACATTT	GTAC	CTCTAT	ATAC	CAAGCAC	ATTTT	AAAA	AGTGCC	ATAA	2280	
DB	2221	ATACCTA	AGAGT	ACATTT	GTAC	CTCTAT	ATAC	CAAGCAC	ATTTT	AAAA	AGTGCC	ATAA	2280	
QY	2281	CAAAATG	TATCA	CTAG	CCCTC	CTTTT	TTTCC	AACAAG	AGGACT	GAGAG	ATGC	AGAAAT	TATT	2340
DB	2281	CAAAATG	TATCA	CTAG	CCCTC	CTTTT	TTTCC	AACAAG	AGGACT	GAGAG	ATGC	AGAAAT	TATT	2340
QY	2341	TGTGAC	AAAAA	ATTAA	GCATTT	TAG	AAAA	ACTT	2372					
DB	2341	TGTGAC	AAAAA	ATTAA	GCATTT	TAG	AAAA	ACTT	2372					

RESULT 7

; Sequence 200, Application US/09909064
 ; Patent No. 6818449
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/909,064
 ; CURRENT FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22

	Query Match	100.0%;	Score 2372;	DB 4;	Length 2372;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2372;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
					0;
QY	1	AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60		
DB	1	AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60		
QY	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120		
DB	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120		
QY	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180		
DB	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180		
QY	181	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240		
DB	181	GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240		
QY	241	GAAGAGCTTTCATCCAGGTGTCAATGCAGAATTATGGGGATCACCCCTTGAGCAAAAAG	300		
DB	241	GAAGAGCTTTCATCCAGGTGTCAATGCAGAATTATGGGGATCACCCCTTGAGCAAAAAG	300		
QY	301	GCGAACCCAGCAGCTGAATTTACAGAAGCTAAGCAGGCCCTGTAGGCTGCTGGGACTAAGT	360		
DB	301	GCGAACCCAGCAGCTGAATTTACAGAAGCTAAGCAGGCCCTGTAGGCTGCTGGGACTAAGT	360		
QY	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420		
DB	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420		
QY	421	GGCTGGGTTGGAGATGGATTGTTGGTCACTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	480		
DB	421	GGCTGGGTTGGAGATGGATTGTTGGTCACTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	480		


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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match      100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

QY      61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY      121 CATCTGAGGTGTTTCCCTGCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CATCTGAGGTGTTTCCCTGCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
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QY      181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

QY      241 GAAGAGCTTTCCATCCAGGTGTGCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAAGAGCTTTCCATCCAGGTGTGCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300

QY      301 GCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360

QY      361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420

QY      421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAACCCCAAGTGTGGG 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAACCCCAAGTGTGGG 480

QY      481 AAAAATGGGTGGGTCTCTGATTGGAAGTTCCAGTGAGCCGACAGATTTCAGACCTAT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 AAAAATGGGTGGGTCTCTGATTGGAAGTTCCAGTGAGCCGACAGATTTCAGACCTAT 540

QY      541 TGTACAACACTCATCTGATACTTGGACTTAACTCGTGCATTCAGAGAAATTATCACCAACAAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TGTACAACACTCATCTGATACTTGGACTTAACTCGTGCATTCAGAGAAATTATCACCAACAAA 600

QY      601 GATCCCATATTTCAACACTCAAACTGCAACACAAAACAGAAATTTATTGTGAGTGACAGT 660
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GATCCCATATTTCAACACTCAAACTGCAACACAAAACAGAAATTTATTGTGAGTGACAGT 660

QY      661 ACCTACTCGGTGGCATCCCCCTTACTCTACAAATACCTGCCCCCTACTACTCTCCTGCT 720
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Db      661 ACCTACTCGGTGGCATCCCCCTTACTCTACAAATACCTGCCCCCTACTACTCTCCTGCT 720

QY      721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATTG 780
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATTG 780

QY      781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAAGCAGCATTTCAAG 840
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAAGCAGCATTTCAAG 840

QY      841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTTC 900
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTTC 900

QY      901 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960

QY      961 TTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAA 1020
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAA 1020

QY      1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080

QY      1081 AAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAA 1140
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAA 1140

QY      1141 TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCTTACCCCTGCCCCAGCTGGGAA 1200
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCTTACCCCTGCCCCAGCTGGGAA 1200

QY      1201 ATCAAAAGGGCCAAAGAAACCAAGAAAGAAAGTCCACCTTGGTTCTTAATGGAATCAGC 1260
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 ATCAAAAGGGCCAAAGAAACCAAGAAAGAAAGTCCACCTTGGTTCTTAATGGAATCAGC 1260
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QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAAC 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTCTAGCCTGGCTAT 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTCTAGCCTGGCTAT 1380
QY 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTTAAACATC 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGACCTTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 CAAGGAGTCACTGAGACCAAGGCTTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGTAAAGCAAA 1620
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGTAAAGCAAA 1620
QY 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
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1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAAGCTAAAAATAAGAAATAGAACAAAGCTGAGGATACGACAGTACACTGTCA 1740
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 TCTCTGTAAAGCTAAAAATAAGAAATAGAACAAAGCTGAGGATACGACAGTACACTGTCA 1740
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTTCTCTGAACACATGAGTTGGAAT 1800
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1741 GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTTCTCTGAACACATGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCAGTCTGATATTTCTCT 1860
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCAGTCTGATATTTCTCT 1860
QY 1861 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAA 1980
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAA 1980
QY 1981 TTCAACAAACATTTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1981 TTCAACAAACATTTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAATTGAATATTATTCCTCAAAAAAATTGCACATAGTAGAACCGTATCTGGGAAGCTAT 2100
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2041 TGTAATTGAATATTATTCCTCAAAAAAATTGCACATAGTAGAACCGTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTCTAATATGSCAACCATATATAACCTTAATTTATTTAATTAAC 2220
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2161 GACTAATCTTATTCATTTTCTCTAATATGSCAACCATATATAACCTTAATTTATTTAATTAAC 2220
QY 2221 ATACCTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 ATACCTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCCAACAAGAGGGACTGAGAGATGCAGAAAATATT 2340
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2281 CAAATGTATCACTAGCCCTCCTTTTCCCAACAAGAGGGACTGAGAGATGCAGAAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
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RESULT 9
; Sequence 200, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423

: SEQ ID NO 200									
; LENGTH: 2372									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
Query Match 100.0%; Score 2372; DB 4; Length 2372;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCAGGAAATCCGGATGTC	CGGTATGAAGTGGAGCAGT	GTGAGCTTCAACATA	60				
Dd	1	AGCAGGAAATCCGGATGTC	CGGTATGAAGTGGAGCAGT	GTGAGCTTCAACATA	60				
Qy	61	GTTCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTG	CCCTCTCATATCACCAGTGC	120				
Dd	61	GTTCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTG	CCCTCTCATATCACCAGTGC	120				
Qy	121	CATCTGAGGTGTTTCCCTG	CTGAAGGGGTAGGCACGAT	GGCCAGGTGCTTCAGCCTG	180				
Dd	121	CATCTGAGGTGTTTCCCTG	CTGAAGGGGTAGGCACGAT	GGCCAGGTGCTTCAGCCTG	180				
Qy	181	GTGTGCTTCTCACTTCCAT	CTGGACACGAGGCTCCTG	GTCCAAAGGCTCTTTGCGTGCA	240				
Dd	181	GTGTGCTTCTCACTTCCAT	CTGGACACGAGGCTCCTG	GTCCAAAGGCTCTTTGCGTGCA	240				
Qy	241	GAAGAGCTTCCATCCAGGT	GTCAATGAGGATATGCGG	ATACACCTTTGTGAGCAAAAG	300				
Dd	241	GAAGAGCTTCCATCCAGGT	GTCAATGAGGATATGCGG	ATACACCTTTGTGAGCAAAAG	300				
Qy	301	GCGAACAGCAGCTGAATT	TCACAGAAGCTAAGGAGCC	TGTAGGCTGCTGGGACTAAGT	360				
Dd	301	GCGAACAGCAGCTGAATT	TCACAGAAGCTAAGGAGCC	TGTAGGCTGCTGGGACTAAGT	360				
Qy	361	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGC	TAGCTTTGAAACTTTGCAGCTAT	420				
Dd	361	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGC	TAGCTTTGAAACTTTGCAGCTAT	420				
Qy	421	GGCTGGGTTGGAGATGGAT	TCGTGGTCATCTTAGGATT	AGCCAAACCCCAAGTGTGGG	480				
Dd	421	GGCTGGGTTGGAGATGGAT	TCGTGGTCATCTTAGGATT	AGCCAAACCCCAAGTGTGGG	480				
Qy	481	AAAAATGGGTTGGGTGTC	CTGATTGGAAGGTTCCAGT	GTAGCGGACAGTTTGCAGCCTAT	540				
Dd	481	AAAAATGGGTTGGGTGTC	CTGATTGGAAGGTTCCAGT	GTAGCGGACAGTTTGCAGCCTAT	540				
Qy	541	TGTTACAACTCATCTGATA	CTTGGACTAATCGTGCATT	CCAGAAATTATCACCACCAA	600				
Dd	541	TGTTACAACTCATCTGATA	CTTGGACTAATCGTGCATT	CCAGAAATTATCACCACCAA	600				
Qy	601	GATCCCATATTCAACACT	CAAACTGCAACACAAACAG	AAATTATTGTCAGTGACAGT	660				
Dd	601	GATCCCATATTCAACACT	CAAACTGCAACACAAACAG	AAATTATTGTCAGTGACAGT	660				
Qy	661	ACCTACTCGGTGGCATCCC	CTTACTCTACAATACCTG	CCCCCTACTACTCTCCTGCT	720				
Dd	661	ACCTACTCGGTGGCATCCC	CTTACTCTACAATACCTG	CCCCCTACTACTCTCCTGCT	720				
Qy	721	CCAGTTCCACTTCTATTCC	ACGAGAAAAAATTGATTG	TGTCACAGAAAGTTTATG	780				
Dd	721	CCAGTTCCACTTCTATTCC	ACGAGAAAAAATTGATTG	TGTCACAGAAAGTTTATG	780				
Qy	781	GAACTAGCACCATGTCTAC	AGAACTGAACCATTTGTTG	AAAAATAAAGCAGCATTCAAG	840				
Dd	781	GAACTAGCACCATGTCTAC	AGAACTGAACCATTTGTTG	AAAAATAAAGCAGCATTCAAG	840				
Qy	841	AATGAAGCTGCTGGGTTTG	GAGGTGTCACCGGCTCTG	CTAGTGTCTCCTCTTC	900				
Dd	841	AATGAAGCTGCTGGGTTTG	GAGGTGTCACCGGCTCTG	CTAGTGTCTCCTCTTC	900				
Qy	901	TTTGGTGCAGCTGGTCTTG	GATTTTGCTATGTCAAAGG	TATGTGAAGGCCCTTCCCT	960				
Dd	901	TTTGGTGCAGCTGGTCTTG	GATTTTGCTATGTCAAAGG	TATGTGAAGGCCCTTCCCT	960				

Qy	961	TTTACAAACAAGAAATCAG	CAGAAAGAAATGATCGAA	ACCAAAAGTAGTAAAGGAG	GAG 1020				
Dd	961	TTTACAAACAAGAAATCAG	CAGAAAGAAATGATCGAA	ACCAAAAGTAGTAAAGGAG	GAG 1020				
Qy	1021	GCCAATGATAGCAACCTTA	TAGAGGAATCAAAGAAAACT	GATAAAAAACCCAGAGATCC	1080				
Dd	1021	GCCAATGATAGCAACCTTA	TAGAGGAATCAAAGAAAACT	GATAAAAAACCCAGAGATCC	1080				
Qy	1081	AAGAGTCCAAGCAAACTAC	CGTGCGATGCCTGGAAGCT	GAAAGTTTAGATGAGACAGAA	1140				
Dd	1081	AAGAGTCCAAGCAAACTAC	CGTGCGATGCCTGGAAGCT	GAAAGTTTAGATGAGACAGAA	1140				
Qy	1141	TGAGGAGACACACCTGAG	SGCTGGTTTCTTTATGCTC	CTTACCCCTGCCCAGCTGGGAA	1200				
Dd	1141	TGAGGAGACACACCTGAG	SGCTGGTTTCTTTATGCTC	CTTACCCCTGCCCAGCTGGGAA	1200				
Qy	1201	ATCAAAAGGGCCAAAGAAC	CAAAAGAAAGTCCACCCCT	TGGTTCCTAACTGGAATCAGC	1260				
Dd	1201	ATCAAAAGGGCCAAAGAAC	CAAAAGAAAGTCCACCCCT	TGGTTCCTAACTGGAATCAGC	1260				
Qy	1261	TCAGGACTGCCATTGGACT	ATATGGAGTGCACCAAAAG	AGAAATGCCCTTCTCCTTAT	TGTAAC 1320				
Dd	1261	TCAGGACTGCCATTGGACT	ATATGGAGTGCACCAAAAG	AGAAATGCCCTTCTCCTTAT	TGTAAC 1320				
Qy	1321	CCTGTCTGGATCCTATCCT	CTACCTCCAAGCTTCCAC	GGCCTTTCTAGCCTGGCTAT	1380				
Dd	1321	CCTGTCTGGATCCTATCCT	CTACCTCCAAGCTTCCAC	GGCCTTTCTAGCCTGGCTAT	1380				
Qy	1381	GTCTTAATAATATCCACT	GGGAGAAAGGAGTTTGTG	CAAAAGTGCAAGGACCTAAA	ACATC 1440				
Dd	1381	GTCTTAATAATATCCACT	GGGAGAAAGGAGTTTGTG	CAAAAGTGCAAGGACCTAAA	ACATC 1440				
Qy	1441	TCATCAGTATCCAGTGGT	TAATAAGGCCTCCTGGCT	GTCTGAGGCTAGGTGGTTG	AAAGC 1500				
Dd	1441	TCATCAGTATCCAGTGGT	TAATAAGGCCTCCTGGCT	GTCTGAGGCTAGGTGGTTG	AAAGC 1500				
Qy	1501	CAAGGAGTCACTGAGACCA	AGGCTTTCTCTACTGATTC	CCGAGCTCAGACCCCTTTCT	TCA 1560				
Dd	1501	CAAGGAGTCACTGAGACCA	AGGCTTTCTCTACTGATTC	CCGAGCTCAGACCCCTTTCT	TCA 1560				
Qy	1561	GCTCTGAAAGAGAAACAC	GTATCCCACCTGCATGTCT	CTTGAGCCCCGGTAAGAGCAA	1620				
Dd	1561	GCTCTGAAAGAGAAACAC	GTATCCCACCTGCATGTCT	CTTGAGCCCCGGTAAGAGCAA	1620				
Qy	1621	AGAATGGCAGAAAGTTTAG	CCCCCTGAAAGCCATGGAG	ATTCTCATAACTTGAGACCTAA	1680				
Dd	1621	AGAATGGCAGAAAGTTTAG	CCCCCTGAAAGCCATGGAG	ATTCTCATAACTTGAGACCTAA	1680				
Qy	1681	TCTCTGTAAGCTAAATAA	AGAAATAGAACCAAGGCT	GAGGATACGACAGTACACTGTCA	1740				
Dd	1681	TCTCTGTAAGCTAAATAA	AGAAATAGAACCAAGGCT	GAGGATACGACAGTACACTGTCA	1740				
Qy	1741	GCAGGGACTGTAAACACAG	ACAGGGTCAAAGTGTTTTCT	CTGAAACACATTGAGTTGGAAT	1800				
Dd	1741	GCAGGGACTGTAAACACAG	ACAGGGTCAAAGTGTTTTCT	CTGAAACACATTGAGTTGGAAT	1800				
Qy	1801	CACGTGTTTAGAACACAC	ACACTTACTTTTCTGGTCT	CTACCACCTGCTGATATTTCTCT	1860				
Dd	1801	CACGTGTTTAGAACACAC	ACACTTACTTTTCTGGTCT	CTACCACCTGCTGATATTTCTCT	1860				
Qy	1861	AGGAAATATACCTTTTACA	AGTAACAAAACTTTATAAA	ATTTCTATTTTATCT 1920					
Dd	1861	AGGAAATATACCTTTTACA	AGTAACAAAACTTTATAAA	ATTTCTATTTTATCT 1920					
Qy	1921	GAGTTACAGAAATGATTACT	AAAGGAGATTACTCAGTAAT	TTGTTTAAAAAGTAATAAAA	1980				
Dd	1921	GAGTTACAGAAATGATTACT	AAAGGAGATTACTCAGTAAT	TTGTTTAAAAAGTAATAAAA	1980				
Qy	1981	TTCAACAAACATTTGCTGA	ATAGCTACTATATGTCAAG	TGCTGTGCAAGGTATTACACTC	2040				
Dd	1981	TTCAACAAACATTTGCTGA	ATAGCTACTATATGTCAAG	TGCTGTGCAAGGTATTACACTC	2040				
Qy	2041	TGTAATTGAATATTATTTC	CTCAAAAAATTGCACATAG	TAGTAACGCTATCTCGGGA	AGCTAT 2100				

Db 2041 TGTAATTGAATATTATTCTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGAAGCTAT 2100
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Db 2101 TTTTTCAGTTTTTGATATTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTTGCTGA 2160
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Db 2221 ATACCTAAGAGTACATTTGTTACCTCTATATACCAAAAGCACATTTTAAAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAAGCATTTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAAGCATTTTAGAAAACTT 2372

RESULT 10
US-09-949-016-1894
; Sequence 1894, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1894
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1894

Query Match 96.9%; Score 2299.4; DB 4; Length 2301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 69 ACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCCAGTGGCCATCTGAG 128
Db 1 ACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCCAGTGGCCATCTGAG 60
QY 129 GTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCT 188
Db 61 GTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCT 120
QY 189 TCTCACTTCCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGCT 248
Db 121 TCTCACTTCCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGCT 180
QY 249 TTCCATCCAGGTGTATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCA 308
Db 181 TTCCATCCAGGTGTATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCA 240
QY 309 GCAGCTGAATTTACAGAAGCTTAAGGAGGCTGTGAGGCTGTGGACTAAGTTTGGCCGG 368
Db 241 GCAGCTGAATTTACAGAAGCTTAAGGAGGCTGTGAGGCTGTGGACTAAGTTTGGCCGG 300

QY 369 CAAGGACCAAGTTGAAACACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGT 428
Db 301 CAAGGACCAAGTTGAAACACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGT 360
QY 429 TGGAGATGGATTCTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGG 488
Db 361 TGGAGATGGATTCTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGG 420
QY 489 GGTGGGTGCTCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAA 548
Db 421 GGTGGGTGCTCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAA 480
QY 549 CTCATCTGATACTTGGACTAACTCGTGCATTTCCAGAAATTATCACCAACCAAGATCCCAT 608
Db 481 CTCATCTGATACTTGGACTAACTCGTGCATTTCCAGAAATTATCACCAACCAAGATCCCAT 540
QY 609 ATTCAACACTCAAACTGCAACACAAACAGAAATTTATTGTGACGACAGTACCTACTC 668
Db 541 ATTCAACACTCAAACTGCAACACAAACAGAAATTTATTGTGACGACAGTACCTACTC 600
QY 669 GGTGGCATCCCTTACTCTACAAATACCTGCCCTTACTACTACTCTCCTCTGCTCCAGCTTC 728
Db 601 GGTGGCATCCCTTACTCTACAAATACCTGCCCTTACTACTACTCTCCTCTGCTCCAGCTTC 660
QY 729 CACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAACTAG 788
Db 661 CACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAACTAG 720
QY 789 CACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAGAATGAAGC 848
Db 721 CACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAGAATGAAGC 780
QY 849 TGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTCCTCTCTTTTGGTGC 908
Db 781 TGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTCCTCTCTTTTGGTGC 840
QY 909 TGCAGTGTGCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCTTTTACAAA 968
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QY 969 CAAGAATCAGCAGAAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGAGAGGCCAATGA 1028
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QY 1029 TAGCAACCTTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAGAGTCCAAGAGTCC 1088
Db 961 TAGCAACCTTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAGAGTCCAAGAGTCC 1020
QY 1089 AAGCAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAAAATGAGGAGA 1148
Db 1021 AAGCAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAAAATGAGGAGA 1080
QY 1149 CACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCCCTGCCCCAGCTGGGAAAAATCAAAG 1208
Db 1081 CACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCCCTGCCCCAGCTGGGAAAAATCAAAG 1140
QY 1209 GGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACT 1268
Db 1141 GGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGCTCAGGACT 1200
QY 1269 GCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTTGTAACCCCTGTCTG 1328
Db 1201 GCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTTGTAACCCCTGTCTG 1260
QY 1329 GATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCCTAAT 1388
Db 1261 GATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCCTAAT 1320
QY 1389 AATATCCCACTGGGAGAAAGGAGTTTTCAAAAGTCAAGGACCTAAAACATCTCATCAGT 1448
Db 1321 AATATCCCACTGGGAGAAAGGAGTTTTCAAAAGTCAAGGACCTAAAACATCTCATCAGT 1380
QY 1449 ATCCAGTGGTAAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCCAAGGAGT 1508

||||| 1381 ATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCAAAGGAGT 1440
QY 1509 CACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCAGCTCTGAA 1568
Db 1441 CACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCAGCTCTGAA 1500
QY 1569 AGAGAAACACGATATCCCACCTGACATGTCTCTTGAGCCCGTAAGAGCAAAAGATGGC 1628
Db 1501 AGAGAAACACGATATCCCACCTGACATGTCTCTTGAGCCCGTAAGAGCAAAAGATGGC 1560
QY 1629 AGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTA 1688
Db 1561 AGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTA 1620
QY 1689 AAGCTAAATAAAGAAATAGAACAGGCTGAGGATCTCATAACTTGAGACCTAATCTCTGTA 1748
Db 1621 AAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCTCAGCAGGGAC 1680
QY 1749 TGTAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTTGAGTTGGAATCACTGTTT 1808
Db 1681 TGTAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTTGAGTTGGAATCACTGTTT 1740
QY 1809 AGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCTAGGAAATA 1868
Db 1741 AGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCTAGGAAATA 1800
QY 1869 TACTTTTACAAGTAACAAATAAATAAACTCTTATAAATTTCTATTTTATCTGAGTTACA 1928
Db 1801 TACTTTTACAAGTAACAAATAAATAAACTCTTATAAATTTCTATTTTATCTGAGTTACA 1860
QY 1929 GAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAA 1988
Db 1861 GAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAA 1920
QY 1989 ACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTAAATTG 2048
Db 1921 ACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTAAATTG 1980
QY 2049 AATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTCA 2108
Db 1981 AATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTCA 2040
QY 2109 GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTGCTGAGACTAATC 2168
Db 2041 GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTGTGTTTGTGCTGAGACTAATC 2100
QY 2169 TTATTCATTTTCTCTAATATGCAACCATTTATAACCTTAATTTATTTAATACATACCTAA 2228
Db 2101 TTATTCATTTTCTCTAATATGCAACCATTTATAACCTTAATTTATTTAATACATACCTAA 2160
QY 2229 GAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTTAACAATGTA 2288
Db 2161 GAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTTAACAATGTA 2220
QY 2289 TCACTAGCCCTCCTTTTCCAAAGAAAGGACTGAGAGATGCAGAAATATTTGTGACAA 2348
Db 2221 TCACTAGCCCTCCTTTTCCAAAGAAAGGACTGAGAGATGCAGAAATATTTGTGACAA 2280
QY 2349 AAAATTAAAGCATTTAGAAAA 2369
Db 2281 AAAATTAAAGCATTTAGAAAA 2301

RESULT 11

US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 91..1056
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1056
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..153
US-08-892-880-1

Query Match 96.6%; Score 2290.2; DB 2; Length 2313;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 75 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTT 134
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QY 135 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTTGCGTGCAGAAAGAGCTTTCCAT 194
Db 66 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTTGCGTGCAGAAAGAGCTTTCCAT 125
QY 195 TTCCATCTGGACCAAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCAT 254
Db 126 TTCCATCTGGACCAAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCAT 185
QY 255 CCAGGTGTTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAGGGCGAACAGCAGCT 314
Db 186 CCAGGTGTTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAGGGCGAACAGCAGCT 245
QY 315 GAATTTACAGAAAGCTAAGGAGGCTCTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGA 374
Db 246 GAATTTACAGAAAGCTAAGGAGGCTCTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGA 305
QY 375 CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA 434
Db 306 CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGCGA 365

QY 435 TGGATTTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGG 494
Db 366 TGGATTTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGG 425
QY 495 TGTCTGATTTCGGAAGGTTCCAGTGAGCCGACAGTTTCAGCCCTATTGTTACAACACTCATC 554
Db 426 TGTCTGATTTCGGAAGGTTCCAGTGAGCCGACAGTTTCAGCCCTATTGTTACAACACTCATC 485
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QY 615 CACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGC 674
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Db 1146 AGAACCAAGAAGAAAGTCCACCCCTTGGTTCTTAATCTGGAATCAGCTCAGGACTGCCATT 1205
QY 1275 GGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAACCCTGTCTGGATCCT 1334
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QY 1395 CCACTGGGAGAAAGGAGTTTTCGCAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAG 1454
Db 1326 CCACTGGGAGAAAGGAGTTTTCGCAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAG 1385
QY 1455 TGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGA 1514
Db 1386 TGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGA 1445
QY 1515 GACCAAGGCTTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAA 1574

Db 1446 GACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAA 1505
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QY 1695 AAATAAAGAAATPAGAAACAAGGCTGAGGATPACGACAGTACACTGTGAGAGGACTGTAAA 1754
Db 1626 AAATAAAGAAATPAGAAACAAGGCTGAGGATPACGACAGTACACTGTGAGAGGACTGTAAA 1685
QY 1755 CACAGACAGGTCAAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACCA 1814
Db 1686 CACAGACAGGTCCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACCA 1745
QY 1815 CACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCTAGAAAAATATACTTT 1874
Db 1746 CACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCTAGAAAAATATACTTT 1805
QY 1875 TACAAGTAACAAAAATAAAAACTCTTTATAAAATTTCTATTTTATCTGAGTTACAGAAATG 1934
Db 1806 TACAAGTAACAAAAATAAAAACTCTTTATAAAATTTCTATTTTATCTGAGTTACAGAAATG 1865
QY 1935 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAAACAAACATTT 1994
Db 1866 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAAACAAACATTT 1925
QY 1995 GCTGAATAGCTACTATATGTCAAAGTGTGCAAGCTATCTGGGAAGCTATTTTTTTCAGTTTGT 2054
Db 1926 GCTGAATAGCTACTATATGTCAAAGTGTGCAAGCTATCTGGGAAGCTATTTTTTTCAGTTTGT 1985
QY 2055 ATTCTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTTTGT 2114
Db 1986 ATTCTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCAGTTTGT 2045
QY 2115 ATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTGAGACTAAATCTTATTC 2174
Db 2046 ATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTGAGACTAAATCTTATTC 2105
QY 2175 ATTTTCTCTAATATGGCAACCATTTATAACCTTAATTTATTATTAAACATACCTAAGAACTA 2234
Db 2106 ATTTTCTCTAATATGGCAACCATTTATAACCTTAATTTATTATTAAACATACCTAAGAACTA 2165
QY 2235 CATTGTTACCTCTATATACCAAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA 2294
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QY 2295 GCCCTCCTTTTCCAAACAAGAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATT 2354
Db 2226 GCCCTCCTTTTCCAAACAAGAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATT 2285
QY 2355 AAAGCATTTTAGAAAA 2369
Db 2286 AAAGCATTTTAGAAAA 2300

RESULT 12
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160

; CURRENT FILING DATE: 1999-01-15									
; NUMBER OF SEQ ID NOS: 23									
; SOFTWARE: PERL Program									
; SEQ ID NO 13									
; LENGTH: 2029									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE: -									
; OTHER INFORMATION: 3044710									
US-09-232-160-13									
Query Match 84.1%; Score 1994; DB 3; Length 2029;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
QY	1	ACGAGGGAAATCCGGATGTC	TCGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	60				
Db	24	ACGAGGGAAATCCGGATGTC	CGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	83				
QY	61	GTTCCAGAACTCTCCATCCG	GA	CTAGTTATTGAGCATCTGCCT	CTCATATCACCAGTGGC	120			
Db	84	GTTCCAGAACTCTCCATCCG	GA	CTAGTTATTGAGCATCTGCCT	CTCATATCACCAGTGGC	143			
QY	121	CATCTGAGGTGTTTCCCTGG	CTCTGAAGGGTAGGCAGAT	GGCCAGGTGCTTCAGCCTG	180				
Db	144	CATCTGAGGTGTTTCCCTGG	CTCTGAAGGGTAGGCAGAT	GGCCAGGTGCTTCAGCCTG	203				
QY	181	GTGTTGCTTCTCACTTCCAT	CTGGACCA	CGAGGCTCTGGTCCAAGGCTCT	TTGCGTGCA	240			
Db	204	GTGTTGCTTCTCACTTCCAT	CTGGACCA	CGAGGCTCTGGTCCAAGGCTCT	TTGCGTGCA	263			
QY	241	GAAGAGCTTTCATCCAGGTG	TCATGCAGAA	TTATGGGGATCACCC	TTGTGAGCAAAAAG	300			
Db	264	GAAGAGCTTTCATCCAGGTG	TCATGCAGAA	TTATGGGGATCACCC	TTGTGAGCAAAAAG	323			
QY	301	GCGAACCCAGCAGCTGAAT	TTACAGAA	GCTAAGGAGCTGTAGGCTGT	GAGCTTGA	360			
Db	324	GCGAACCCAGCAGCTGAAT	TTACAGAA	GCTAAGGAGCTGTAGGCTGT	GAGCTTGA	383			
QY	361	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCT	GTAGCTTTGAAACTTG	CAGCTAT	420			
Db	384	TTGGCCGGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCT	GTAGCTTTGAAACTTG	CAGCTAT	443			
QY	421	GGCTGGGTGGAGATGGAT	TCGTGGTCACTCTAGGAT	TAGCCAAACCCCAAGTGGG	480				
Db	444	GGCTGGGTGGAGATGGAT	TCGTGGTCACTCTAGGAT	TAGCCAAACCCCAAGTGGG	503				
QY	481	AAAAATGGGTGGGTGTCCT	GATTTGGAAGGTTCCAGT	GAGCCGACAGTTTG	CAGCCTAT	540			
Db	504	AAAAATGGGTGGGTGTCCT	GATTTGGAAGGTTCCAGT	GAGCCGACAGTTTG	CAGCCTAT	563			
QY	541	TGTTACAACTCATCTGAT	ACTTGGACTAACTCGTGC	ATTCCAGAAATTTAT	CACCAACAAA	600			
Db	564	TGTTACAACTCATCTGAT	ACTTGGACTAACTCGTGC	ATTCCAGAAATTTAT	CACCAACAAA	623			
QY	601	GATCCCATATTTCAACACT	CAAACTGCAACAAACAG	AAATTTATTGTCAGTGACAGT	660				
Db	624	GATCCCATATTTCAACACT	CAAACTGCAACAAACAG	AAATTTATTGTCAGTGACAGT	683				
QY	661	ACCTACTCGGTGGCATCC	CCCTACTCTACAATACCT	GCCCCCTACTACTCTCTCT	CTGCT	720			
Db	684	ACCTACTCGGTGGCATCC	CCCTACTCTACAATACCT	GCCCCCTACTACTCTCTCT	CTGCT	743			
QY	721	CCAGCTTCCACTTCTATT	CCAGGAGAAAAAATTTG	ATTGTCACAGAAATTTTATG	780				
Db	744	CCAGCTTCCACTTCTATT	CCAGGAGAAAAAATTTG	ATTGTCACAGAAATTTTATG	803				
QY	781	GAAACTAGCACCATGTCT	ACAGAAACTGAACCAAT	TTGTTGAAAAATAAAGC	AGCATTC	840			
Db	804	GAAACTAGCACCATGTCT	ACAGAAACTGAACCAAT	TTGTTGAAAAATAAAGC	AGCATTC	863			
QY	841	AATGAAGCTGCTGGGTT	GTGAGGTGTCCCCACGG	CTCTGCTAGTGTCTCTCT	CTCTC	900			

Db	864	AATGAAGCTGCTGGGTTT	GGAGGTGTCCCCACGG	CTCTGCTAGTGTCTCTCT	CTCTC	923
QY	901	TTTGGTGTGCAGCTGCT	GTCTTTGGATTTTGCT	ATGTCAAAAAGGTATGT	GAAAGCCCTTCCCT	960
Db	924	TTTGGTGTGCAGCTGCT	GTCTTTGGATTTTGCT	ATGTCAAAAAGGTATGT	GAAAGCCCTTCCCT	983
QY	961	TTTACAAACAAGAAATC	AGCAGAAAGAAATGAT	CGAAACCAAAAGTAG	TAAAGGAGGAGAA	1020
Db	984	TTTACAAACAAGAAATC	AGCAGAAAGAAATGAT	CGAAACCAAAAGTAG	TAAAGGAGGAGAA	1043
QY	1021	GCCAATGATAGCAACCT	TAATGAGGAATCAA	AGAAACTGATAAAAA	CCCAGAAAGTCC	1080
Db	1044	GCCAATGATAGCAACCT	TAATGAGGAATCAA	AGAAACTGATAAAAA	CCCAGAAAGTCC	1103
QY	1081	AAGAGTCCAAGCAAACT	ACCGTGC	GATGCCTGGAGCTG	AAAGTTTAGATGAG	1140
Db	1104	AAGAGTCCAAGCAAACT	ACCGTGC	GATGCCTGGAGCTG	AAAGTTTAGATGAG	1163
QY	1141	TGAGGAGACACACCTG	AGGCTGGTTTCTT	CATGCTCCTTAC	CCCTGCCCCAGCT	1200
Db	1164	TGAGGAGACACACCTG	AGGCTGGTTTCTT	CATGCTCCTTAC	CCCTGCCCCAGCT	1223
QY	1201	ATCAAAAGGGCCAAAG	AAACCAAGAAAGT	CCACCCCTTGGT	TCCTAACTGGAAT	1260
Db	1224	ATCAAAAGGGCCAAAG	AAACCAAGAAAGT	CCACCCCTTGGT	TCCTAACTGGAAT	1283
QY	1261	TCAGGACTGCCATTG	GACTATGGAGTG	CAACAAAGAAAT	GCCCCCTTCTCCT	1320
Db	1284	TCAGGACTGCCATTG	GACTATGGAGTG	CAACAAAGAAAT	GCCCCCTTCTCCT	1343
QY	1321	CCTGTCTGGATCCTAT	CCTCTACCTCCA	AAAGTTTCCCACGG	CCCTTTCTAGCCT	1380
Db	1344	CCTGTCTGGATCCTAT	CCTCTACCTCCA	AAAGTTTCCCACGG	CCCTTTCTAGCCT	1403
QY	1381	GTCTTAATAATATCC	CACTGGGAGAAAG	GAGTTTTC	GCAAAAGTGCAAGG	1440
Db	1404	GTCTTAATAATATCC	CACTGGGAGAAAG	GAGTTTTC	GCAAAAGTGCAAGG	1463
QY	1441	TCATCAGTATCCAGT	TGTA	AAAAGGCCTCCTGG	CTGTCTGAGGCT	1500
Db	1464	TCATCAGTATCCAGT	TGTA	AAAAGGCCTCCTGG	CTGTCTGAGGCT	1523
QY	1501	CAAGGAGTCACTG	AGACCAAGGCTTT	CTCTACTGAT	TCGCGAGCTCAG	1560
Db	1524	CAAGGAGTCACTG	AGACCAAGGCTTT	CTCTACTGAT	TCGCGAGCTCAG	1583
QY	1561	GCTCTGAAAGAGAA	ACAGTATCCAC	CTGACATGTCTCT	GAGCCCGTAA	1620
Db	1584	GCTCTGAAAGAGAA	ACAGTATCCAC	CTGACATGTCTCT	GAGCCCGTAA	1643
QY	1621	AGAATGGCAGAAA	AGTTTAGCCCTG	AAAAGCCATGG	AGATTCTCAT	1680
Db	1644	AGAATGGCAGAAA	AGTTTAGCCCTG	AAAAGCCATGG	AGATTCTCAT	1703
QY	1681	TCTCTGTAAAGCT	AAAAATAAAGAA	ATAGAACAG	SGCTGAGGAT	1740
Db	1704	TCTCTGTAAAGCT	AAAAATAAAGAA	ATAGAACAG	SGCTGAGGAT	1763
QY	1741	GCAGGGACTGTAA	ACACAGACAGGG	TCAAAGTGT	TTCTCTGAA	1800
Db	1764	GCAGGGACTGTAA	ACACAGACAGGG	TCAAAGTGT	TTCTCTGAA	1823
QY	1801	CAC	TGTTTAGAACACAC	ACACTTACTTTT	CTGGTCTCTAC	1860
Db	1824	CAC	TGTTTAGAACACAC	ACACTTACTTTT	CTGGTCTCTAC	1883
QY	1861	AGGAAATATAC	TTTACAAAGTAA	CAAAAAATA	AAAAACTTT	1920
Db	1884	AGGAAATATAC	TTTACAAAGTAA	CAAAAAATA	AAAAACTTT	1943
QY	1921	GAGTTACAGAA	ATGATTACTAAG	GAGATTACTCAG	TAAATTTG	1980
Db	1944	GAGTTACAGAA	ATGATTACTAAG	GAGATTACTCAG	TAAATTTG	2003


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; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0

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Query Match 25.4%; Score 603.6; DB 3; Length 1896;
Best Local Similarity 76.2%; Pred. No. 1.7e-163;
Matches 786; Conservative 0; Mismatches 234; Indels 12;

QY	140	GCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTGGTGTGCTTCTCACTTCCA	199
Db	42	GCCCCGAGGGATCTGCACAATGCTCCAGCACACTAGCCTGGTGTACTCTCGCCTCTA	101
QY	200	TCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAAGAGCTTTCCATCCAGG	259
Db	102	TTTGGACCACTAGGCACCCAGTCCAAGGTCCGACCTCGTGCAAGACCTTTCCAT--TT	158
QY	260	TGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATT	319
Db	159	CTACATGCAGAATCATGGGGCGTTGCCCTTGTGGGCAGAAAACAAAACCCACAGATGAATT	218
QY	320	TCACAGAAGCTAAGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAG	379
Db	219	TCACAGAAGCCAACGAGGCCTGTAAGATGCTGGGACTGACTCTGGCCAGCAGGACCAGG	278
QY	380	TTGAAACAGCCTTGAAAGCTAGCTTTTGAAACCTTGCAGCTATGGCTGGGTTGGAGATGGAT	439
Db	279	TAGAGTCAGCGCAGAAAATCTGGCTTTGAGACTTGCACTTGCACTATGGATGGGTGGAGAACGT	338
QY	440	TCGTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCC	499
Db	339	TCTCTGTCATCCCTCGGATTTTCTCAAACCCCGAGGTGTGGGAAGAATGGCAAAGGTGTCC	398
QY	500	TGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGTATA	559
Db	399	TGATTTGGAATGCTCCCTCCAGCCCAAAGTTCAAAGCCTATTGCCACAACTCATCCGACA	458
QY	560	CTTGGACTAACTCTGTGCATTCCAGAAAATTATACCAACCAAAAGATCCCATATTCAACACTC	619
Db	459	CCTGGGTTAACTCCTGCAATCCAGAAAATCGTTACCACATTTTACCCCGTGTGGACACTC	518
QY	620	AAACTGCAACACAAAACAACAGAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCC	679
Db	519	A-----AACACCCGCAACAGAGTTTCTGTGAGCAGCAGCGCCTACTTGGCTTCATCCC	572
QY	680	CTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGTCTCCAGCTTCCACTTCTATTCT	739
Db	573	CTGACTCCACAAACACCTG--TTTCTGCCACCCACCCGGGCTCCACCTTTGACCTCCATGG	629
QY	740	CACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTATA	799
Db	630	CACGGAAGCAAAAAAAGATTGTATCACGGAAGTTTATACAGAACCTATCACCATGGCTA	689
QY	800	CAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCAATCAAGAAATGAAGCTGCTGGGTTG	859
Db	690	CAGAAACAGAAAGCATTTGTTGCAAGTGGAGCAGCAATCAAGAAACGAAAGCAGCTGGGTTG	749
QY	860	GAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCAAGCTGGTC	919
Db	750	GAGGTGTCCCCACCGCCCTGCTGGTCTGCTGCTCTCTCTCTTTTGGTGTGCGCTGTGC	809
QY	920	TTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGC	979
Db	810	TGGCTGTTTGCTACGTGAAAAGGTATGTGAAGGCCCTTCCCTTTTCAAAACCAAGAAATCAAC	869
QY	980	AGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAAATGATAGCAACCCCTA	1039

Db	870	AGAAGGAATGATCGAAACCAAGGTTGTAAAGGAAGAGAGGCTGATGACGTCAACGCTA	929
QY	1040	ATGAGGAATCAAAGAAAACTGATATAAAAAACCCAGAAAGAGTCCAAGAGAGTCCAAGCAAAAACTA	1099
Db	930	ATGAAGAATCAAAGAAAAACCATTAATAAACCCAGAGGAGGCCAAGAGTCCACCCAAAACTA	989
QY	1100	CCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAAAATGAGGAGACACACCTTGAGG	1159
Db	990	CGGTGCGATGCTTAGAAGCTGAAGTTTAGATGCAAGAGAGTGGAGAAGGTGCACACGAGG	1049
QY	1160	CTGGTTTCTTTC	1171
Db	1050	CAAGTTTCATGC	1061

RESULT 15
 US-08-892-880-11/c
 ; Sequence 11, Application US/08892880
 ; Patent No. 5942417
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER L.
 ; APPLICANT: DILLON, PATRICK J.
 ; TITLE OF INVENTION: CD44-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/892,880
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/021,762
 ; FILING DATE: 15-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0490001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 339 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-892-880-11

	Query Match	14.1%; Score 334; DB 2;	Length 339;
	Best Local Similarity	98.5%; Pred. No.	4.e-86;
	Matches 334; Conservative	0; Mismatches	5; Indels 0; Gaps 0;
QY	1466 CCTCTGGCGTGTCTGAGGCTAGTGGGTTGAAGCCAAGGAGTCAC TGAGACCAAGGC TT	1525	
Dd	339 CCTCTGGCGTGTCTGAGGCTAGTGGGTTGAAGCNAAGGAGTCAC TGAGACCAAGGC TT	280	
QY	1526 TCTCTACTGATTCGCGAGCTCACGCCCTTTCTTCAGCTCTGAAAGAGAAAA CAGTATCCC	1585	
Dd	279 NCTCTACTGATTCCGCGAGCTCAGACCCTTNCTTCAGCTCTGAAAGAGAAAA CAGTATCCC	220	

Qy	1586	ACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCT	1645
Db	219	ACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCT	160
Qy	1646	GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAATAAAGAAA	1705
Db	159	GAAAGCCATGGAGANTCTCATAACTTGAGACCTAATCTCTGTAAAGCTNAATAAAGAAA	100
Qy	1706	TAGAACAAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGACAGGG	1765
Db	99	TAGAACAAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGACAGGG	40
Qy	1766	TCAAAGTGTTTCTCTGAACACATTGAGTTGGAATCACT	1804
Db	39	TCAAAGTGTTTCTCTGAACACATTGAGTTGGAATCACT	1

Search completed: October 8, 2005, 16:31:23
Job time : 493 secs

Run on: October 8, 2005, 08:05:13 ; Search time 1268 Seconds (without alignments)
11073.838 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccggatgtc.....ttaaagcatttagaaaaactt 2372
Scoring table: IDENTITY NUC

Searched: Gapop 10.0 , Gapext 1.0
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAX52250	standard; DNA; 2372 BP.				
DE	Protein PRO263	cdNA clone DNA34431-1171.				
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 2372;	DB 2;	Length 2372;		
RESULT 2						
ID	ADC78520	standard; cdNA; 2372 BP.				
DE	Human PRO263	cdNA.				
PN	WO200015796-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 2372;	DB 3;	Length 2372;		
RESULT 3						
ID	AAF72408	standard; cdNA; 2372 BP.				
DE	Human PRO263	cdNA.				
PN	WO200104311-A1.					
PD	18-JAN-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 2372;	DB 4;	Length 2372;		
RESULT 4						
ID	AAF92060	standard; cdNA; 2372 BP.				
DE	Human PRO263	cdNA.				
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 2372;	DB 4;	Length 2372;		
RESULT 5						
ID	ABS74380	standard; cdNA; 2372 BP.				
DE	Human cdNA encoding secreted/transmembrane protein PRO263.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					

Query Match
Best Local Similarity 100.0%; Score 2372; DB 6; Length 2372;
RESULT 6
ID ABL88087 standard; cdNA; 2372 BP.
DE Human PRO263 cdNA sequence SEQ ID NO:31.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 6; Length 2372;
RESULT 7
ID ABL95576 standard; cdNA; 2372 BP.
DE Human angiogenesis related cdNA PRO263 SEQ ID NO: 31.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 6; Length 2372;
RESULT 8
ID ACA60164 standard; cdNA; 2372 BP.
DE Human cdNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 8; Length 2372;
RESULT 9
ID ACD07564 standard; cdNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 8; Length 2372;
RESULT 10
ID ACA91166 standard; cdNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 8; Length 2372;
RESULT 11
ID ACD81543 standard; cdNA; 2372 BP.
DE Human cdNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 8; Length 2372;
RESULT 12
ID ACA60365 standard; cdNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cdNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 8; Length 2372;

RESULT 13
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACA58812 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACA91252 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22

ID ACD20169 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACH66246 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ACD02300 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ACA89291 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ACA68928 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ACA54972 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ACA98450 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ACA63375 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ACD19807 standard; cDNA; 2372 BP.

DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADB29405 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADB17062 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ACH03578 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADA18261 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ACD66954 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADA19867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADB17250 standard; cDNA; 2372 BP.
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ACD83115 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADA16236 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.

PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADA20039 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ACD82092 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADA42381 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACD23293 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADA00336 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADA16660 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADA13089 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADA41957 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADA17304 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003017498-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADA42807 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ACD23655 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADB85578 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADB77726 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADB74862 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB68257 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADB68064 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ADB90881 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ADC28508 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059772-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADC39708 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADC40222 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADC19046 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADC34346 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ADC29401 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADC28932 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADC40817 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADC19474 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADC06961 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADC17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADD36009 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADE34833 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADG01010 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADG08563 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADF95184 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADH24037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADH34063 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 86
ID ADH29896 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADH23867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADG85271 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADH24547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADH37403 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADH01992 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADH37573 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADG85611 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADH24207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95

ID ADH38501 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADG83622 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADH29430 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADH27546 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADH37743 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADH37920 standard; cDNA; 2372 BP.
DE Human secreted and transmembrane protein PRO263 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADH57340 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADH59316 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADH53482 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADH53652 standard; cDNA; 2372 BP.

DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADH51988 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADH49843 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADI25353 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADH90146 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADI25523 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADH97697 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADI38095 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADI03545 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADI11902 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.

PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADH89976 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADH98377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADI11052 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADI11562 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.

PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADI05025 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ADI03375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADI04770 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ADH78224 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADI19568 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADH90316 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADI03035 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADH77884 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADH97867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADI01252 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADI01947 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADI03205 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADI11392 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADI02294 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADI11732 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADI05369 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADH79441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADI19398 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ADI05199 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADH79611 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADI01437 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ADI01607 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ADI01777 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ADH79781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ADI04599 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ADI02735 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ADH78054 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADI25693 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ADI25863 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ADK65375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ADH98717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ADH79958 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ADJ26363 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ADL93689 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 11; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ADE79278 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ADE79702 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 159
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADE41281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.

PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADH06405 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADG68826 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADH27716 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADH25057 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADH33689 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADG92296 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADH02332 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADH07939 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180845-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADG69336 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADH39157 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADG92723 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ADG83897 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADG85441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ADH06235 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADH30231 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADH24377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADG69506 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADH07769 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ADG85781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADH39327 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADH33519 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ADH33859 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADH01069 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADG69676 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADH02162 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADG69166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 195
ID ADG85951 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 196
ID ADH24887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 197
ID ADH39504 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 198
ID ADH02502 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 199
ID ADG68996 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 200
ID ADH07599 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 201
ID ADG86121 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 202
ID ADH24717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 203
ID ADH25765 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 204
ID ADH38331 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 205
ID ADH20512 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 206
ID ADH57170 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 207
ID ADH43464 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 208
ID ADH07367 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 209
ID ADH52158 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 210
ID ADH59912 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 211
ID ADH49524 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;
RESULT 212
ID ADH06940 standard; cDNA; 2372 BP.

DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADH90486 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ADI11222 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ADI18682 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ADH98887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ADI02117 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ADH90656 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ADI37665 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ADH97461 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190610-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ADI65829 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ADH60572 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ADJ99629 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ADL08822 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADJ98531 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ADJ98701 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADH78860 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADJ99094 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 229
ID ADJ99264 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ADJ98882 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ADH79030 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ADK00890 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ADK14411 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ADM25163 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADM29913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADK82809 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ADM80860 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238

ID ADO06235 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ADR11087 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ADRI7996 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 13; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ADT03672 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 13; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADS74635 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane cDNA #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 13; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ADC52143 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 2370.4; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ADQ25003 standard; DNA; 2667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 99.9%; Score 2369; DB 12; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ADR41319 standard; cDNA; 2369 BP.
DE Human CD-like molecule HEMFC27 cDNA, SEQ ID NO:118.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.8%; Score 2343; DB 7; Length 2369;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ABL90698 standard; cDNA; 2369 BP.
DE Human polynucleotide SEQ ID NO 1260.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.7%; Score 2342.2; DB 6; Length 2369;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 247
ID ABA09223 standard; cDNA; 2324 BP.
DE Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 97.5%; Score 2313.2; DB 4; Length 2324;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 248
ID AAV22687 standard; DNA; 2313 BP.
DE DNA encoding a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.6%; Score 2290.2; DB 2; Length 2313;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 249
ID ADP65684 standard; DNA; 2313 BP.
DE Human extracellular link domain containing 1 (XLKD1) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 96.2%; Score 2282.2; DB 11; Length 2313;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 250
ID ADM67137 standard; DNA; 2313 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 273.
PN WO2004011618-A2.
PD 05-FEB-2004.

PA (HMGE-) HMGENE INC.
Query Match 96.2%; Score 2282.2; DB 12; Length 2313;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 251
ID ADN05865 standard; cDNA; 2313 BP.
DE Antipsoriatic cDNA sequence #1164.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 96.2%; Score 2282.2; DB 12; Length 2313;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 252
ID ADQ21088 standard; DNA; 2313 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 96.2%; Score 2282.2; DB 12; Length 2313;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 253
ID ADE71449 standard; cDNA; 2027 BP.
DE Human cDNA encoding PDEBC #2.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 84.1%; Score 1994; DB 12; Length 2027;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 254
ID AAZ98172 standard; cDNA; 2029 BP.
DE Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.
PN WO200000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 84.1%; Score 1994; DB 3; Length 2029;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 255
ID ADE71445 standard; cDNA; 2029 BP.
DE Human cDNA encoding PDEBC incyte 3044710CB1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 84.1%; Score 1994; DB 12; Length 2029;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 256
ID AAC59803 standard; DNA; 2967 BP.
DE Human secreted protein encoding DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 73.1%; Score 1733; DB 3; Length 2967;
Best Local Similarity 79.6%; Pred. No. 0;
RESULT 257
ID AAF93818 standard; cDNA; 1755 BP.
DE Human cDNA encoding a membrane or secretory protein clone PSEC0135.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 72.2%; Score 1712.4; DB 5; Length 1755;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 258
ID ADD04999 standard; cDNA; 1680 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 43.4%; Score 1029; DB 10; Length 1680;
Best Local Similarity 98.1%; Pred. No. 1.1e-246;
RESULT 259
ID ACA10111 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN WO200290504-A2.

PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP. 40.8%; Score 967.4; DB 8; Length 1127;
Query Match
Best Local Similarity 93.2%; Pred. No. 2.3e-231;
RESULT 260
ID ADO08254 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOEROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match
Best Local Similarity 40.8%; Score 967.4; DB 12; Length 1127;
RESULT 261
ID AAF94017 standard; DNA; 716 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 451.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 26.6%; Score 631.8; DB 5; Length 716;
RESULT 262
ID ADM67136 standard; DNA; 1516 BP.
DE Murine adipocyte specific DNA SeqID 272.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Query Match
Best Local Similarity 26.0%; Score 616.4; DB 12; Length 1516;
RESULT 263
ID AAD10132 standard; cDNA; 1896 BP.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 25.4%; Score 603.6; DB 4; Length 1896;
RESULT 264
ID ABL35066 standard; cDNA; 1896 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 595.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 25.4%; Score 603.6; DB 6; Length 1896;
RESULT 265

ID ABT09892 standard; cDNA; 596 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 26.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 22.2%; Score 526; DB 6; Length 596;
RESULT 266
ID ABL65949 standard; DNA; 516 BP.
DE Lung cancer related gene sequence SEQ ID NO:4286.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 267
ID ABL64470 standard; DNA; 516 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2807.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 268
ID ABL63363 standard; DNA; 516 BP.
DE Breast cancer related gene sequence SEQ ID NO:1700.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 269
ID ABL63772 standard; DNA; 516 BP.
DE Breast cancer related gene sequence SEQ ID NO:2109.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 270
ID ABL65524 standard; DNA; 516 BP.
DE Lung cancer related gene sequence SEQ ID NO:3861.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 271
ID ABN93616 standard; DNA; 516 BP.
DE Gene #114 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 21.1%; Score 500.2; DB 6; Length 516;
RESULT 272
ID AAH55571 standard; DNA; 506 BP.
DE Human breast tumour protein contig 55 DNA sequence.
PN WO200140269-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 20.5%; Score 485.8; DB 4; Length 506;
RESULT 273
ID ADN40341 standard; cDNA; 506 BP.
DE Human breast cancer associated cDNA sequence #93.
PN US2004101899-A1.
PD 27-MAY-2004.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 20.5%; Score 485.8; DB 12; Length 506;
RESULT 274
ID AAF94160 standard; DNA; 591 BP.

DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 594.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 19.3%; Score 458.8; DB 5; Length 591;
Best Local Similarity 88.9%; Pred. No. 3e-104;
RESULT 275
ID AAX41156 standard; cDNA; 451 BP.
DE Human secreted protein 5' EST SEQ ID NO:100.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 19.0%; Score 450; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 4.3e-102;
RESULT 276
ID ACH22904 standard; cDNA; 486 BP.
DE Human adult ovary cDNA #1284.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 18.5%; Score 440; DB 9; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
RESULT 277
ID ACH22239 standard; cDNA; 472 BP.
DE Human adult ovary cDNA #619.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 17.7%; Score 419.4; DB 9; Length 472;
Best Local Similarity 99.8%; Pred. No. 2e-94;
RESULT 278
ID ACH30085 standard; cDNA; 499 BP.
DE Human testis cDNA #471.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 17.1%; Score 406; DB 9; Length 499;
Best Local Similarity 99.8%; Pred. No. 4.5e-91;
RESULT 279
ID ACH17082 standard; cDNA; 441 BP.
DE Human adult heart cDNA #1396.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 17.0%; Score 403; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
RESULT 280
ID ACH20895 standard; cDNA; 411 BP.
DE Human adult liver cDNA #507.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 16.7%; Score 397; DB 9; Length 411;

Best Local Similarity 98.8%; Pred. No. 7.4e-89;
RESULT 281
ID ADE71448 standard; cDNA; 820 BP.
DE Dog cDNA encoding PDEBC variant Incyte 704113673J1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 16.3%; Score 387.6; DB 12; Length 820;
Best Local Similarity 77.5%; Pred. No. 2.3e-86;
RESULT 282
ID AAX41003 standard; cDNA; 363 BP.
DE Human secreted protein 5' EST SEQ ID NO: 215.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.5%; Score 343; DB 2; Length 363;
Best Local Similarity 97.0%; Pred. No. 2.3e-75;
RESULT 283
ID AAX51631 standard; cDNA; 373 BP.
DE Human secreted protein 5' EST SEQ ID NO:210.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.0%; Score 331.8; DB 2; Length 373;
Best Local Similarity 99.4%; Pred. No. 1.5e-72;
RESULT 284
ID ADE71446 standard; cDNA; 559 BP.
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 13.9%; Score 328.6; DB 12; Length 559;
Best Local Similarity 78.4%; Pred. No. 1.1e-71;
RESULT 285
ID AAF17836 standard; cDNA; 241 BP.
DE Human breast cancer associated 23232 coding sequence.
PN WO200060076-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2e-49;
RESULT 286
ID AAS47266 standard; cDNA; 241 BP.
DE Human breast cancer cDNA clone 23232.
PN WO200179286-A2.
PD 25-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2e-49;
RESULT 287
ID ABS63867 standard; cDNA; 241 BP.
DE Human breast tumour polynucleotide #319.
PN US2002085998-A1.
PD 04-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.1%; Score 239; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 2e-49;
RESULT 288
ID ABT33079 standard; DNA; 241 BP.
DE Human tumour-related DNA sequence - SEQ ID No 324.
PN WO200283956-A1.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 10.1%; Score 239; DB 10; Length 241;
Best Local Similarity 100.0%; Pred. No. 2e-49;
RESULT 289
ID ADL92986 standard; cDNA; 241 BP.
DE Human breast cancer-associated polypeptide cDNA #319.
PN US2003166022-A1.
PD 04-SEP-2003.
PA (CORI-) CORIXA CORP.

Query Match
Best Local Similarity 10.1%; Score 239; DB 11; Length 241;
RESULT 290
ID ADE44276 standard; cDNA; 241 BP.
DE Human cDNA associated with breast cancer #319.
PN US2003104366-A1.
PD 05-JUN-2003.
PA (JIAN/) JIANG Y.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (XUJJ/) XU J.
PA (HARL/) HARLOCKER S L.
Query Match
Best Local Similarity 10.1%; Score 239; DB 12; Length 241;
RESULT 291
ID ABL63797 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:2134.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 10.0%; Score 238; DB 6; Length 308;
RESULT 292
ID ABL63384 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:1721.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 10.0%; Score 238; DB 6; Length 308;
RESULT 293
ID ABL63798 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:2135.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 10.0%; Score 238; DB 6; Length 308;
RESULT 294
ID ABN95189 standard; DNA; 308 BP.
DE Gene #1687 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 10.0%; Score 238; DB 6; Length 308;
RESULT 295
ID AAF17835 standard; cDNA; 241 BP.
DE Human breast cancer associated 23182 coding sequence.
PN WO200060076-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.0%; Score 237; DB 4; Length 241;
RESULT 296
ID AAS47265 standard; cDNA; 241 BP.
DE Human breast cancer cDNA clone 23182.
PN WO200179286-A2.
PD 25-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.0%; Score 237; DB 4; Length 241;
RESULT 297
ID ABS63866 standard; cDNA; 241 BP.
DE Human breast tumour polynucleotide #318.
PN US2002085998-A1.
PD 04-JUL-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.0%; Score 237; DB 6; Length 241;
RESULT 298
ID ABT33078 standard; DNA; 241 BP.
DE Human tumour-related DNA sequence - SEQ ID No 323.

PN WO200283956-A1.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.0%; Score 237; DB 10; Length 241;
RESULT 299
ID ADL92985 standard; cDNA; 241 BP.
DE Human breast cancer-associated polypeptide cDNA #318.
PN US2003166022-A1.
PD 04-SEP-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 10.0%; Score 237; DB 11; Length 241;
RESULT 300
ID ADE44275 standard; cDNA; 241 BP.
DE Human cDNA associated with breast cancer #318.
PN US2003104366-A1.
PD 05-JUN-2003.
PA (JIAN/) JIANG Y.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (XUJJ/) XU J.
PA (HARL/) HARLOCKER S L.
Query Match
Best Local Similarity 10.0%; Score 237; DB 12; Length 241;
RESULT 301
ID ABL65603 standard; DNA; 239 BP.
DE Lung cancer related gene sequence SEQ ID NO:3940.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 9.5%; Score 226.2; DB 6; Length 239;
RESULT 302
ID ABL63605 standard; DNA; 239 BP.
DE Breast cancer related gene sequence SEQ ID NO:1942.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 9.5%; Score 226.2; DB 6; Length 239;
RESULT 303
ID ABL66203 standard; DNA; 239 BP.
DE Lung cancer related gene sequence SEQ ID NO:4540.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 9.5%; Score 226.2; DB 6; Length 239;
RESULT 304
ID ABL64015 standard; DNA; 239 BP.
DE Breast cancer related gene sequence SEQ ID NO:2352.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 9.5%; Score 226.2; DB 6; Length 239;
RESULT 305
ID ABN94227 standard; DNA; 239 BP.
DE Gene #725 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 9.5%; Score 226.2; DB 6; Length 239;
RESULT 306
ID ADE71447 standard; cDNA; 279 BP.
DE Rat cDNA encoding PDEBC variant Incyte 701647942H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match
Best Local Similarity 8.9%; Score 212.2; DB 12; Length 279;

Best Local Similarity 86.1%; Pred. No. 1.1e-42;
RESULT 307
ID ABA54110 standard; DNA; 469 BP.
DE Human foetal liver single exon nucleic acid probe #2415.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 4; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 308
ID AAI33763 standard; DNA; 469 BP.
DE Probe #2449 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 4; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 309
ID ABA23859 standard; DNA; 469 BP.
DE Probe #2325 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 4; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 310
ID AAK27829 standard; DNA; 469 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2386.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 4; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 311
ID ABS27409 standard; DNA; 469 BP.
DE Human liver single exon probe, SEQ ID No 2399.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 4; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 312
ID ABS02280 standard; DNA; 469 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2271.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.6%; Score 179.2; DB 6; Length 469;
Best Local Similarity 98.0%; Pred. No. 2.4e-34;
RESULT 313
ID AAI33382 standard; DNA; 457 BP.
DE Probe #2068 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.4%; Score 175; DB 4; Length 457;
Best Local Similarity 94.8%; Pred. No. 2.7e-33;
RESULT 314
ID ABS01959 standard; DNA; 457 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1950.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.4%; Score 175; DB 6; Length 457;
Best Local Similarity 94.8%; Pred. No. 2.7e-33;
RESULT 315
ID ABA66678 standard; DNA; 141 BP.
DE Human foetal liver single exon nucleic acid probe #14983.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 4; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;

RESULT 316
ID AAI46891 standard; DNA; 141 BP.
DE Probe #15577 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 4; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;
RESULT 317
ID ABA33740 standard; DNA; 141 BP.
DE Probe #12206 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 4; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;
RESULT 318
ID AAK40837 standard; DNA; 141 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15394.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 4; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;
RESULT 319
ID ABS40414 standard; DNA; 141 BP.
DE Human liver single exon probe, SEQ ID No 15404.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 4; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;
RESULT 320
ID ABS14788 standard; DNA; 141 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14779.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.4%; Score 129; DB 6; Length 141;
Best Local Similarity 99.3%; Pred. No. 5.1e-22;
RESULT 321
ID AAI46523 standard; DNA; 106 BP.
DE Probe #15209 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.5%; Score 106; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
RESULT 322
ID ABS14478 standard; DNA; 106 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14469.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.5%; Score 106; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
RESULT 323
ID ABN38121 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:10869.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 2.5%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
RESULT 324
ID ABQ56694 standard; cDNA; 641 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:389.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 2.5%; Score 58.2; DB 6; Length 641;
Best Local Similarity 38.9%; Pred. No. 0.00051;
RESULT 325

Query Match 2.4%; Score 57.4; DB 13; Length 110000;
Best Local Similarity 46.4%; Pred. No. 0.0079;
RESULT 326
ID ABZ10100 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.4%; Score 56.8; DB 8; Length 8056;
Best Local Similarity 44.9%; Pred. No. 0.0035;
RESULT 327
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 56.6; DB 8; Length 2000;
Best Local Similarity 9.0%; Pred. No. 0.0021;
RESULT 328
ID ABK39932 standard; DNA; 6216 BP.
DE Human chemically pretreated gene sequence #7 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.4%; Score 56.6; DB 6; Length 6216;
Best Local Similarity 49.0%; Pred. No. 0.0035;
RESULT 329
ID ABL70139 standard; DNA; 6216 BP.
DE Chemically treated cell signalling DNA sequence#15.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.4%; Score 56.6; DB 6; Length 6216;
Best Local Similarity 49.0%; Pred. No. 0.0035;
RESULT 330
ID ABZ10246 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.4%; Score 55.8; DB 8; Length 8056;
Best Local Similarity 45.7%; Pred. No. 0.0063;
RESULT 331
ID ACC43051 standard; DNA; 339 BP.
DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGE/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 2.3%; Score 55.4; DB 8; Length 339;
Best Local Similarity 50.2%; Pred. No. 0.0019;
RESULT 332
ID ABZ10246 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.3%; Score 55.2; DB 8; Length 8056;
Best Local Similarity 44.7%; Pred. No. 0.0088;
RESULT 333
ID ABQ67093 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 123.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.3%; Score 55; DB 6; Length 83391;
Best Local Similarity 45.9%; Pred. No. 0.028;
RESULT 334
ID AAA70187 standard; DNA; 11922 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:320.
PN WO200025728-A2.
PD 11-MAY-2000.

PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 2.3%; Score 54.2; DB 3; Length 11922;
Best Local Similarity 49.0%; Pred. No. 0.019;
RESULT 335
ID ABL32467 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 440.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.3%; Score 54.2; DB 6; Length 15373;
Best Local Similarity 46.5%; Pred. No. 0.021;
RESULT 336
ID ABL32542 standard; DNA; 11790 BP.
DE Human immune system associated gene SEQ ID NO: 515.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.3%; Score 53.8; DB 6; Length 11790;
Best Local Similarity 46.2%; Pred. No. 0.023;
RESULT 337
ID AAH93026 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR3319a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match 2.3%; Score 53.6; DB 4; Length 700;
Best Local Similarity 47.6%; Pred. No. 0.0076;
RESULT 338
ID AAS45340 standard; DNA; 6544 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #23.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 53; DB 4; Length 6544;
Best Local Similarity 44.0%; Pred. No. 0.029;
RESULT 339
ID ABL32646 standard; DNA; 6544 BP.
DE Human immune system associated gene SEQ ID NO: 619.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 53; DB 6; Length 6544;
Best Local Similarity 44.0%; Pred. No. 0.029;
RESULT 340
ID ABL33979 standard; DNA; 8101 BP.
DE Human immune system associated gene SEQ ID NO: 1952.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 53; DB 6; Length 8101;
Best Local Similarity 45.0%; Pred. No. 0.031;
RESULT 341
ID ABL33317 standard; DNA; 13574 BP.
DE Human immune system associated gene SEQ ID NO: 1290.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 53; DB 6; Length 13574;
Best Local Similarity 48.7%; Pred. No. 0.039;
RESULT 342
ID ABL32656 standard; DNA; 9832 BP.
DE Human immune system associated gene SEQ ID NO: 629.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 51.8; DB 6; Length 9832;
Best Local Similarity 49.8%; Pred. No. 0.068;
RESULT 343
ID AAS46314 standard; DNA; 16750 BP.

DE Tumour suppressor gene derived chemically modified sequence #36.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 51.6; DB 4; Length 16750;
Best Local Similarity 44.0%; Pred. No. 0.097;
RESULT 344
ID ABL32521 standard; DNA; 16750 BP.
DE Human immune system associated gene SEQ ID NO: 494.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 51.6; DB 6; Length 16750;
Best Local Similarity 44.0%; Pred. No. 0.097;
RESULT 345
ID ADH10017 standard; DNA; 365186 BP.
DE Human chromosome 2p21-22 fragment containing the DRIP gene.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 2.2%; Score 51.6; DB 10; Length 110000;
Best Local Similarity 46.2%; Pred. No. 0.22;
RESULT 346
ID ADR01991 standard; DNA; 724 BP.
DE A. gossypii genomic DNA PAG1453RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.2%; Score 51.2; DB 2; Length 724;
Best Local Similarity 48.5%; Pred. No. 0.031;
RESULT 347
ID ABQ67074 standard; DNA; 20579 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 104.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.2%; Score 51; DB 6; Length 20579;
Best Local Similarity 47.2%; Pred. No. 0.15;
RESULT 348
ID ABL34090 standard; DNA; 5407 BP.
DE Human immune system associated gene SEQ ID NO: 2063.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50.8; DB 6; Length 5407;
Best Local Similarity 45.6%; Pred. No. 0.093;
RESULT 349
ID ABX39643 standard; cDNA; 392 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4808.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.1%; Score 50.6; DB 8; Length 392;
Best Local Similarity 52.1%; Pred. No. 0.033;
RESULT 350
ID ABL70350 standard; DNA; 5504 BP.
DE Chemically treated cell signalling DNA sequence complementary to#120.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50.6; DB 6; Length 5504;
Best Local Similarity 43.8%; Pred. No. 0.11;
RESULT 351
ID AAS61309 standard; DNA; 5504 BP.
DE Human gene regulation-associated gene oligonucleotide #264.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50.6; DB 6; Length 5504;
Best Local Similarity 43.8%; Pred. No. 0.11;

RESULT 352
ID ABZ10100 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50.4; DB 8; Length 8056;
Best Local Similarity 47.4%; Pred. No. 0.14;
RESULT 353
ID ABL34358 standard; DNA; 12237 BP.
DE Human immune system associated gene SEQ ID NO: 2331.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50.4; DB 6; Length 12237;
Best Local Similarity 45.1%; Pred. No. 0.17;
RESULT 354
ID AAX52401 standard; DNA; 50 BP.
DE Probe used to isolate a cDNA clone encoding PRO263.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 355
ID ADC78525 standard; DNA; 50 BP.
DE Human PRO protein-related probe SEQ ID 205.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 356
ID AAF72559 standard; DNA; 50 BP.
DE Human PRO polypeptide gene hybridisation probe SEQ ID NO: 205.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 357
ID ACA60168 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein PRO263 probe.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 358
ID ACD07568 standard; DNA; 50 BP.
DE Novel human secreted and transmembrane protein PCR probe #31.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 359
ID ABX71616 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein PRO263 probe.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 360
ID ACH06948 standard; DNA; 50 BP.
DE Human secreted/transmembrane polypeptide PRO263 probe.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 361

ID ABX96185 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein cDNA, #38, probe.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 362
ID ACA05506 standard; DNA; 50 BP.
DE Human secreted protein PRO263 probe.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 363
ID ACD20173 standard; DNA; 50 BP.
DE Human secreted / transmembrane polypeptide PRO263 probe.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 364
ID ACA54976 standard; DNA; 50 BP.
DE Novel secreted and transmembrane protein associated primer #90.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 365
ID ACD19811 standard; DNA; 50 BP.
DE Human secreted / transmembrane polypeptide PRO263 probe.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 366
ID ADB29410 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 367
ID ADA18266 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 368
ID ACD66958 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein PRO263 probe.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 369
ID ACD83119 standard; DNA; 50 BP.
DE Human PRO probe #40.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 370
ID ADA16241 standard; DNA; 50 BP.

DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 371
ID ADA42386 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 372
ID ACD23297 standard; DNA; 50 BP.
DE Human PRO probe #37.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 373
ID ADA16665 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 374
ID ADA13094 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 375
ID ADA41962 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 376
ID ADA17309 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 377
ID ADA42812 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 378
ID ACD23659 standard; DNA; 50 BP.
DE Human PRO probe #37.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 379
ID ADB77731 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.

PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 380
ID ADB74867 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 381
ID ADC28513 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 382
ID ADC39713 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 383
ID ADC40227 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 384
ID ADC19051 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 385
ID ADC34351 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 386
ID ADC29406 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 387
ID ADC28937 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 388
ID ADC40822 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054400-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 389
ID ADC19479 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 390
ID ADC33927 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 391
ID ADC12997 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 392
ID ADC12449 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 393
ID ADD05004 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 394
ID ADD04010 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 395
ID ADD03586 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 396
ID ADE34838 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;
Query Match 100.0%; Pred. No. 0.019;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 397
ID ADH59321 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003039972-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 398
ID ADI38100 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 399
ID ACA59064 standard; DNA; 50 BP.
DE Human PRO probe #37.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 400
ID ACA58461 standard; DNA; 50 BP.
DE Probe #38 used to isolate cDNA encoding a human PRO polypeptide.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 401
ID ADJ26368 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 402
ID ADE79283 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 403
ID ADE79707 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 404
ID ADE73383 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 405
ID ADE73918 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 406
ID ADE99472 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 407
ID ADE98591 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 408
ID ADE99018 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 409
ID ADG40488 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 410
ID ADF73882 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 411
ID ADF73458 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 412
ID ADG92301 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 413
ID ADG92728 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 414
ID ADH20517 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 415

ID ADH07372 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 416
ID ADH59917 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 417
ID ADH06945 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 418
ID ADI18687 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 419
ID ADI65407 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 420
ID ADI37670 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 421
ID ADH97466 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 422
ID ADI65834 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.

Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 423
ID ADH60577 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 424
ID ADJ99634 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 425
ID ADL08827 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 426
ID ADM25168 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 427
ID ADM29918 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 428
ID ADO06240 standard; DNA; 50 BP.
DE Human PRO probe #37.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 429
ID ADR11092 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 430
ID ADR18001 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.

PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 431
ID ADT03677 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 2.1%; Score 50; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 432
ID ADS74640 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.1%; Score 50; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.019;
RESULT 433
ID ABQ66998 standard; DNA; 37515 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 28.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 50; DB 6; Length 37515;
Best Local Similarity 45.0%; Pred. No. 0.35;
RESULT 434
ID ADP71270 standard; DNA; 600 BP.
DE Human aggrecan B-B' domain gene region SeqID5.
PN JP2004154038-A.

PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 2.1%; Score 49.6; DB 12; Length 600;
Best Local Similarity 51.9%; Pred. No. 0.071;
RESULT 435
ID ADL13490 standard; DNA; 6951 BP.
DE Osteoarthritis-associated polymorphic nucleotide #22.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.1%; Score 49.6; DB 10; Length 6951;
Best Local Similarity 51.9%; Pred. No. 0.21;
RESULT 436
ID ADL13489 standard; DNA; 7137 BP.
DE Osteoarthritis-associated polymorphic nucleotide #21.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.1%; Score 49.6; DB 10; Length 7137;
Best Local Similarity 51.9%; Pred. No. 0.21;
RESULT 437
ID ADP65694 standard; DNA; 7137 BP.
DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 2.1%; Score 49.6; DB 11; Length 7137;
Best Local Similarity 51.9%; Pred. No. 0.21;
RESULT 438
ID ADP65777 standard; DNA; 7137 BP.
DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 2.1%; Score 49.6; DB 11; Length 7137;
Best Local Similarity 51.9%; Pred. No. 0.21;
RESULT 439
ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.6; DB 6; Length 47108;
Best Local Similarity 44.5%; Pred. No. 0.48;
RESULT 440
ID ABL33569 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1542.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.4; DB 6; Length 8305;
Best Local Similarity 45.3%; Pred. No. 0.25;
RESULT 441
ID ABQ80553 standard; DNA; 47841 BP.
DE Human Canlon gene fragment #3.
PN WO200246404-A2.
PD 13-JUN-2002.
PA (GEST) GENSET.
Query Match 2.1%; Score 49.4; DB 6; Length 47841;
Best Local Similarity 44.4%; Pred. No. 0.55;
RESULT 442
ID ABL34125 standard; DNA; 73334 BP.
DE Human immune system associated gene SEQ ID NO: 2098.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.4; DB 6; Length 73334;
Best Local Similarity 47.6%; Pred. No. 0.66;
RESULT 443
ID ABL92319 standard; DNA; 73334 BP.
DE Chemically treated DNA repair gene fragment complementary to#64.
PN WO200181622-A2.
PD 01-NOV-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.4; DB 6; Length 73334;
Best Local Similarity 47.6%; Pred. No. 0.66;
RESULT 444
ID ADR01499 standard; DNA; 663 BP.
DE A. gossypii genomic DNA PAG1076UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 49.2; DB 2; Length 663;
Best Local Similarity 48.1%; Pred. No. 0.093;
RESULT 445
ID ADR02344 standard; DNA; 732 BP.
DE A. gossypii genomic DNA PAG1633UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 49.2; DB 2; Length 732;
Best Local Similarity 48.3%; Pred. No. 0.097;
RESULT 446
ID ADR01842 standard; DNA; 854 BP.
DE A. gossypii genomic DNA PAG1372UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 49.2; DB 2; Length 854;
Best Local Similarity 48.9%; Pred. No. 0.1;
RESULT 447
ID ABL33784 standard; DNA; 7461 BP.
DE Human immune system associated gene SEQ ID NO: 1757.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.2; DB 6; Length 7461;
Best Local Similarity 44.8%; Pred. No. 0.27;
RESULT 448
ID AAS46815 standard; DNA; 21354 BP.
DE Tumour suppressor gene derived chemically modified sequence #512.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49.2; DB 4; Length 21354;
Best Local Similarity 47.2%; Pred. No. 0.43;
RESULT 449
ID ABL67703 standard; DNA; 302250 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6040.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.1%; Score 49.2; DB 6; Length 302250;
Best Local Similarity 47.2%; Pred. No. 1.4;
RESULT 450
ID AAS46292 standard; DNA; 5430 BP.
DE Tumour suppressor gene derived chemically modified sequence #14.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49; DB 4; Length 5430;
Best Local Similarity 48.0%; Pred. No. 0.26;
RESULT 451
ID AAS46429 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #151.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49; DB 4; Length 6106;
Best Local Similarity 45.9%; Pred. No. 0.28;
RESULT 452
ID ABK40031 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.1%; Score 49; DB 6; Length 6106;
Best Local Similarity 45.9%; Pred. No. 0.28;
RESULT 453
ID ABL33472 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1445.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49; DB 6; Length 6106;
Best Local Similarity 45.9%; Pred. No. 0.28;
RESULT 454
ID ABL33207 standard; DNA; 15767 BP.
DE Human immune system associated gene SEQ ID NO: 1180.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49; DB 6; Length 15767;
Best Local Similarity 48.9%; Pred. No. 0.42;
RESULT 455
ID ABL34553 standard; DNA; 15767 BP.
DE Human metastasis associated gene SEQ ID NO: 106.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 49; DB 6; Length 15767;
Best Local Similarity 48.9%; Pred. No. 0.42;
RESULT 456
ID ADS99814 standard; DNA; 15767 BP.
DE Complement of bisulphite treated metastasis-associated human gene #53.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.1%; Score 49; DB 7; Length 15767;
Best Local Similarity 48.9%; Pred. No. 0.42;
RESULT 457
ID ADR01595 standard; DNA; 860 BP.
DE A. gossypii genomic DNA PAG1240UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.8; DB 2; Length 860;
Best Local Similarity 50.0%; Pred. No. 0.13;
RESULT 458
ID ABL32426 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 399.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 48.8; DB 6; Length 9810;
Best Local Similarity 44.9%; Pred. No. 0.38;
RESULT 459
ID ABL33299 standard; DNA; 12025 BP.
DE Human immune system associated gene SEQ ID NO: 1272.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 48.8; DB 6; Length 12025;
Best Local Similarity 45.6%; Pred. No. 0.42;
RESULT 460
ID ABL33485 standard; DNA; 13202 BP.
DE Human immune system associated gene SEQ ID NO: 1458.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.1%; Score 48.8; DB 6; Length 13202;
Best Local Similarity 46.1%; Pred. No. 0.44;
RESULT 461
ID ABL33530 standard; DNA; 13712 BP.
DE Human immune system associated gene SEQ ID NO: 1503.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG. 2.1%; Score 48.8; DB 6; Length 13712;
Query Match 46.1%; Pred. No. 0.45;
Best Local Similarity
RESULT 462
ID ABL56203 standard; DNA; 32392 BP.
DE AmEPV genome fragment#5.
PN WO200213526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 2.1%; Score 48.8; DB 6; Length 32392;
Best Local Similarity 45.5%; Pred. No. 0.65;
RESULT 463
ID ABK31200 standard; DNA; 6154 BP.
DE Signal transduction associated gene modified DNA #22.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.6; DB 6; Length 6154;
Best Local Similarity 45.8%; Pred. No. 0.35;
RESULT 464
ID ABL70167 standard; DNA; 6154 BP.
DE Chemically treated cell signalling DNA sequence#29.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.6; DB 6; Length 6154;
Best Local Similarity 45.8%; Pred. No. 0.35;
RESULT 465
ID AAS61112 standard; DNA; 6154 BP.
DE Human gene regulation-associated gene oligonucleotide #67.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.6; DB 6; Length 6154;
Best Local Similarity 45.8%; Pred. No. 0.35;
RESULT 466
ID AAX20257 standard; DNA; 10749 BP.
DE Borrelia burgdorferi polynucleotide sequence #10.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 2.0%; Score 48.6; DB 2; Length 10749;
Best Local Similarity 47.5%; Pred. No. 0.45;
RESULT 467
ID ABL34053 standard; DNA; 11172 BP.
DE Human immune system associated gene SEQ ID NO: 2026.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.6; DB 6; Length 11172;
Best Local Similarity 49.2%; Pred. No. 0.46;
RESULT 468
ID ABL32191 standard; DNA; 17137 BP.
DE Human immune system associated gene SEQ ID NO: 164.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.6; DB 6; Length 17137;
Best Local Similarity 43.4%; Pred. No. 0.55;
RESULT 469
ID ABQ67160 standard; DNA; 6775 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 190.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.4; DB 6; Length 6775;
Best Local Similarity 47.4%; Pred. No. 0.41;
RESULT 470
Query Match 2.0%; Score 48.4; DB 6; Length 110000;
Best Local Similarity 48.2%; Pred. No. 1.4;
RESULT 471
ID ACH93277 standard; DNA; 334 BP.

DE Human genome derived single exon probe #26472.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.0%; Score 48.2; DB 12; Length 334;
Best Local Similarity 52.8%; Pred. No. 0.12;
RESULT 472
ID ACH79577 standard; DNA; 538 BP.
DE Human genome derived single exon probe #12772.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.0%; Score 48.2; DB 12; Length 538;
Best Local Similarity 52.8%; Pred. No. 0.15;
RESULT 473
ID ABA06490 standard; cDNA; 972 BP.
DE Human cDNA SEQ ID NO: 156.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 48.2; DB 4; Length 972;
Best Local Similarity 52.8%; Pred. No. 0.2;
RESULT 474
ID ABV83827 standard; cDNA; 972 BP.
DE Human polynucleotide SEQ ID NO 156.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.0%; Score 48.2; DB 6; Length 972;
Best Local Similarity 52.8%; Pred. No. 0.2;
RESULT 475
ID AAV41923 standard; cDNA; 1587 BP.
DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 2.0%; Score 48.2; DB 2; Length 1587;
Best Local Similarity 52.8%; Pred. No. 0.24;
RESULT 476
ID AAV34196 standard; DNA; 1720 BP.
DE Human secreted protein gene 43 clone HSXCK41.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 48.2; DB 2; Length 1720;
Best Local Similarity 52.8%; Pred. No. 0.25;
RESULT 477
ID ACD08067 standard; cDNA; 1720 BP.
DE cDNA encoding novel human secreted protein #43.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.

PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Query Match 2.0%; Score 48.2; DB 8; Length 1720;
Best Local Similarity 52.8%; Pred. No. 0.25;
RESULT 478
ID AAF29460 standard; cDNA; 2013 BP.
DE Human TANGO 332 cDNA open reading frame.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 4; Length 2013;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 479
ID ACD66767 standard; cDNA; 2013 BP.
DE Secreted polypeptide-related cDNA #51.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 2.0%; Score 48.2; DB 8; Length 2013;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 480
ID ADB90775 standard; cDNA; 2013 BP.
DE Human TANGO 332 open reading frame.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 9; Length 2013;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 481
ID ADF71510 standard; cDNA; 2013 BP.
DE Human TANGO 332 CDS.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 10; Length 2013;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 482
ID ADQ10328 standard; cDNA; 2013 BP.
DE Human polynucleotide #58.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 12; Length 2013;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 483
ID AAX20297 standard; DNA; 2496 BP.
DE Borrelia burgdorferi polynucleotide sequence #50.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 2.0%; Score 48.2; DB 2; Length 2496;
Best Local Similarity 45.6%; Pred. No. 0.3;
RESULT 484
ID AAF29459 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 4; Length 2730;

Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 485
ID ACD66766 standard; cDNA; 2730 BP.
DE Secreted polypeptide-related cDNA #50.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 2.0%; Score 48.2; DB 8; Length 2730;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 486
ID ADB90774 standard; cDNA; 2730 BP.
DE Human cDNA encoding TANGO 332.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 9; Length 2730;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 487
ID ADF71509 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 10; Length 2730;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 488
ID ADQ10327 standard; cDNA; 2730 BP.
DE Human polynucleotide #57.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 48.2; DB 12; Length 2730;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 489
ID AAD48133 standard; DNA; 2878 BP.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 2.0%; Score 48.2; DB 8; Length 2878;
Best Local Similarity 52.8%; Pred. No. 0.32;
RESULT 490
ID ADN38941 standard; cDNA; 2878 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.0%; Score 48.2; DB 11; Length 2878;
Best Local Similarity 52.8%; Pred. No. 0.32;
RESULT 491
ID ADK67783 standard; DNA; 2878 BP.
DE Human glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 2.0%; Score 48.2; DB 12; Length 2878;
Best Local Similarity 52.8%; Pred. No. 0.32;
RESULT 492
ID ACN37482 standard; cDNA; 3275 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 2.0%; Score 48.2; DB 13; Length 3275;
Best Local Similarity 52.8%; Pred. No. 0.33;
RESULT 493
ID ADH18923 standard; cDNA; 3293 BP.
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 12; Length 3293;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 494
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMCAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.0%; Score 48.2; DB 6; Length 3438;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 495
ID ADQ83194 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.0%; Score 48.2; DB 12; Length 3467;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 496
ID ADQ85107 standard; cDNA; 3467 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.0%; Score 48.2; DB 12; Length 3467;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 497
ID AAA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 4; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 498
ID ABK69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 6; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 499
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 500
ID ADA43748 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 501
ID ADA43516 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 502
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 503
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 504
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 505
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 506
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 507
ID ADB99675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 508
ID ADB86958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 509
ID ADB66113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 9; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 510
ID ADB99791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 511
ID ADB99446 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 512
ID ADB65997 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 513
ID ADC23395 standard; cDNA; 3476 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 514
ID ADC26088 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 515
ID ADE04915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 516
ID ADE11221 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 517
ID ADD88152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 518
ID ADD95447 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 519
ID ADE06377 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073195-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 520
ID ADE38152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 521
ID ADD88268 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 522
ID ADD90849 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 523
ID ADF99404 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 524
ID ADG06497 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 525
ID ADG05448 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 526
ID ADG82449 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 10; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 527
ID ADE51702 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 528
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 529
ID ADE37676 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 530
ID ADE37560 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 531
ID ADD95331 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 532
ID ADE38031 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 533
ID ADE76120 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 534
ID ADE39443 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 535
ID ADE04247 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 536
ID ADE39844 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 537
ID ADEi9709 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;

Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 538
ID ADE77287 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 539
ID ADE65395 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 540
ID ADE76004 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 541
ID ADE37915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 542
ID ADE64525 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 543
ID ADE38860 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 544
ID ADE51934 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 545
ID ADD90965 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 546
ID ADE38744 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;
RESULT 547
ID ADEi9709 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 3476;

RESULT 547
ID ADE37444 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 548
ID ADE06261 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US200313898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 549
ID ADD90120 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 550
ID ADE38628 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 551
ID ADE39559 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 552
ID ADD89164 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 553
ID ADD88931 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 554
ID ADE19825 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 555
ID ADE77403 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 556

ID ADE65279 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 557
ID ADE39327 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 558
ID ADE38512 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 559
ID ADG11065 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 560
ID ADG10949 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 561
ID ADH31477 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 562
ID ADH38725 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 563
ID ADH29360 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 564
ID ADH23663 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 565
ID ADH26993 standard; cDNA; 3476 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 566
ID ADH38261 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 567
ID ADH26877 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 568
ID ADH38145 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 569
ID ADH38841 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 570
ID ADH23779 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 571
ID ADH40155 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 572
ID ADH40039 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 573
ID ADH31361 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 574
ID ADH29239 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 575
ID ADH49454 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 576
ID ADH51918 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 577
ID ADH49773 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 578
ID ADH52374 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 579
ID ADH52490 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 580
ID ADH58487 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 581
ID ADH51802 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 582
ID ADH58363 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 583
ID ADI13560 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003119131-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 584
ID ADK00816 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 585
ID ADL08557 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 48.2; DB 12; Length 3476;
Best Local Similarity 52.8%; Pred. No. 0.34;
RESULT 586
ID ACN42086 standard; cDNA; 4353 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 13; Length 4353;
Best Local Similarity 52.8%; Pred. No. 0.38;
RESULT 587
ID ACN42085 standard; cDNA; 4391 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:960.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 13; Length 4391;
Best Local Similarity 52.8%; Pred. No. 0.38;
RESULT 588
ID ACN42084 standard; cDNA; 4536 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 13; Length 4536;
Best Local Similarity 52.8%; Pred. No. 0.39;
RESULT 589
ID ACN42083 standard; cDNA; 4545 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 13; Length 4545;
Best Local Similarity 52.8%; Pred. No. 0.39;
RESULT 590
ID ACN42082 standard; cDNA; 4659 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48.2; DB 13; Length 4659;
Best Local Similarity 52.8%; Pred. No. 0.39;
RESULT 591
ID ADR06936 standard; cDNA; 4966 BP.
DE Full length human cDNA useful for treating neurological disease Seq 442.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.0%; Score 48.2; DB 13; Length 4966;
Best Local Similarity 54.1%; Pred. No. 0.4;
RESULT 592
ID AAS28917 standard; DNA; 5430 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID No 279.
PN WO200155315-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 48.2; DB 4; Length 5430;
Best Local Similarity 52.8%; Pred. No. 0.42;
RESULT 593
ID ADB31758 standard; DNA; 5430 BP.
DE Human novel protein DNA SEQ ID NO 279.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 48.2; DB 10; Length 5430;
Best Local Similarity 52.8%; Pred. No. 0.42;
RESULT 594
ID AAS46429 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #151.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.2; DB 4; Length 6106;
Best Local Similarity 44.7%; Pred. No. 0.44;
RESULT 595
ID ABK40031 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.2; DB 6; Length 6106;
Best Local Similarity 44.7%; Pred. No. 0.44;
RESULT 596
ID ABL33472 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1445.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48.2; DB 6; Length 6106;
Best Local Similarity 44.7%; Pred. No. 0.44;
RESULT 597
ID ADH12179 standard; cDNA; 9646 BP.
DE Human CHD5 (chromodomain, helicase, DNA-binding 5)-encoding cDNA.
PN WO2003106650-A2.
PD 24-DEC-2003.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
Query Match 2.0%; Score 48.2; DB 12; Length 9646;
Best Local Similarity 54.1%; Pred. No. 0.54;
RESULT 598
ID ADQ17729 standard; DNA; 143239 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 546.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.0%; Score 48.2; DB 12; Length 143239;
Best Local Similarity 44.9%; Pred. No. 1.8;
RESULT 599
ID ADS89278 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:294.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48; DB 13; Length 5286;
Best Local Similarity 45.3%; Pred. No. 0.46;
RESULT 600
ID ADS89552 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:568.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 48; DB 13; Length 5286;
Best Local Similarity 45.3%; Pred. No. 0.46;
RESULT 601
ID ABK28414 standard; DNA; 5362 BP.
DE DNA transcription associated complementary genomic DNA #144.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 48; DB 6; Length 5362;
Best Local Similarity 44.9%; Pred. No. 0.47;
RESULT 602
ID ACN42826 standard; cDNA; 7678 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48; DB 13; Length 7678;
Best Local Similarity 51.4%; Pred. No. 0.55;
RESULT 603
ID ACN42825 standard; cDNA; 7975 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 48; DB 13; Length 7975;
Best Local Similarity 51.4%; Pred. No. 0.56;
RESULT 604
ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.8; DB 6; Length 47108;
Best Local Similarity 46.5%; Pred. No. 1.4;
RESULT 605
ID AAH93026 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR3319a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match 2.0%; Score 47.6; DB 4; Length 700;
Best Local Similarity 47.5%; Pred. No. 0.24;
RESULT 606
ID ABL33527 standard; DNA; 9965 BP.
DE Human immune system associated gene SEQ ID NO: 1500.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.6; DB 6; Length 9965;
Best Local Similarity 45.3%; Pred. No. 0.77;
RESULT 607
ID AAS4660 standard; DNA; 12578 BP.
DE Tumour suppressor gene derived chemically modified sequence #382.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.6; DB 4; Length 12578;
Best Local Similarity 48.6%; Pred. No. 0.86;
RESULT 608
ID AAS46385 standard; DNA; 12781 BP.
DE Tumour suppressor gene derived chemically modified sequence #107.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.6; DB 4; Length 12781;
Best Local Similarity 49.6%; Pred. No. 0.86;
RESULT 609
ID ABL92228 standard; DNA; 12781 BP.
DE Chemically treated DNA repair gene fragment#19.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.6; DB 6; Length 12781;
Best Local Similarity 49.6%; Pred. No. 0.86;
RESULT 610
ID ADB54127 standard; DNA; 12781 BP.
DE Pretreated genomic DNA region 51.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 47.6; DB 10; Length 12781;
Best Local Similarity 49.6%; Pred. No. 0.86;
RESULT 611
ID ADB54255 standard; DNA; 12781 BP.
DE Pretreated genomic DNA region 179.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.6; DB 10; Length 12781;
Best Local Similarity 49.6%; Pred. No. 0.86;
RESULT 612
ID ABL56203 standard; DNA; 32392 BP.
DE AmEPV genome fragment#5.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 2.0%; Score 47.6; DB 6; Length 32392;
Best Local Similarity 44.8%; Pred. No. 1.3;
RESULT 613
ID ABL34073 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2046.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.4; DB 6; Length 40862;
Best Local Similarity 50.2%; Pred. No. 1.6;
RESULT 614
ID ADH30232 standard; DNA; 161671 BP.
DE Human PLOD2 DNA.
PN US2003124535-A1.
PD 03-JUL-2003.
PA (VITI-) VITIVITY INC.
Query Match 2.0%; Score 47.4; DB 12; Length 161671;
Best Local Similarity 46.7%; Pred. No. 3;
RESULT 615
ID AAL15210 standard; cDNA; 883 BP.
DE Human breast cancer expressed polynucleotide 7667.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.0%; Score 47.2; DB 4; Length 883;
Best Local Similarity 39.8%; Pred. No. 0.33;
RESULT 616
ID ACN85231 standard; DNA; 960 BP.
DE Breast cancer related marker, seq id 6381.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 47.2; DB 11; Length 960;
Best Local Similarity 39.8%; Pred. No. 0.35;
RESULT 617
ID AAS46694 standard; DNA; 5413 BP.
DE Tumour suppressor gene derived chemically modified sequence #417.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 4; Length 5413;
Best Local Similarity 46.9%; Pred. No. 0.74;
RESULT 618
ID ABK28374 standard; DNA; 6074 BP.
DE DNA transcription associated complementary genomic DNA #124.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 6074;
Best Local Similarity 45.9%; Pred. No. 0.78;
RESULT 619
ID AAS46433 standard; DNA; 6174 BP.
DE Tumour suppressor gene derived chemically modified sequence #155.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 4; Length 6174;

Best Local Similarity 44.4%; Pred. No. 0.79;
RESULT 620
ID ABL33216 standard; DNA; 6191 BP.
DE Human immune system associated gene SEQ ID NO: 1189.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 6191;
Best Local Similarity 44.8%; Pred. No. 0.79;
RESULT 621
ID ABK31306 standard; DNA; 6191 BP.
DE Signal transduction associated gene modified DNA #75.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 6191;
Best Local Similarity 44.8%; Pred. No. 0.79;
RESULT 622
ID ABL70281 standard; DNA; 6191 BP.
DE Chemically treated cell signalling DNA sequence#86.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 6191;
Best Local Similarity 44.8%; Pred. No. 0.79;
RESULT 623
ID ABN80160 standard; DNA; 6191 BP.
DE Human chemically modified disease associated gene SEQ ID NO 177.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 6191;
Best Local Similarity 44.8%; Pred. No. 0.79;
RESULT 624
ID ABL32628 standard; DNA; 7669 BP.
DE Human immune system associated gene SEQ ID NO: 601.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 7669;
Best Local Similarity 51.4%; Pred. No. 0.87;
RESULT 625
ID ABL32191 standard; DNA; 17137 BP.
DE Human immune system associated gene SEQ ID NO: 164.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 17137;
Best Local Similarity 44.8%; Pred. No. 1.2;
RESULT 626
ID AAS46665 standard; DNA; 17144 BP.
DE Tumour suppressor gene derived chemically modified sequence #387.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 4; Length 17144;
Best Local Similarity 53.2%; Pred. No. 1.2;
RESULT 627
ID ABN80227 standard; DNA; 19236 BP.
DE Human chemically modified disease associated gene SEQ ID NO 244.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47.2; DB 6; Length 19236;
Best Local Similarity 49.5%; Pred. No. 1.3;
RESULT 628
ID AAI61373 standard; DNA; 513445 BP.
DE Soybean 318013 region A3, SEQ ID NO: 4.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 2.0%; Score 47.2; DB 5; Length 110000;
Best Local Similarity 47.3%; Pred. No. 2.8;

RESULT 629
ID AAS46740 standard; DNA; 4045 BP.
DE Tumour suppressor gene derived chemically modified sequence #464.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 4; Length 4045;
Best Local Similarity 51.2%; Pred. No. 0.73;
RESULT 630
ID AAD22381 standard; DNA; 5006 BP.
DE Cotton oleoyl-PC delta12-desaturase (ghFAD2-1) gene.
PN WO200179499-A1.
PD 25-OCT-2001.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 2.0%; Score 47; DB 5; Length 5006;
Best Local Similarity 47.2%; Pred. No. 0.81;
RESULT 631
ID AAS46601 standard; DNA; 7057 BP.
DE Tumour suppressor gene derived chemically modified sequence #323.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 4; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 632
ID ABL33848 standard; DNA; 7057 BP.
DE Human immune system associated gene SEQ ID NO: 1821.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 633
ID ABL34594 standard; DNA; 7057 BP.
DE Human metastasis associated gene SEQ ID NO: 147.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 634
ID ABL70407 standard; DNA; 7057 BP.
DE Chemically treated cell signalling DNA sequence#149.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 635
ID AAS61354 standard; DNA; 7057 BP.
DE Human gene regulation-associated gene oligonucleotide #309.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 636
ID ADS99855 standard; DNA; 7057 BP.
DE Bisulphite treated human gene associated with metastasis #74.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.0%; Score 47; DB 7; Length 7057;
Best Local Similarity 46.4%; Pred. No. 0.94;
RESULT 637
ID ABQ67025 standard; DNA; 11964 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 55.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 11964;

Best Local Similarity 46.5%; Pred. No. 1.2;
RESULT 638
ID ABK40038 standard; DNA; 16258 BP.
DE Human chemically pretreated gene sequence #60 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 16258;
Best Local Similarity 45.3%; Pred. No. 1.4;
RESULT 639
ID ABL70376 standard; DNA; 16258 BP.
DE Chemically treated cell signalling DNA sequence complementary to#133.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 47; DB 6; Length 16258;
Best Local Similarity 45.3%; Pred. No. 1.4;
RESULT 640
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.0%; Score 47; DB 11; Length 172569;
Best Local Similarity 54.3%; Pred. No. 3.8;
RESULT 641
ID ADL38504 standard; DNA; 319 BP.
DE Human ovarian cancer DNA marker #12394.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.0%; Score 46.8; DB 5; Length 319;
Best Local Similarity 44.7%; Pred. No. 0.27;
RESULT 642
ID ADI73373 standard; DNA; 319 BP.
DE Human ovarian cancer DNA marker #6115.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.0%; Score 46.8; DB 5; Length 319;
Best Local Similarity 44.7%; Pred. No. 0.27;
RESULT 643
ID ADS89604 standard; DNA; 2987 BP.
DE Oligonucleotide of the invention SEQ ID NO:620.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 13; Length 2987;
Best Local Similarity 44.4%; Pred. No. 0.72;
RESULT 644
ID ADS89330 standard; DNA; 2987 BP.
DE Oligonucleotide of the invention SEQ ID NO:346.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 13; Length 2987;
Best Local Similarity 44.4%; Pred. No. 0.72;
RESULT 645
ID AAF29464 standard; cDNA; 3153 BP.
DE Murine brevidin cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 46.8; DB 4; Length 3153;
Best Local Similarity 54.7%; Pred. No. 0.74;
RESULT 646
ID ACD66770 standard; cDNA; 3153 BP.
DE Secreted polypeptide-related cDNA #76.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.

PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 2.0%; Score 46.8; DB 8; Length 3153;
Best Local Similarity 54.7%; Pred. No. 0.74;
RESULT 647
ID ADB90788 standard; cDNA; 3153 BP.
DE Mouse cDNA encoding brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 46.8; DB 9; Length 3153;
Best Local Similarity 54.7%; Pred. No. 0.74;
RESULT 648
ID ADF71523 standard; cDNA; 3153 BP.
DE Murine brevidin protein cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 46.8; DB 10; Length 3153;
Best Local Similarity 54.7%; Pred. No. 0.74;
RESULT 649
ID ADQ10339 standard; cDNA; 3153 BP.
DE Human polynucleotide #61.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 46.8; DB 12; Length 3153;
Best Local Similarity 54.7%; Pred. No. 0.74;
RESULT 650
ID ABL33563 standard; DNA; 5987 BP.
DE Human immune system associated gene SEQ ID NO: 1536.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 5987;
Best Local Similarity 44.4%; Pred. No. 0.98;
RESULT 651
ID ABQ67102 standard; DNA; 5987 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 132.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 5987;
Best Local Similarity 44.4%; Pred. No. 0.98;
RESULT 652
ID ADB54180 standard; DNA; 5987 BP.
DE Pretreated genomic DNA region 104.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 10; Length 5987;
Best Local Similarity 44.4%; Pred. No. 0.98;
RESULT 653
ID ADB54308 standard; DNA; 5987 BP.
DE Pretreated genomic DNA region 232.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 10; Length 5987;
Best Local Similarity 44.4%; Pred. No. 0.98;
RESULT 654
ID ABL32052 standard; DNA; 6301 BP.
DE Human immune system associated gene SEQ ID NO: 25.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 6301;

Best Local Similarity 45.5%; Pred. No. 1;
RESULT 655
ID ABK31243 standard; DNA; 9760 BP.
DE Signal transduction associated gene modified complementary DNA #43.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 9760;
Best Local Similarity 45.8%; Pred. No. 1.2;
RESULT 656
ID ABL70198 standard; DNA; 9760 BP.
DE Chemically treated cell signalling DNA sequence complementary to#44.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 9760;
Best Local Similarity 45.8%; Pred. No. 1.2;
RESULT 657
ID AAS61156 standard; DNA; 9760 BP.
DE Human gene regulation-associated gene oligonucleotide #111.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 9760;
Best Local Similarity 45.8%; Pred. No. 1.2;
RESULT 658
ID AAS45494 standard; DNA; 12968 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #100.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 4; Length 12968;
Best Local Similarity 43.2%; Pred. No. 1.4;
RESULT 659
ID AAS46779 standard; DNA; 12968 BP.
DE Tumour suppressor gene derived chemically modified sequence #504.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 4; Length 12968;
Best Local Similarity 43.2%; Pred. No. 1.4;
RESULT 660
ID ABL34085 standard; DNA; 12968 BP.
DE Human immune system associated gene SEQ ID NO: 2058.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 12968;
Best Local Similarity 43.2%; Pred. No. 1.4;
RESULT 661
ID ABK28424 standard; DNA; 12968 BP.
DE DNA transcription associated complementary genomic DNA #149.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 12968;
Best Local Similarity 43.2%; Pred. No. 1.4;
RESULT 662
ID ABN80285 standard; DNA; 12968 BP.
DE Human chemically modified disease associated gene SEQ ID NO 302.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.8; DB 6; Length 12968;
Best Local Similarity 43.2%; Pred. No. 1.4;
RESULT 663
ID ABL56202 standard; DNA; 50000 BP.
DE AmEPV genome fragment#4.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 2.0%; Score 46.8; DB 6; Length 50000;
Best Local Similarity 46.4%; Pred. No. 2.5;

RESULT 664
ID ADQ59452 standard; DNA; 168198 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:88.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.0%; Score 46.8; DB 12; Length 168198;
Best Local Similarity 48.8%; Pred. No. 4.3;
RESULT 665
ID AAC02796 standard; cDNA; 315 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2794.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.0%; Score 46.6; DB 3; Length 315;
Best Local Similarity 51.9%; Pred. No. 0.3;
RESULT 666
ID AAL15210 standard; cDNA; 883 BP.
DE Human breast cancer expressed polynucleotide 7667.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.0%; Score 46.6; DB 4; Length 883;
Best Local Similarity 39.7%; Pred. No. 0.47;
RESULT 667
ID ACN85231 standard; DNA; 960 BP.
DE Breast cancer related marker, seq id 6381.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.0%; Score 46.6; DB 11; Length 960;
Best Local Similarity 39.7%; Pred. No. 0.49;
RESULT 668
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.0%; Score 46.6; DB 8; Length 2000;
Best Local Similarity 8.8%; Pred. No. 0.68;
RESULT 669
ID ABN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 2.0%; Score 46.6; DB 6; Length 2747;
Best Local Similarity 50.5%; Pred. No. 0.78;
RESULT 670
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.0%; Score 46.6; DB 6; Length 2747;
Best Local Similarity 50.5%; Pred. No. 0.78;
RESULT 671
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 2.0%; Score 46.6; DB 2; Length 3207;
Best Local Similarity 50.5%; Pred. No. 0.83;
RESULT 672
ID ABL33248 standard; DNA; 5163 BP.
DE Human immune system associated gene SEQ ID NO: 1221.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 46.6; DB 6; Length 5163;
Best Local Similarity 45.5%; Pred. No. 1;
RESULT 673
ID ABL34598 standard; DNA; 7676 BP.
DE Human metastasis associated gene SEQ ID NO: 151.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 7676;
Best Local Similarity 46.2%; Pred. No. 1.2;
RESULT 674
ID ABL70409 standard; DNA; 7676 BP.
DE Chemically treated cell signalling DNA sequence#150.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 7676;
Best Local Similarity 46.2%; Pred. No. 1.2;
RESULT 675
ID ADS99859 standard; DNA; 7676 BP.
DE Bisulphite treated human gene associated with metastasis #76.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.0%; Score 46.6; DB 7; Length 7676;
Best Local Similarity 46.2%; Pred. No. 1.2;
RESULT 676
ID ABL32465 standard; DNA; 10891 BP.
DE Human immune system associated gene SEQ ID NO: 438.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 9180;
Best Local Similarity 48.4%; Pred. No. 1.3;
RESULT 677
ID ABL32465 standard; DNA; 10891 BP.
DE Human immune system associated gene SEQ ID NO: 438.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 10891;
Best Local Similarity 45.0%; Pred. No. 1.4;
RESULT 678
ID ABL33512 standard; DNA; 11092 BP.
DE Human immune system associated gene SEQ ID NO: 1485.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 11092;
Best Local Similarity 44.4%; Pred. No. 1.4;
RESULT 679
ID ABL32298 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 271.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 12507;
Best Local Similarity 46.9%; Pred. No. 1.5;
RESULT 680
ID ABL34155 standard; DNA; 15548 BP.
DE Human immune system associated gene SEQ ID NO: 2128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 15548;
Best Local Similarity 44.4%; Pred. No. 1.7;
RESULT 681
ID ABL34073 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2046.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.6; DB 6; Length 40862;
Best Local Similarity 47.8%; Pred. No. 2.6;
RESULT 682
ID ABL55643 standard; DNA; 50000 BP.
DE AmEPV genome fragment#1.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 2.0%; Score 46.6; DB 6; Length 50000;
Best Local Similarity 47.3%; Pred. No. 2.8;
RESULT 683
ID ADQ97266 standard; DNA; 355211 BP.
DE Human cancer associated sequence HD08-023, SEQ ID 242.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.0%; Score 46.6; DB 12; Length 110000;
Best Local Similarity 48.4%; Pred. No. 4;
RESULT 684
Query Match 2.0%; Score 46.6; DB 13; Length 110000;
Best Local Similarity 47.5%; Pred. No. 4;
RESULT 685
ID AAH54899 standard; DNA; 4092 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4263.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.0%; Score 46.4; DB 4; Length 4092;
Best Local Similarity 46.3%; Pred. No. 1;
RESULT 686
ID ABL32714 standard; DNA; 4172 BP.
DE Human immune system associated gene SEQ ID NO: 687.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 4172;
Best Local Similarity 45.9%; Pred. No. 1.1;
RESULT 687
ID ABL92301 standard; DNA; 6040 BP.
DE Chemically treated DNA repair gene fragment complementary to#55.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 6040;
Best Local Similarity 47.0%; Pred. No. 1.2;
RESULT 688
ID ABL49370 standard; DNA; 6040 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 70.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 6040;
Best Local Similarity 47.0%; Pred. No. 1.2;
RESULT 689
ID ABL70459 standard; DNA; 16228 BP.
DE Chemically treated cell signalling DNA sequence#175.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 16228;
Best Local Similarity 47.3%; Pred. No. 1.9;
RESULT 690
ID AAS61424 standard; DNA; 16228 BP.
DE Human gene regulation-associated gene oligonucleotide #379.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 16228;
Best Local Similarity 47.3%; Pred. No. 1.9;
RESULT 691
ID ABL34026 standard; DNA; 17594 BP.
DE Human immune system associated gene SEQ ID NO: 1999.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 6; Length 17594;
Best Local Similarity 45.4%; Pred. No. 2;
RESULT 692
ID AAS46717 standard; DNA; 19131 BP.
DE Tumour suppressor gene derived chemically modified sequence #440.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.0%; Score 46.4; DB 4; Length 19131;
Best Local Similarity 58.8%; Pred. No. 2.1;
RESULT 693
ID AAN60472 standard; DNA; 4590 BP.
DE Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).
PN WO8601802-A.
PD 27-MAR-1986.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 1.9%; Score 46.2; DB 1; Length 4590;
Best Local Similarity 44.6%; Pred. No. 1.2;
RESULT 694
ID ADS89612 standard; DNA; 4930 BP.
DE Oligonucleotide of the invention SEQ ID NO:628.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 13; Length 4930;
Best Local Similarity 46.0%; Pred. No. 1.3;
RESULT 695
ID AAS46331 standard; DNA; 5880 BP.
DE Tumour suppressor gene derived chemically modified sequence #53.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 4; Length 5880;
Best Local Similarity 43.5%; Pred. No. 1.4;
RESULT 696
ID ABK28177 standard; DNA; 5880 BP.
DE DNA transcription associated genomic DNA #26.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 5880;
Best Local Similarity 43.5%; Pred. No. 1.4;
RESULT 697
ID ABL33763 standard; DNA; 5981 BP.
DE Human immune system associated gene SEQ ID NO: 1736.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 5981;
Best Local Similarity 44.3%; Pred. No. 1.4;
RESULT 698
ID ADS89769 standard; DNA; 6001 BP.
DE Oligonucleotide of the invention SEQ ID NO:785.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 13; Length 6001;
Best Local Similarity 46.0%; Pred. No. 1.4;
RESULT 699
ID ABL33487 standard; DNA; 6831 BP.
DE Human immune system associated gene SEQ ID NO: 1460.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 6831;
Best Local Similarity 45.9%; Pred. No. 1.5;
RESULT 700
ID ADB54312 standard; DNA; 7833 BP.
DE Pretreated genomic DNA region 236.
PN WO2003072821-A2.

PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 10; Length 7833;
Best Local Similarity 46.0%; Pred. No. 1.6;
RESULT 701
ID ADE37779 standard; DNA; 7833 BP.
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:25.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 10; Length 7833;
Best Local Similarity 46.0%; Pred. No. 1.6;
RESULT 702
ID ADS89608 standard; DNA; 7833 BP.
DE Oligonucleotide of the invention SEQ ID NO:624.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 13; Length 7833;
Best Local Similarity 46.0%; Pred. No. 1.6;
RESULT 703
ID ABL32299 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 272.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 12507;
Best Local Similarity 46.4%; Pred. No. 1.9;
RESULT 704
ID ABK28396 standard; DNA; 15743 BP.
DE DNA transcription associated complementary genomic DNA #135.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 15743;
Best Local Similarity 46.2%; Pred. No. 2.1;
RESULT 705
ID AAS61427 standard; DNA; 19380 BP.
DE Human gene regulation-associated gene oligonucleotide #382.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 6; Length 19380;
Best Local Similarity 45.3%; Pred. No. 2.3;
RESULT 706
ID ADB37663 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:5.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46.2; DB 10; Length 29993;
Best Local Similarity 44.0%; Pred. No. 2.8;
RESULT 707
ID ABL55643 standard; DNA; 50000 BP.
DE AmEPV genome fragment#1.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 1.9%; Score 46.2; DB 6; Length 50000;
Best Local Similarity 48.6%; Pred. No. 3.5;
RESULT 708
ID ADH10017 standard; DNA; 365186 BP.
DE Human chromosome 2p21-22 fragment containing the DRIP gene.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 1.9%; Score 46.2; DB 10; Length 110000;
Best Local Similarity 44.4%; Pred. No. 5;
RESULT 709
ID ACA64845 standard; DNA; 115218 BP.
DE Human HNRNP GP43 DNA corresponding to AL034397.
PN DE10127572-A1.
PD 05-DEC-2002.

PA (PATH-) PATHOARRAY GMBH.
Query Match 1.9%; Score 46.2; DB 8; Length 115218;
Best Local Similarity 45.9%; Pred. No. 5.1;
RESULT 710
ID ABD32715 standard; DNA; 337344 BP.
DE Human cancer-associated genomic DNA HD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.9%; Score 46.2; DB 13; Length 337344;
Best Local Similarity 43.8%; Pred. No. 8.2;
RESULT 711
ID AAX99555 standard; DNA; 3057 BP.
DE Nucleic acid sequence from U. urealyticum.
PN WO9939007-A1.
PD 05-AUG-1999.
PA (UABR-) UAB RES FOUND.
Query Match 1.9%; Score 46; DB 2; Length 3057;
Best Local Similarity 43.1%; Pred. No. 1.2;
RESULT 712
ID ABQ67021 standard; DNA; 4661 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 51.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 4661;
Best Local Similarity 46.7%; Pred. No. 1.4;
RESULT 713
ID ABL32430 standard; DNA; 6113 BP.
DE Human immune system associated gene SEQ ID NO: 403.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 6113;
Best Local Similarity 45.2%; Pred. No. 1.6;
RESULT 714
ID ABL92204 standard; DNA; 6113 BP.
DE Chemically treated DNA repair gene fragment#7.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 6113;
Best Local Similarity 45.2%; Pred. No. 1.6;
RESULT 715
ID ABL49313 standard; DNA; 6113 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 13.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 6113;
Best Local Similarity 45.2%; Pred. No. 1.6;
RESULT 716
ID ABQ67062 standard; DNA; 9095 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 92.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 9095;
Best Local Similarity 43.4%; Pred. No. 1.9;
RESULT 717
ID ABK39994 standard; DNA; 9524 BP.
DE Human chemically pretreated gene sequence #38 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 9524;
Best Local Similarity 47.5%; Pred. No. 1.9;
RESULT 718
ID ABL32839 standard; DNA; 9524 BP.
DE Human immune system associated gene SEQ ID NO: 812.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 46; DB 6; Length 9524;
Best Local Similarity 47.5%; Pred. No. 1.9;
RESULT 719
ID ABK31519 standard; DNA; 14316 BP.
DE Signal transduction associated gene modified complementary DNA #181.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 14316;
Best Local Similarity 46.9%; Pred. No. 2.3;
RESULT 720
ID ABL70606 standard; DNA; 14316 BP.
DE Chemically treated cell signalling DNA sequence complementary to#248.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 14316;
Best Local Similarity 46.9%; Pred. No. 2.3;
RESULT 721
ID AAS61445 standard; DNA; 14316 BP.
DE Human gene regulation-associated gene oligonucleotide #400.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 14316;
Best Local Similarity 46.9%; Pred. No. 2.3;
RESULT 722
ID ABK31343 standard; DNA; 15587 BP.
DE Signal transduction associated gene modified complementary DNA #93.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 15587;
Best Local Similarity 50.9%; Pred. No. 2.4;
RESULT 723
ID ABL70304 standard; DNA; 15587 BP.
DE Chemically treated cell signalling DNA sequence complementary to#97.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 15587;
Best Local Similarity 50.9%; Pred. No. 2.4;
RESULT 724
ID AAS61238 standard; DNA; 15587 BP.
DE Human gene regulation-associated gene oligonucleotide #193.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 15587;
Best Local Similarity 50.9%; Pred. No. 2.4;
RESULT 725
ID ABL32625 standard; DNA; 16217 BP.
DE Human immune system associated gene SEQ ID NO: 598.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 16217;
Best Local Similarity 45.2%; Pred. No. 2.4;
RESULT 726
ID ABL33998 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1971.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 46; DB 6; Length 21537;
Best Local Similarity 47.7%; Pred. No. 2.7;
RESULT 727
ID AAF12929 standard; cDNA; 1132 BP.
DE Aspergillus oryzae EST SEQ ID NO:5452.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.

Query Match 1.9%; Score 45.8; DB 3; Length 1132;
Best Local Similarity 46.2%; Pred. No. 0.84;
RESULT 728
ID ADQ25148 standard; DNA; 1533 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.9%; Score 45.8; DB 12; Length 1533;
Best Local Similarity 48.0%; Pred. No. 0.96;
RESULT 729
ID ABL33518 standard; DNA; 5520 BP.
DE Human immune system associated gene SEQ ID NO: 1491.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 5520;
Best Local Similarity 47.3%; Pred. No. 1.7;
RESULT 730
ID ABL32374 standard; DNA; 5659 BP.
DE Human immune system associated gene SEQ ID NO: 347.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 731
ID ABK33931 standard; DNA; 5659 BP.
DE Human DNA for staging of Astrocytomas #7.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 732
ID ABL34486 standard; DNA; 5659 BP.
DE Human metastasis associated gene SEQ ID NO: 39.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 733
ID ADS99747 standard; DNA; 5659 BP.
DE Bisulphite treated human gene associated with metastasis #20.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.9%; Score 45.8; DB 7; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 734
ID ADA20366 standard; DNA; 5659 BP.
DE Prostate tumour related genomic DNA sample #16.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 8; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 735
ID ADA84173 standard; DNA; 5659 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:31.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 8; Length 5659;
Best Local Similarity 51.2%; Pred. No. 1.7;
RESULT 736
ID ABL32505 standard; DNA; 6065 BP.
DE Human immune system associated gene SEQ ID NO: 478.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 6065;
Best Local Similarity 51.7%; Pred. No. 1.8;
RESULT 737
ID ABL32030 standard; DNA; 6072 BP.
DE Human immune system associated gene SEQ ID NO: 3.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 6072;
Best Local Similarity 44.8%; Pred. No. 1.8;
RESULT 738
ID ABL32493 standard; DNA; 6120 BP.
DE Human immune system associated gene SEQ ID NO: 466.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 6120;
Best Local Similarity 45.3%; Pred. No. 1.8;
RESULT 739
ID ABL33140 standard; DNA; 6361 BP.
DE Human immune system associated gene SEQ ID NO: 1113.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 6361;
Best Local Similarity 46.9%; Pred. No. 1.8;
RESULT 740
ID ABL32257 standard; DNA; 7498 BP.
DE Human immune system associated gene SEQ ID NO: 230.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 7498;
Best Local Similarity 47.1%; Pred. No. 1.9;
RESULT 741
ID ABK31207 standard; DNA; 7508 BP.
DE Signal transduction associated gene modified complementary DNA #25.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 7508;
Best Local Similarity 44.4%; Pred. No. 1.9;
RESULT 742
ID ABZ10177 standard; DNA; 8093 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #317.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 8; Length 8093;
Best Local Similarity 46.4%; Pred. No. 2;
RESULT 743
ID ADB54267 standard; DNA; 8093 BP.
DE Pretreated genomic DNA region 191.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 10; Length 8093;
Best Local Similarity 46.4%; Pred. No. 2;
RESULT 744
ID ADE84189 standard; DNA; 8093 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #125.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 10; Length 8093;
Best Local Similarity 46.4%; Pred. No. 2;
RESULT 745
ID ADS89565 standard; DNA; 8093 BP.
DE Oligonucleotide of the invention SEQ ID NO:581.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 45.8; DB 13; Length 8093;
Best Local Similarity 46.4%; Pred. No. 2;
RESULT 746
ID ABL333949 standard; DNA; 18218 BP.
DE Human immune system associated gene SEQ ID NO: 1922.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.8; DB 6; Length 18218;
Best Local Similarity 45.7%; Pred. No. 2.8;
RESULT 747
ID AAH51601 standard; DNA; 319608 BP.
DE Human chromosome 13q31-q33 genomic nucleotide sequence.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 1.9%; Score 45.8; DB 3; Length 319608;
Best Local Similarity 48.1%; Pred. No. 10;
RESULT 748
ID AAS09301 standard; DNA; 319608 BP.
DE Human schizopfhrenia associated gene g35030 and biallelic markers A1-A71.
Query Match 1.9%; Score 45.8; DB 5; Length 319608;
Best Local Similarity 48.1%; Pred. No. 10;
RESULT 749
ID AAX08523 standard; DNA; 6265 BP.
DE NBP46 (root lectin) genomic DNA.
PN WO9907223-A1.
PD 18-FEB-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.9%; Score 45.6; DB 2; Length 6265;
Best Local Similarity 44.7%; Pred. No. 2;
RESULT 750
ID ABL32604 standard; DNA; 11155 BP.
DE Human immune system associated gene SEQ ID NO: 577.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.6; DB 6; Length 11155;
Best Local Similarity 45.5%; Pred. No. 2.6;
RESULT 751
Query Match 1.9%; Score 45.6; DB 6; Length 110000;
Best Local Similarity 46.8%; Pred. No. 7;
RESULT 752
ID ADS89278 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:294. .
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 13; Length 5286;
Best Local Similarity 45.4%; Pred. No. 2.1;
RESULT 753
ID ADS89552 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:568.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 13; Length 5286;
Best Local Similarity 45.4%; Pred. No. 2.1;
RESULT 754
ID AAX08523 standard; DNA; 6265 BP.
DE NBP46 (root lectin) genomic DNA.
PN WO9907223-A1.
PD 18-FEB-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.9%; Score 45.4; DB 2; Length 6265;
Best Local Similarity 48.5%; Pred. No. 2.2;
RESULT 755
ID ABL32257 standard; DNA; 7498 BP.
DE Human immune system associated gene SEQ ID NO: 230.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 7498;

Best Local Similarity 44.8%; Pred. No. 2.4;
RESULT 756
ID ABL54354 standard; DNA; 9881 BP.
DE Chemically treated apoptosis gene complementary to gene #27.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 9881;
Best Local Similarity 45.0%; Pred. No. 2.7;
RESULT 757
ID ABL33591 standard; DNA; 10279 BP.
DE Human immune system associated gene SEQ ID NO: 1564.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 10279;
Best Local Similarity 44.5%; Pred. No. 2.8;
RESULT 758
ID ABL92277 standard; DNA; 10279 BP.
DE Chemically treated DNA repair gene fragment complementary to#43.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 10279;
Best Local Similarity 44.5%; Pred. No. 2.8;
RESULT 759
ID AAD2328 standard; DNA; 10279 BP.
DE Chemically treated human genomic DNA #18 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 10279;
Best Local Similarity 44.5%; Pred. No. 2.8;
RESULT 760
ID AAS45315 standard; DNA; 11260 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #10.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 4; Length 11260;
Best Local Similarity 47.2%; Pred. No. 2.9;
RESULT 761
ID ABK28154 standard; DNA; 11260 BP.
DE DNA transcription associated complementary genomic DNA #14.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 11260;
Best Local Similarity 47.2%; Pred. No. 2.9;
RESULT 762
ID ABN80039 standard; DNA; 11260 BP.
DE Human chemically modified disease associated gene SEQ ID NO 56.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 11260;
Best Local Similarity 47.2%; Pred. No. 2.9;
RESULT 763
ID ABL34493 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 46.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 11996;
Best Local Similarity 47.2%; Pred. No. 2.9;
RESULT 764
ID ADS99754 standard; DNA; 11996 BP.
DE Complement of bisulphite treated metastasis-associated human gene #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.

Query Match 1.9%; Score 45.4; DB 7; Length 11996;
Best Local Similarity 48.1%; Pred. No. 3;
RESULT 765
ID ABL32917 standard; DNA; 13420 BP.
DE Human immune system associated gene SEQ ID NO: 890.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 13420;
Best Local Similarity 53.0%; Pred. No. 3.1;
RESULT 766
ID ABL70543 standard; DNA; 15649 BP.
DE Chemically treated cell signalling DNA sequence#217.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 15649;
Best Local Similarity 54.5%; Pred. No. 3.3;
RESULT 767
ID ABL70604 standard; DNA; 34548 BP.
DE Chemically treated cell signalling DNA sequence complementary to#247.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 34548;
Best Local Similarity 44.3%; Pred. No. 4.7;
RESULT 768
ID ABQ67149 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.4; DB 6; Length 40324;
Best Local Similarity 46.5%; Pred. No. 5.1;
RESULT 769
Query Match 1.9%; Score 45.4; DB 6; Length 40681;
Best Local Similarity 48.0%; Pred. No. 5.1;
RESULT 770
Query Match 1.9%; Score 45.4; DB 6; Length 110000;
Best Local Similarity 48.0%; Pred. No. 7.9;
RESULT 771
ID ADL13728 standard; DNA; 151212 BP.
DE Osteoarthritis-associated polymorphic nucleotide #260.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.9%; Score 45.4; DB 10; Length 151212;
Best Local Similarity 46.0%; Pred. No. 9.1;
RESULT 772
ID AAQ34622 standard; DNA; 1939 BP.
DE Cytosolic GS3A glutamine synthase promoter element.
PN WO9222582-A1.
PD 23-DEC-1992.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 1.9%; Score 45.2; DB 2; Length 1939;
Best Local Similarity 46.1%; Pred. No. 1.5;
RESULT 773
ID AAQ12540 standard; DNA; 1942 BP.
DE GS3A promoter element.
PN WO9109050-A.
PD 27-JUN-1991.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 1.9%; Score 45.2; DB 2; Length 1942;
Best Local Similarity 46.1%; Pred. No. 1.5;
RESULT 774
ID ACN91743 standard; DNA; 2432 BP.
DE Breast cancer related marker, seq id 12893.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.9%; Score 45.2; DB 11; Length 2432;
Best Local Similarity 54.1%; Pred. No. 1.7;
RESULT 775

ID ADS89338 standard; DNA; 4930 BP.
DE Oligonucleotide of the invention SEQ ID NO:354.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 13; Length 4930;
Best Local Similarity 46.4%; Pred. No. 2.3;
RESULT 776
ID ABQ67043 standard; DNA; 5267 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 73.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 5267;
Best Local Similarity 44.8%; Pred. No. 2.3;
RESULT 777
ID ADS89495 standard; DNA; 6001 BP.
DE Oligonucleotide of the invention SEQ ID NO:511.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 13; Length 6001;
Best Local Similarity 46.4%; Pred. No. 2.5;
RESULT 778
ID ADQ24856 standard; DNA; 6816 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.9%; Score 45.2; DB 12; Length 6816;
Best Local Similarity 37.7%; Pred. No. 2.6;
RESULT 779
ID ABK31206 standard; DNA; 7508 BP.
DE Signal transduction associated gene modified DNA #25.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 7508;
Best Local Similarity 47.2%; Pred. No. 2.7;
RESULT 780
ID ADB54184 standard; DNA; 7833 BP.
DE Pretreated genomic DNA region 108.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 10; Length 7833;
Best Local Similarity 46.4%; Pred. No. 2.8;
RESULT 781
ID ADE37769 standard; DNA; 7833 BP.
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:15.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 10; Length 7833;
Best Local Similarity 46.4%; Pred. No. 2.8;
RESULT 782
ID ADS89334 standard; DNA; 7833 BP.
DE Oligonucleotide of the invention SEQ ID NO:350.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 13; Length 7833;
Best Local Similarity 46.4%; Pred. No. 2.8;
RESULT 783
ID ABL34076 standard; DNA; 8876 BP.
DE Human immune system associated gene SEQ ID NO: 2049.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 8876;
Best Local Similarity 45.2%; Pred. No. 2.9;
RESULT 784
ID ABN79996 standard; DNA; 10710 BP.

DE Human chemically modified disease associated gene SEQ ID NO 13.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 10710;
Best Local Similarity 51.0%; Pred. No. 3.2;
RESULT 785
ID ABL32487 standard; DNA; 17183 BP.
DE Human immune system associated gene SEQ ID NO: 460.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 17183;
Best Local Similarity 46.2%; Pred. No. 3.9;
RESULT 786
ID AAS45393 standard; DNA; 17419 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #49.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 4; Length 17419;
Best Local Similarity 44.3%; Pred. No. 3.9;
RESULT 787
ID ABL33295 standard; DNA; 17419 BP.
DE Human immune system associated gene SEQ ID NO: 1268.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 17419;
Best Local Similarity 44.3%; Pred. No. 3.9;
RESULT 788
ID ABK28238 standard; DNA; 17419 BP.
DE DNA transcription associated complementary genomic DNA #56.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45.2; DB 6; Length 17419;
Best Local Similarity 44.3%; Pred. No. 3.9;
RESULT 789
ID ACN47153 standard; CDNA; 535 BP.
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-N6-G4, SEQ:1934.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.9%; Score 45; DB 13; Length 535;
Best Local Similarity 47.0%; Pred. No. 0.95;
RESULT 790
ID ADQ24856 standard; DNA; 6816 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.9%; Score 45; DB 12; Length 6816;
Best Local Similarity 36.7%; Pred. No. 2.9;
RESULT 791
ID ABL33673 standard; DNA; 12142 BP.
DE Human immune system associated gene SEQ ID NO: 1646.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45; DB 6; Length 12142;
Best Local Similarity 43.7%; Pred. No. 3.8;
RESULT 792
ID ABL32630 standard; DNA; 14987 BP.
DE Human immune system associated gene SEQ ID NO: 603.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45; DB 6; Length 14987;
Best Local Similarity 47.1%; Pred. No. 4.1;

RESULT 793
ID ABK40018 standard; DNA; 18133 BP.
DE Human chemically pretreated gene sequence #50 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45; DB 6; Length 18133;
Best Local Similarity 48.3%; Pred. No. 4.5;
RESULT 794
ID ABL32941 standard; DNA; 18133 BP.
DE Human immune system associated gene SEQ ID NO: 914.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45; DB 6; Length 18133;
Best Local Similarity 48.3%; Pred. No. 4.5;
RESULT 795
ID ABL32766 standard; DNA; 19659 BP.
DE Human immune system associated gene SEQ ID NO: 739.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 45; DB 6; Length 19659;
Best Local Similarity 48.6%; Pred. No. 4.7;
RESULT 796
ID AAX20253 standard; DNA; 26811 BP.
DE Borrelia burgdorferi polynucleotide sequence #6.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 1.9%; Score 45; DB 2; Length 26811;
Best Local Similarity 48.0%; Pred. No. 5.3;
RESULT 797
ID ADQ97050 standard; DNA; 687411 BP.
DE Human cancer associated sequence HD08-001, SEQ ID 26.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.9%; Score 45; DB 12; Length 110000;
Best Local Similarity 44.1%; Pred. No. 10;
RESULT 798
ID AAQ02047 standard; DNA; 3101 BP.
DE Sequence encoding a circumsporozoite (CS)-related protein of Plasmodium
DE falciparum.
PN WO9001496-A.
PD 22-FEB-1990.
PA (REEX-) RES EXPLOITATION LTD.
PA (THRE-) 3I RES EXPL LTD.
Query Match 1.9%; Score 44.8; DB 2; Length 3101;
Best Local Similarity 45.7%; Pred. No. 2.3;
RESULT 799
ID ABQ67022 standard; DNA; 4661 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 52.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 4661;
Best Local Similarity 47.0%; Pred. No. 2.8;
RESULT 800
ID ABL33161 standard; DNA; 5593 BP.
DE Human immune system associated gene SEQ ID NO: 1134.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 5593;
Best Local Similarity 50.5%; Pred. No. 3;
RESULT 801
ID ABL32738 standard; DNA; 6759 BP.
DE Human immune system associated gene SEQ ID NO: 711.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 44.8; DB 6; Length 6759;
Best Local Similarity 47.2%; Pred. No. 3.3;
RESULT 802
ID ABL54323 standard; DNA; 7231 BP.
DE Chemically treated apoptosis gene #12.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 7231;
Best Local Similarity 44.9%; Pred. No. 3.4;
RESULT 803
ID ABQ67015 standard; DNA; 10048 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 45.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 10048;
Best Local Similarity 46.7%; Pred. No. 3.9;
RESULT 804
ID ABQ67074 standard; DNA; 20579 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 104.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 20579;
Best Local Similarity 44.6%; Pred. No. 5.3;
RESULT 805
ID ABL70603 standard; DNA; 34548 BP.
DE Chemically treated cell signalling DNA sequence#247.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.8; DB 6; Length 34548;
Best Local Similarity 49.2%; Pred. No. 6.7;
RESULT 806
ID ADR02094 standard; DNA; 711 BP.
DE A. gossypii genomic DNA PAG1504UP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.6; DB 2; Length 711;
Best Local Similarity 48.3%; Pred. No. 1.4;
RESULT 807
ID AAS45313 standard; DNA; 5979 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #9.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 4; Length 5979;
Best Local Similarity 46.9%; Pred. No. 3.5;
RESULT 808
ID ABK28152 standard; DNA; 5979 BP.
DE DNA transcription associated complementary genomic DNA #13.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 5979;
Best Local Similarity 46.9%; Pred. No. 3.5;
RESULT 809
ID ABK28394 standard; DNA; 6063 BP.
DE DNA transcription associated complementary genomic DNA #134.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 6063;
Best Local Similarity 57.6%; Pred. No. 3.5;
RESULT 810
ID ABL32739 standard; DNA; 6759 BP.
DE Human immune system associated gene SEQ ID NO: 712.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 6759;

Best Local Similarity 44.6%; Pred. No. 3.7;
RESULT 811
ID AAX20263 standard; DNA; 8905 BP.
DE Borrelia burgdorferi polynucleotide sequence #16.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 1.9%; Score 44.6; DB 2; Length 8905;
Best Local Similarity 44.4%; Pred. No. 4.1;
RESULT 812
ID ABK40061 standard; DNA; 13784 BP.
DE Human chemically pretreated gene sequence #72 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 13784;
Best Local Similarity 48.9%; Pred. No. 5;
RESULT 813
ID AAS45414 standard; DNA; 14649 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #60.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 4; Length 14649;
Best Local Similarity 44.6%; Pred. No. 5.2;
RESULT 814
ID ABK28267 standard; DNA; 14649 BP.
DE DNA transcription associated genomic DNA #71.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 14649;
Best Local Similarity 44.6%; Pred. No. 5.2;
RESULT 815
ID ABL33022 standard; DNA; 16236 BP.
DE Human immune system associated gene SEQ ID NO: 995.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 16236;
Best Local Similarity 45.7%; Pred. No. 5.4;
RESULT 816
ID ADB54246 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 170.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 10; Length 16579;
Best Local Similarity 43.3%; Pred. No. 5.4;
RESULT 817
ID ADE37773 standard; DNA; 16579 BP.
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:19.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 10; Length 16579;
Best Local Similarity 43.3%; Pred. No. 5.4;
RESULT 818
ID ADS89548 standard; DNA; 16579 BP.
DE Oligonucleotide of the invention SEQ ID NO:564.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 13; Length 16579;
Best Local Similarity 43.3%; Pred. No. 5.4;
RESULT 819
ID ABL70502 standard; DNA; 18283 BP.
DE Chemically treated cell signalling DNA sequence complementary to#196.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 18283;

Best Local Similarity 44.9%; Pred. No. 5.7;
RESULT 820
ID AAS61363 standard; DNA; 18283 BP.
DE Human gene regulation-associated gene oligonucleotide #318.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.6; DB 6; Length 18283;
Best Local Similarity 44.9%; Pred. No. 5.7;
RESULT 821
ID ABL56201 standard; DNA; 50000 BP.
DE AmEPV genome fragment#3.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 1.9%; Score 44.6; DB 6; Length 50000;
Best Local Similarity 46.9%; Pred. No. 8.9;
RESULT 822
Query Match 1.9%; Score 44.6; DB 12; Length 82256;
Best Local Similarity 46.3%; Pred. No. 11;
RESULT 823
ID ADC85260 standard; DNA; 96588 BP.
DE Human PtpRK genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.9%; Score 44.6; DB 10; Length 96588;
Best Local Similarity 53.8%; Pred. No. 12;
RESULT 824
ID ADA02780 standard; DNA; 96589 BP.
DE Human PTPRK carcinoma associated gene, SEQ ID NO:1298.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.9%; Score 44.6; DB 9; Length 96589;
Best Local Similarity 53.8%; Pred. No. 12;
RESULT 825
ID ADB72518 standard; DNA; 96589 BP.
DE Human PTPRK gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.9%; Score 44.6; DB 10; Length 96589;
Best Local Similarity 53.8%; Pred. No. 12;
RESULT 826
ID ADM74375 standard; DNA; 96589 BP.
DE Human carcinoma associated (CA) nucleic acid #22.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 1.9%; Score 44.6; DB 12; Length 96589;
Best Local Similarity 53.8%; Pred. No. 12;
RESULT 827
ID ABQ88126 standard; cDNA; 159400 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 33.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 1.9%; Score 44.6; DB 6; Length 159400;
Best Local Similarity 48.6%; Pred. No. 15;
RESULT 828
ID ABD32659 standard; DNA; 163382 BP.
DE Human cancer-associated genomic DNA HD13-065.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.9%; Score 44.6; DB 13; Length 163382;
Best Local Similarity 45.6%; Pred. No. 15;
RESULT 829
ID ADL43635 standard; DNA; 388 BP.
DE Human ovarian cancer DNA marker #17525.

PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.9%; Score 44.4; DB 5; Length 388;
Best Local Similarity 49.6%; Pred. No. 1.2;
RESULT 830
ID ADB09790 standard; DNA; 714 BP.
DE Allolococcus otitis antigenic protein encoding DNA SEQ ID NO:3835.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 1.9%; Score 44.4; DB 9; Length 714;
Best Local Similarity 46.7%; Pred. No. 1.5;
RESULT 831
ID AAZ37082 standard; DNA; 1431 BP.
DE DNA sequence encoding a yeast SceI endonuclease.
PN EP972836-A2.
PD 19-JAN-2000.
PA (RIKA) INST PHYSICAL & CHEM RES.
Query Match 1.9%; Score 44.4; DB 3; Length 1431;
Best Local Similarity 48.6%; Pred. No. 2.1;
RESULT 832
ID ABZ10188 standard; DNA; 1501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #328.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 8; Length 1501;
Best Local Similarity 45.1%; Pred. No. 2.1;
RESULT 833
ID ADE84162 standard; DNA; 1501 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #98.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 10; Length 1501;
Best Local Similarity 45.1%; Pred. No. 2.1;
RESULT 834
ID AAQ24134 standard; DNA; 1671 BP.
DE 50 kD subunit of SceI.
PN JP04104793-A.
PD 07-APR-1992.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 1.9%; Score 44.4; DB 2; Length 1671;
Best Local Similarity 48.6%; Pred. No. 2.2;
RESULT 835
ID ABZ59722 standard; DNA; 3410 BP.
DE T. thermophila metallothionein gene (MTT1).
PN WO2003006480-A1.
PD 23-JAN-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 1.9%; Score 44.4; DB 8; Length 3410;
Best Local Similarity 47.4%; Pred. No. 3;
RESULT 836
ID ABL34102 standard; DNA; 4993 BP.
DE Human immune system associated gene SEQ ID NO: 2075.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 4993;
Best Local Similarity 45.1%; Pred. No. 3.6;
RESULT 837
ID ADS89374 standard; DNA; 5034 BP.
DE Oligonucleotide of the invention SEQ ID NO:390.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 13; Length 5034;
Best Local Similarity 47.2%; Pred. No. 3.6;
RESULT 838
ID ADS89648 standard; DNA; 5034 BP.
DE Oligonucleotide of the invention SEQ ID NO:664.
PN WO2004035803-A2.

PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 13; Length 5034;
Best Local Similarity 47.2%; Pred. No. 3.6;
RESULT 839
ID ABL33666 standard; DNA; 5798 BP.
DE Human immune system associated gene SEQ ID NO: 1639.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 5798;
Best Local Similarity 47.4%; Pred. No. 3.8;
RESULT 840
ID ABL32820 standard; DNA; 6123 BP.
DE Human immune system associated gene SEQ ID NO: 793.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 6123;
Best Local Similarity 46.4%; Pred. No. 3.9;
RESULT 841
ID ABK31185 standard; DNA; 6239 BP.
DE Signal transduction associated gene modified complementary DNA #14.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 6239;
Best Local Similarity 46.8%; Pred. No. 4;
RESULT 842
ID ABL70146 standard; DNA; 6239 BP.
DE Chemically treated cell signalling DNA sequence complementary to#18.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 6239;
Best Local Similarity 46.8%; Pred. No. 4;
RESULT 843
ID AAS61072 standard; DNA; 6239 BP.
DE Human gene regulation-associated gene oligonucleotide #27.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 6239;
Best Local Similarity 46.8%; Pred. No. 4;
RESULT 844
ID ABL92231 standard; DNA; 7168 BP.
DE Chemically treated DNA repair gene fragment complementary to#20.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 7168;
Best Local Similarity 47.0%; Pred. No. 4.2;
RESULT 845
ID AAD22318 standard; DNA; 7168 BP.
DE Chemically treated human genomic DNA #8 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 7168;
Best Local Similarity 47.0%; Pred. No. 4.2;
RESULT 846
ID ABN80026 standard; DNA; 7189 BP.
DE Human chemically modified disease associated gene SEQ ID NO 43.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 7189;
Best Local Similarity 46.4%; Pred. No. 4.2;
RESULT 847
ID ABK31479 standard; DNA; 8032 BP.
DE Signal transduction associated gene modified complementary DNA #161.
PN WO200200926-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 8032;
Best Local Similarity 47.2%; Pred. No. 4.4;
RESULT 848
ID ABL70448 standard; DNA; 8032 BP.
DE Chemically treated cell signalling DNA sequence complementary to#169.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 8032;
Best Local Similarity 47.2%; Pred. No. 4.4;
RESULT 849
ID AAS61409 standard; DNA; 8032 BP.
DE Human gene regulation-associated gene oligonucleotide #364.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 8032;
Best Local Similarity 47.2%; Pred. No. 4.4;
RESULT 850
ID ABL33568 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1541.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 8305;
Best Local Similarity 47.4%; Pred. No. 4.5;
RESULT 851
ID AAZ29911 standard; DNA; 8310 BP.
DE cDNA encoding a SC4 protein of soybean.
PN WO9953067-A2.
PD 21-OCT-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 1.9%; Score 44.4; DB 2; Length 8310;
Best Local Similarity 44.2%; Pred. No. 4.5;
RESULT 852
ID ABL32668 standard; DNA; 11049 BP.
DE Human immune system associated gene SEQ ID NO: 641.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 11049;
Best Local Similarity 47.8%; Pred. No. 5.1;
RESULT 853
ID ABL92218 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment#14.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 11049;
Best Local Similarity 47.8%; Pred. No. 5.1;
RESULT 854
ID ABL49321 standard; DNA; 11049 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 21.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 11049;
Best Local Similarity 47.8%; Pred. No. 5.1;
RESULT 855
ID AAS46698 standard; DNA; 11694 BP.
DE Tumour suppressor gene derived chemically modified sequence #421.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 4; Length 11694;
Best Local Similarity 44.4%; Pred. No. 5.2;
RESULT 856
ID ABN79985 standard; DNA; 16633 BP.
DE Human chemically modified disease associated gene SEQ ID NO 2.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 44.4; DB 6; Length 16633;
Best Local Similarity 47.1%; Pred. No. 6.1;
RESULT 857
ID ABL70501 standard; DNA; 18283 BP.
DE Chemically treated cell signalling DNA sequence#196.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 18283;
Best Local Similarity 44.7%; Pred. No. 6.4;
RESULT 858
ID AAS61362 standard; DNA; 18283 BP.
DE Human gene regulation-associated gene oligonucleotide #317.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 18283;
Best Local Similarity 44.7%; Pred. No. 6.4;
RESULT 859
ID ABQ67060 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 90.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 34688;
Best Local Similarity 43.7%; Pred. No. 8.5;
RESULT 860
ID ABQ67094 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.4; DB 6; Length 83391;
Best Local Similarity 45.7%; Pred. No. 12;
RESULT 861
Query Match 1.9%; Score 44.4; DB 9; Length 110000;
Best Local Similarity 46.7%; Pred. No. 14;
RESULT 862
ID ADL37588 standard; DNA; 608 BP.
DE Human ovarian cancer DNA marker #11478.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.9%; Score 44.2; DB 5; Length 608;
Best Local Similarity 41.0%; Pred. No. 1.6;
RESULT 863
ID ADI72448 standard; DNA; 608 BP.
DE Human ovarian cancer DNA marker #5190.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.9%; Score 44.2; DB 5; Length 608;
Best Local Similarity 41.0%; Pred. No. 1.6;
RESULT 864
ID AAS28824 standard; cDNA; 697 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 70.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.9%; Score 44.2; DB 4; Length 697;
Best Local Similarity 52.5%; Pred. No. 1.7;
RESULT 865
ID ABA06691 standard; cDNA; 697 BP.
DE Human cDNA SEQ ID NO: 357.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.9%; Score 44.2; DB 4; Length 697;
Best Local Similarity 52.5%; Pred. No. 1.7;
RESULT 866
ID ABV84028 standard; cDNA; 697 BP.
DE Human polynucleotide SEQ ID NO 357.
PN US2002090672-A1.

PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.9%; Score 44.2; DB 6; Length 697;
Best Local Similarity 52.5%; Pred. No. 1.7;
RESULT 867
ID ADB31549 standard; cDNA; 697 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 70.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.9%; Score 44.2; DB 10; Length 697;
Best Local Similarity 52.5%; Pred. No. 1.7;
RESULT 868
ID AAQ31693 standard; DNA; 731 BP.
DE RsaI restriction fragment from Dd ras genomic clone.
PN WO9220806-A2.
PD 26-NOV-1992.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 1.9%; Score 44.2; DB 2; Length 731;
Best Local Similarity 43.0%; Pred. No. 1.7;
RESULT 869
ID AAZ17145 standard; cDNA; 1351 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:4616.
PN WO938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 1.9%; Score 44.2; DB 2; Length 1351;
Best Local Similarity 37.6%; Pred. No. 2.3;
RESULT 870
ID ABZ17044 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4849.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 2000;
Best Local Similarity 45.4%; Pred. No. 2.7;
RESULT 871
ID ADG65091 standard; DNA; 2000 BP.
DE Promoter region sequence #3.
PN EP1209228-A2.
PD 29-MAY-2002.
PA (RIKE) RIKEN KK.
PA (TOYT) TOYOTA JIDOSHA KK.
Query Match 1.9%; Score 44.2; DB 6; Length 2000;
Best Local Similarity 45.4%; Pred. No. 2.7;
RESULT 872
ID ADA69322 standard; DNA; 2000 BP.
DE Arabidopsis thaliana gene, SEQ ID 2645.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.2; DB 8; Length 2000;
Best Local Similarity 45.4%; Pred. No. 2.7;
RESULT 873
ID ADS91270 standard; DNA; 2648 BP.
DE alpha-1 tubulin coding sequence, SEQ ID 166.
PN WO2004074479-A1.
PD 02-SEP-2004.
PA (PHYL-) PHYLOGICA LTD.
Query Match 1.9%; Score 44.2; DB 13; Length 2648;
Best Local Similarity 46.3%; Pred. No. 3.1;
RESULT 874
ID ABL32341 standard; DNA; 5349 BP.
DE Human immune system associated gene SEQ ID NO: 314.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 5349;
Best Local Similarity 51.4%; Pred. No. 4.2;

RESULT 875
ID ABK31370 standard; DNA; 6012 BP.
DE Signal transduction associated gene modified DNA #107.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6012;
Best Local Similarity 48.6%; Pred. No. 4.4;
RESULT 876
ID ABL70327 standard; DNA; 6012 BP.
DE Chemically treated cell signalling DNA sequence#109.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6012;
Best Local Similarity 48.6%; Pred. No. 4.4;
RESULT 877
ID AAS61274 standard; DNA; 6012 BP.
DE Human gene regulation-associated gene oligonucleotide #229.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6012;
Best Local Similarity 48.6%; Pred. No. 4.4;
RESULT 878
ID ABL32326 standard; DNA; 6109 BP.
DE Human immune system associated gene SEQ ID NO: 299.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6109;
Best Local Similarity 45.6%; Pred. No. 4.4;
RESULT 879
ID AAS61077 standard; DNA; 6109 BP.
DE Human gene regulation-associated gene oligonucleotide #32.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6109;
Best Local Similarity 45.6%; Pred. No. 4.4;
RESULT 880
ID ABL32890 standard; DNA; 6131 BP.
DE Human immune system associated gene SEQ ID NO: 863.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6131;
Best Local Similarity 46.9%; Pred. No. 4.4;
RESULT 881
ID ABK31353 standard; DNA; 6147 BP.
DE Signal transduction associated gene modified complementary DNA #98.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6147;
Best Local Similarity 44.1%; Pred. No. 4.4;
RESULT 882
ID ABL33047 standard; DNA; 6290 BP.
DE Human immune system associated gene SEQ ID NO: 1020.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 6290;
Best Local Similarity 43.8%; Pred. No. 4.5;
RESULT 883
ID ABL33930 standard; DNA; 7456 BP.
DE Human immune system associated gene SEQ ID NO: 1903.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 7456;
Best Local Similarity 53.1%; Pred. No. 4.8;
RESULT 884

ID ABL92292 standard; DNA; 7456 BP.
DE Chemically treated DNA repair gene fragment#51.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 7456;
Best Local Similarity 53.1%; Pred. No. 4.8;
RESULT 885
ID ABL32530 standard; DNA; 7644 BP.
DE Human immune system associated gene SEQ ID NO: 503.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 7644;
Best Local Similarity 51.2%; Pred. No. 4.9;
RESULT 886
ID AAS46435 standard; DNA; 8093 BP.
DE Tumour suppressor gene derived chemically modified sequence #157.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 4; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 887
ID ABK33973 standard; DNA; 8093 BP.
DE Human DNA for staging of Astrocytomas #29.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 888
ID ABL92236 standard; DNA; 8093 BP.
DE Chemically treated DNA repair gene fragment#23.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 889
ID ABL49331 standard; DNA; 8093 BP.
DE Human MLH1 gene associated with DNA replication SEQ ID NO 31.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 890
ID ABZ10031 standard; DNA; 8093 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #171.
PN WO20027272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 8; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 891
ID ADA20360 standard; DNA; 8093 BP.
DE Prostate tumour related genomic DNA sample #13.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 8; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 892
ID ADA84167 standard; DNA; 8093 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:25.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 8; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 893
ID ADB54139 standard; DNA; 8093 BP.

DE Pretreated genomic DNA region 63.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 10; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 894
ID ADE84113 standard; DNA; 8093 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #49.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 10; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 895
ID ADS89291 standard; DNA; 8093 BP.
DE Oligonucleotide of the invention SEQ ID NO:307.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 13; Length 8093;
Best Local Similarity 46.1%; Pred. No. 5;
RESULT 896
ID ABL33068 standard; DNA; 9117 BP.
DE Human immune system associated gene SEQ ID NO: 1041.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 9117;
Best Local Similarity 51.4%; Pred. No. 5.3;
RESULT 897
ID AAS45453 standard; DNA; 9515 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #79.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 4; Length 9515;
Best Local Similarity 45.3%; Pred. No. 5.4;
RESULT 898
ID ABK28308 standard; DNA; 9515 BP.
DE DNA transcription associated complementary genomic DNA #91.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 9515;
Best Local Similarity 45.3%; Pred. No. 5.4;
RESULT 899
ID ABN80245 standard; DNA; 9515 BP.
DE Human chemically modified disease associated gene SEQ ID NO 262.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 9515;
Best Local Similarity 45.3%; Pred. No. 5.4;
RESULT 900
ID ABK28452 standard; DNA; 11187 BP.
DE DNA transcription associated complementary genomic DNA #163.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 11187;
Best Local Similarity 44.8%; Pred. No. 5.8;
RESULT 901
ID ABL70501 standard; DNA; 18283 BP.
DE Chemically treated cell signalling DNA sequence#196.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 18283;
Best Local Similarity 50.2%; Pred. No. 7.2;
RESULT 902
ID AAS61362 standard; DNA; 18283 BP.
DE Human gene regulation-associated gene oligonucleotide #317.

PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 18283;
Best Local Similarity 50.2%; Pred. No. 7.2;
RESULT 903
ID ABQ67006 standard; DNA; 33053 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 36.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44.2; DB 6; Length 33053;
Best Local Similarity 45.7%; Pred. No. 9.3;
RESULT 904
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.9%; Score 44.2; DB 11; Length 198522;
Best Local Similarity 44.5%; Pred. No. 20;
RESULT 905
ID ABX46069 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11234.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.9%; Score 44; DB 8; Length 419;
Best Local Similarity 47.5%; Pred. No. 1.5;
RESULT 906
ID ADQ22935 standard; DNA; 2288 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5755.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.9%; Score 44; DB 12; Length 2288;
Best Local Similarity 50.5%; Pred. No. 3.2;
RESULT 907
ID AAS45511 standard; DNA; 3007 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #108.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 4; Length 3007;
Best Local Similarity 46.3%; Pred. No. 3.6;
RESULT 908
ID ABK28445 standard; DNA; 3007 BP.
DE DNA transcription associated genomic DNA #160.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 3007;
Best Local Similarity 46.3%; Pred. No. 3.6;
RESULT 909
ID ABQ67144 standard; DNA; 3151 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 174.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 3151;
Best Local Similarity 44.9%; Pred. No. 3.7;
RESULT 910
ID AAD48465 standard; DNA; 3750 BP.
DE Brassica napus brevipedicellus (BnBP) genomic fragment DNA.
PN WO200279463-A2.
PD 10-OCT-2002.
PA (CANA) NAT RES COUNCIL CANADA.
Query Match 1.9%; Score 44; DB 8; Length 3750;
Best Local Similarity 44.6%; Pred. No. 4;
RESULT 911

ID ABL32538 standard; DNA; 5820 BP.
DE Human immune system associated gene SEQ ID NO: 511.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 5820;
Best Local Similarity 44.5%; Pred. No. 4.9;
RESULT 912
ID ABK31237 standard; DNA; 6129 BP.
DE Signal transduction associated gene modified complementary DNA #40.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 6129;
Best Local Similarity 44.9%; Pred. No. 5;
RESULT 913
ID ABL70538 standard; DNA; 6129 BP.
DE Chemically treated cell signalling DNA sequence complementary to#214.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 6129;
Best Local Similarity 44.9%; Pred. No. 5;
RESULT 914
ID AAS61150 standard; DNA; 6129 BP.
DE Human gene regulation-associated gene oligonucleotide #105.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 6129;
Best Local Similarity 44.9%; Pred. No. 5;
RESULT 915
ID AAS61176 standard; DNA; 6223 BP.
DE Human gene regulation-associated gene oligonucleotide #131.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 6223;
Best Local Similarity 45.4%; Pred. No. 5;
RESULT 916
ID AAS45422 standard; DNA; 6306 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #64.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 4; Length 6306;
Best Local Similarity 48.0%; Pred. No. 5;
RESULT 917
ID ABL33260 standard; DNA; 6437 BP.
DE Human immune system associated gene SEQ ID NO: 1233.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 6437;
Best Local Similarity 51.5%; Pred. No. 5.1;
RESULT 918
ID ABK31424 standard; DNA; 7321 BP.
DE Signal transduction associated gene modified DNA #134.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 7321;
Best Local Similarity 57.1%; Pred. No. 5.4;
RESULT 919
ID ABL70385 standard; DNA; 7321 BP.
DE Chemically treated cell signalling DNA sequence#138.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 7321;
Best Local Similarity 57.1%; Pred. No. 5.4;
RESULT 920
ID AAS61337 standard; DNA; 7321 BP.

DE Human gene regulation-associated gene oligonucleotide #292.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 7321;
Best Local Similarity 57.1%; Pred. No. 5.4;
RESULT 921
ID ABL32914 standard; DNA; 7522 BP.
DE Human immune system associated gene SEQ ID NO: 887.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 7522;
Best Local Similarity 47.8%; Pred. No. 5.4;
RESULT 922
ID ABL33013 standard; DNA; 7597 BP.
DE Human immune system associated gene SEQ ID NO: 986.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 7597;
Best Local Similarity 43.8%; Pred. No. 5.5;
RESULT 923
ID AAS46445 standard; DNA; 8952 BP.
DE Tumour suppressor gene derived chemically modified sequence #167.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 4; Length 8952;
Best Local Similarity 50.0%; Pred. No. 5.9;
RESULT 924
ID ABQ67026 standard; DNA; 11964 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 56.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 11964;
Best Local Similarity 44.9%; Pred. No. 6.7;
RESULT 925
ID ABQ66975 standard; DNA; 13627 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 5.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 13627;
Best Local Similarity 45.8%; Pred. No. 7.1;
RESULT 926
ID ABL33345 standard; DNA; 17674 BP.
DE Human immune system associated gene SEQ ID NO: 1318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 6; Length 17674;
Best Local Similarity 45.1%; Pred. No. 7.9;
RESULT 927
ID AAS46794 standard; DNA; 56153 BP.
DE Tumour suppressor gene derived chemically modified sequence #520.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.9%; Score 44; DB 4; Length 56153;
Best Local Similarity 45.6%; Pred. No. 13;
RESULT 928
ID ABQ99654 standard; DNA; 95109 BP.
DE Human membrane spanning 4-domain family, subfamily A genomic sequence.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 1.9%; Score 44; DB 6; Length 95109;
Best Local Similarity 46.4%; Pred. No. 17;
RESULT 929
ID ABL33598 standard; DNA; 5487 BP.
DE Human immune system associated gene SEQ ID NO: 1571.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 5487;
Best Local Similarity 49.0%; Pred. No. 5.3;
RESULT 930
ID ABL34448 standard; DNA; 6127 BP.
DE Human metastasis associated gene SEQ ID NO: 1.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6127;
Best Local Similarity 49.4%; Pred. No. 5.6;
RESULT 931
ID ABL70119 standard; DNA; 6127 BP.
DE Chemically treated cell signalling DNA sequence#5.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6127;
Best Local Similarity 49.4%; Pred. No. 5.6;
RESULT 932
ID ADS99709 standard; DNA; 6127 BP.
DE Bisulphite treated human gene associated with metastasis #1.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 43.8; DB 7; Length 6127;
Best Local Similarity 49.4%; Pred. No. 5.6;
RESULT 933
ID AAS46497 standard; DNA; 6233 BP.
DE Tumour suppressor gene derived chemically modified sequence #219.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 4; Length 6233;
Best Local Similarity 48.0%; Pred. No. 5.6;
RESULT 934
ID ABL32323 standard; DNA; 6418 BP.
DE Human immune system associated gene SEQ ID NO: 296.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6418;
Best Local Similarity 46.0%; Pred. No. 5.7;
RESULT 935
ID AAS61074 standard; DNA; 6418 BP.
DE Human gene regulation-associated gene oligonucleotide #29.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6418;
Best Local Similarity 46.0%; Pred. No. 5.7;
RESULT 936
ID ABL34541 standard; DNA; 6811 BP.
DE Human metastasis associated gene SEQ ID NO: 94.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6811;
Best Local Similarity 51.9%; Pred. No. 5.8;
RESULT 937
ID ABL70264 standard; DNA; 6811 BP.
DE Chemically treated cell signalling DNA sequence complementary to#77.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 6811;
Best Local Similarity 51.9%; Pred. No. 5.8;
RESULT 938
ID ADS99802 standard; DNA; 6811 BP.

DE Complement of bisulphite treated metastasis-associated human gene #47.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 43.8; DB 7; Length 6811;
Best Local Similarity 51.9%; Pred. No. 5.8;
RESULT 939
ID ABZ10178 standard; DNA; 8093 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #318.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 8; Length 8093;
Best Local Similarity 47.0%; Pred. No. 6.3;
RESULT 940
ID ADB54268 standard; DNA; 8093 BP.
DE Pretreated genomic DNA region 192.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 10; Length 8093;
Best Local Similarity 47.0%; Pred. No. 6.3;
RESULT 941
ID ADE84190 standard; DNA; 8093 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #126.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 10; Length 8093;
Best Local Similarity 47.0%; Pred. No. 6.3;
RESULT 942
ID ADS89566 standard; DNA; 8093 BP.
DE Oligonucleotide of the invention SEQ ID NO:582.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 13; Length 8093;
Best Local Similarity 47.0%; Pred. No. 6.3;
RESULT 943
ID ABQ67126 standard; DNA; 8227 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 156.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 8227;
Best Local Similarity 45.8%; Pred. No. 6.3;
RESULT 944
ID ABL34492 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 45.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 11996;
Best Local Similarity 45.6%; Pred. No. 7.5;
RESULT 945
ID ADS99753 standard; DNA; 11996 BP.
DE Bisulphite treated human gene associated with metastasis #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 43.8; DB 7; Length 11996;
Best Local Similarity 45.6%; Pred. No. 7.5;
RESULT 946
ID ABL34358 standard; DNA; 12237 BP.
DE Human immune system associated gene SEQ ID NO: 2331.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 12237;

Best Local Similarity 47.3%; Pred. No. 7.6;
RESULT 947
ID ABL33194 standard; DNA; 14861 BP.
DE Human immune system associated gene SEQ ID NO: 1167.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 14861;
Best Local Similarity 47.6%; Pred. No. 8.2;
RESULT 948
ID ABL70553 standard; DNA; 14861 BP.
DE Chemically treated cell signalling DNA sequence#222.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 14861;
Best Local Similarity 47.6%; Pred. No. 8.2;
RESULT 949
ID AAS61202 standard; DNA; 14861 BP.
DE Human gene regulation-associated gene oligonucleotide #157.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 14861;
Best Local Similarity 47.6%; Pred. No. 8.2;
RESULT 950
ID AAS46506 standard; DNA; 14919 BP.
DE Tumour suppressor gene derived chemically modified sequence #228.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 4; Length 14919;
Best Local Similarity 44.8%; Pred. No. 8.2;
RESULT 951
ID ABK28395 standard; DNA; 15743 BP.
DE DNA transcription associated genomic DNA #135.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 15743;
Best Local Similarity 48.3%; Pred. No. 8.4;
RESULT 952
ID ABL33090 standard; DNA; 16724 BP.
DE Human immune system associated gene SEQ ID NO: 1063.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 16724;
Best Local Similarity 52.9%; Pred. No. 8.7;
RESULT 953
ID ABL34536 standard; DNA; 16724 BP.
DE Human metastasis associated gene SEQ ID NO: 89.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 16724;
Best Local Similarity 52.9%; Pred. No. 8.7;
RESULT 954
ID ABL70259 standard; DNA; 16724 BP.
DE Chemically treated cell signalling DNA sequence#75.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 16724;
Best Local Similarity 52.9%; Pred. No. 8.7;
RESULT 955
ID ADS99797 standard; DNA; 16724 BP.
DE Bisulphite treated human gene associated with metastasis #45.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.

Query Match 1.8%; Score 43.8; DB 7; Length 16724;
Best Local Similarity 52.9%; Pred. No. 8.7;
RESULT 956
ID ABK39952 standard; DNA; 17703 BP.
DE Human chemically pretreated gene sequence #17 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 17703;
Best Local Similarity 44.7%; Pred. No. 8.9;
RESULT 957
ID ABL32254 standard; DNA; 18154 BP.
DE Human immune system associated gene SEQ ID NO: 227.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 18154;
Best Local Similarity 44.6%; Pred. No. 9;
RESULT 958
ID ABL32254 standard; DNA; 18154 BP.
DE Human immune system associated gene SEQ ID NO: 227.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.8; DB 6; Length 18154;
Best Local Similarity 44.1%; Pred. No. 9;
RESULT 959
ID AAC66747 standard; DNA; 555 BP.
DE DNA marker B.
PN WO200063432-A1.
PD 26-OCT-2000.
PA (ENZA-) ENZA ZADEN ENKHUIZER ZAADHANDEL BV.
Query Match 1.8%; Score 43.6; DB 3; Length 555;
Best Local Similarity 46.4%; Pred. No. 2.2;
RESULT 960
ID ABQ40113 standard; DNA; 583 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26704.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 583;
Best Local Similarity 47.7%; Pred. No. 2.2;
RESULT 961
ID ABQ40112 standard; DNA; 583 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26703.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 583;
Best Local Similarity 47.7%; Pred. No. 2.2;
RESULT 962
ID AAK03309 standard; DNA; 1988 BP.
DE Human brain expressed single exon probe SEQ ID NO: 3300.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 43.6; DB 4; Length 1988;
Best Local Similarity 44.5%; Pred. No. 3.8;
RESULT 963
ID ABZ10164 standard; DNA; 3128 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #304.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 8; Length 3128;
Best Local Similarity 55.2%; Pred. No. 4.6;
RESULT 964
ID ADS89612 standard; DNA; 4930 BP.
DE Oligonucleotide of the invention SEQ ID NO:628.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 4930;

Best Local Similarity 46.2%; Pred. No. 5.7;
RESULT 965
ID ABL34176 standard; DNA; 5368 BP.
DE Human immune system associated gene SEQ ID NO: 2149.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 5368;
Best Local Similarity 45.6%; Pred. No. 5.9;
RESULT 966
ID ABL34091 standard; DNA; 5407 BP.
DE Human immune system associated gene SEQ ID NO: 2064.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 5407;
Best Local Similarity 44.7%; Pred. No. 5.9;
RESULT 967
ID ABL33870 standard; DNA; 5511 BP.
DE Human immune system associated gene SEQ ID NO: 1843.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 5511;
Best Local Similarity 46.4%; Pred. No. 6;
RESULT 968
ID ADS89769 standard; DNA; 6001 BP.
DE Oligonucleotide of the invention SEQ ID NO:785.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 6001;
Best Local Similarity 46.2%; Pred. No. 6.2;
RESULT 969
ID ADE84206 standard; DNA; 6028 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #142.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 10; Length 6028;
Best Local Similarity 55.2%; Pred. No. 6.2;
RESULT 970
ID AAS46430 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #152.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 4; Length 6106;
Best Local Similarity 43.8%; Pred. No. 6.2;
RESULT 971
ID ABK40032 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6106;
Best Local Similarity 43.8%; Pred. No. 6.2;
RESULT 972
ID ABL33473 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1446.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6106;
Best Local Similarity 43.8%; Pred. No. 6.2;
RESULT 973
ID ABL70354 standard; DNA; 6107 BP.
DE Chemically treated cell signalling DNA sequence complementary to#122.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6107;
Best Local Similarity 45.0%; Pred. No. 6.2;

RESULT 974
ID AAS61315 standard; DNA; 6107 BP.
DE Human gene regulation-associated gene oligonucleotide #270.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6107;
Best Local Similarity 45.0%; Pred. No. 6.2;
RESULT 975
ID AAS46574 standard; DNA; 6126 BP.
DE Tumour suppressor gene derived chemically modified sequence #296.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 4; Length 6126;
Best Local Similarity 47.2%; Pred. No. 6.2;
RESULT 976
ID ABL33831 standard; DNA; 6126 BP.
DE Human immune system associated gene SEQ ID NO: 1804.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6126;
Best Local Similarity 47.2%; Pred. No. 6.2;
RESULT 977
ID ABL32623 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 596.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6161;
Best Local Similarity 47.4%; Pred. No. 6.3;
RESULT 978
ID ABL33586 standard; DNA; 6227 BP.
DE Human immune system associated gene SEQ ID NO: 1559.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6227;
Best Local Similarity 44.3%; Pred. No. 6.3;
RESULT 979
ID ABL92260 standard; DNA; 6227 BP.
DE Chemically treated DNA repair gene fragment#35.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 6227;
Best Local Similarity 44.3%; Pred. No. 6.3;
RESULT 980
ID ABZ79546 standard; DNA; 6459 BP.
DE Radish Rfl DNA # SEQ ID 1.
PN JP2002355042-A.
PD 10-DEC-2002.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 1.8%; Score 43.6; DB 8; Length 6459;
Best Local Similarity 46.0%; Pred. No. 6.4;
RESULT 981
ID AAK86101 standard; DNA; 6558 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40913.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 43.6; DB 4; Length 6558;
Best Local Similarity 44.5%; Pred. No. 6.4;
RESULT 982
ID AAL37138 standard; DNA; 6558 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3503.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 43.6; DB 4; Length 6558;
Best Local Similarity 44.5%; Pred. No. 6.4;
RESULT 983

ID ABA21372 standard; DNA; 6558 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13703.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 43.6; DB 5; Length 6558;
Best Local Similarity 44.5%; Pred. No. 6.4;
RESULT 984
ID ABX60126 standard; cDNA; 6558 BP.
DE CDNA encoding novel human musculoskeletal system antigen #2470.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.8%; Score 43.6; DB 8; Length 6558;
Best Local Similarity 44.5%; Pred. No. 6.4;
RESULT 985
ID ADJ30876 standard; DNA; 6558 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3503.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 43.6; DB 12; Length 6558;
Best Local Similarity 44.5%; Pred. No. 6.4;
RESULT 986
ID ABK31451 standard; DNA; 7131 BP.
DE Signal transduction associated gene modified complementary DNA #147.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 7131;
Best Local Similarity 43.4%; Pred. No. 6.7;
RESULT 987
ID ABL70428 standard; DNA; 7131 BP.
DE Chemically treated cell signalling DNA sequence complementary to#159.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 7131;
Best Local Similarity 43.4%; Pred. No. 6.7;
RESULT 988
ID AAS61361 standard; DNA; 7131 BP.
DE Human gene regulation-associated gene oligonucleotide #316.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 7131;
Best Local Similarity 43.4%; Pred. No. 6.7;
RESULT 989
ID ABL32982 standard; DNA; 7143 BP.
DE Human immune system associated gene SEQ ID NO: 955.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 7143;
Best Local Similarity 45.4%; Pred. No. 6.7;
RESULT 990
ID ABL33775 standard; DNA; 7503 BP.
DE Human immune system associated gene SEQ ID NO: 1748.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 7503;
Best Local Similarity 57.2%; Pred. No. 6.8;
RESULT 991
ID ADB54312 standard; DNA; 7833 BP.
DE Pretreated genomic DNA region 236.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 10; Length 7833;
Best Local Similarity 46.2%; Pred. No. 7;

RESULT 992
ID ADE37779 standard; DNA; 7833 BP.
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:25.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 10; Length 7833;
Best Local Similarity 46.2%; Pred. No. 7;
RESULT 993
ID ADS89608 standard; DNA; 7833 BP.
DE Oligonucleotide of the invention SEQ ID NO:624.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 7833;
Best Local Similarity 46.2%; Pred. No. 7;
RESULT 994
ID AAS45432 standard; DNA; 8866 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #69.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 4; Length 8866;
Best Local Similarity 46.4%; Pred. No. 7.4;
RESULT 995
ID ABK28279 standard; DNA; 8866 BP.
DE DNA transcription associated genomic DNA #77.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 8866;
Best Local Similarity 46.4%; Pred. No. 7.4;
RESULT 996
ID ADS89686 standard; DNA; 8900 BP.
DE Oligonucleotide of the invention SEQ ID NO:702.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 8900;
Best Local Similarity 47.4%; Pred. No. 7.4;
RESULT 997
ID ADS89412 standard; DNA; 8900 BP.
DE Oligonucleotide of the invention SEQ ID NO:428.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 8900;
Best Local Similarity 47.4%; Pred. No. 7.4;
RESULT 998
ID ABK28453 standard; DNA; 10467 BP.
DE DNA transcription associated genomic DNA #164.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 10467;
Best Local Similarity 53.5%; Pred. No. 7.9;
RESULT 999
ID ADB54222 standard; DNA; 11913 BP.
DE Pretreated genomic DNA region 146.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 10; Length 11913;
Best Local Similarity 46.5%; Pred. No. 8.4;
RESULT 1000
ID ADS89520 standard; DNA; 11913 BP.
DE Oligonucleotide of the invention SEQ ID NO:536.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 13; Length 11913;
Best Local Similarity 46.5%; Pred. No. 8.4;
RESULT 1001

ID ABL32299 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 272.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 12507;
Best Local Similarity 49.3%; Pred. No. 8.6;
RESULT 1002
ID ABL33712 standard; DNA; 13326 BP.
DE Human immune system associated gene SEQ ID NO: 1685.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 13326;
Best Local Similarity 49.0%; Pred. No. 8.8;
RESULT 1003
ID ABL34070 standard; DNA; 13503 BP.
DE Human immune system associated gene SEQ ID NO: 2043.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 13503;
Best Local Similarity 47.8%; Pred. No. 8.8;
RESULT 1004
ID AAS46356 standard; DNA; 14537 BP.
DE Tumour suppressor gene derived chemically modified sequence #78.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 14537;
Best Local Similarity 46.0%; Pred. No. 9.1;
RESULT 1005
ID ABL34469 standard; DNA; 16173 BP.
DE Human metastasis associated gene SEQ ID NO: 22.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 16173;
Best Local Similarity 45.9%; Pred. No. 9.6;
RESULT 1006
ID ADS99730 standard; DNA; 16173 BP.
DE Complement of bisulphite treated metastasis-associated human gene #11.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 43.6; DB 7; Length 16173;
Best Local Similarity 45.9%; Pred. No. 9.6;
RESULT 1007
ID ABL33702 standard; DNA; 18624 BP.
DE Human immune system associated gene SEQ ID NO: 1675.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 18624;
Best Local Similarity 50.5%; Pred. No. 10;
RESULT 1008
ID ABL33933 standard; DNA; 19734 BP.
DE Human immune system associated gene SEQ ID NO: 1906.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 19734;
Best Local Similarity 45.4%; Pred. No. 10;
RESULT 1009
ID ABK31510 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 47108;
Best Local Similarity 45.7%; Pred. No. 15;

RESULT 1010
ID ABL55644 standard; DNA; 50000 BP.
DE AmEPV genome fragment#2.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 1.8%; Score 43.6; DB 6; Length 50000;
Best Local Similarity 48.7%; Pred. No. 16;
RESULT 1011
ID ABQ67093 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 123.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.6; DB 6; Length 83391;
Best Local Similarity 45.6%; Pred. No. 20;
RESULT 1012
ID ADQ97960 standard; DNA; 390183 BP.
DE Human cancer associated sequence HD11-029, SEQ ID 937.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 43.6; DB 12; Length 110000;
Best Local Similarity 47.5%; Pred. No. 22;
RESULT 1013
ID ABX41811 standard; cDNA; 337 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6976.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 1.8%; Score 43.4; DB 8; Length 337;
Best Local Similarity 53.2%; Pred. No. 2;
RESULT 1014
ID ABQ14987 standard; DNA; 547 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1578.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 547;
Best Local Similarity 44.9%; Pred. No. 2.4;
RESULT 1015
ID ABQ14986 standard; DNA; 547 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1577.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 547;
Best Local Similarity 44.9%; Pred. No. 2.4;
RESULT 1016
ID ABQ89354 standard; cDNA; 830 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 610.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 43.4; DB 6; Length 830;
Best Local Similarity 51.9%; Pred. No. 2.9;
RESULT 1017
ID ADB82297 standard; cDNA; 830 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 609).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 43.4; DB 9; Length 830;
Best Local Similarity 51.9%; Pred. No. 2.9;
RESULT 1018
ID ABI99480 standard; cDNA; 2196 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:441.
PN WO200188188-A2.

PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 1.8%; Score 43.4; DB 6; Length 2196;
Best Local Similarity 49.3%; Pred. No. 4.5;
RESULT 1019
ID ABL34150 standard; DNA; 5376 BP.
DE Human immune system associated gene SEQ ID NO: 2123.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 5376;
Best Local Similarity 51.0%; Pred. No. 6.6;
RESULT 1020
ID ABK31491 standard; DNA; 6012 BP.
DE Signal transduction associated gene modified complementary DNA #167.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6012;
Best Local Similarity 48.9%; Pred. No. 7;
RESULT 1021
ID ABL70464 standard; DNA; 6012 BP.
DE Chemically treated cell signalling DNA sequence complementary to#177.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6012;
Best Local Similarity 48.9%; Pred. No. 7;
RESULT 1022
ID AAS46430 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #152.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 4; Length 6106;
Best Local Similarity 43.9%; Pred. No. 7;
RESULT 1023
ID ABK40032 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6106;
Best Local Similarity 43.9%; Pred. No. 7;
RESULT 1024
ID ABL33473 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1446.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6106;
Best Local Similarity 43.9%; Pred. No. 7;
RESULT 1025
ID ABL32408 standard; DNA; 6317 BP.
DE Human immune system associated gene SEQ ID NO: 381.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6317;
Best Local Similarity 45.9%; Pred. No. 7.1;
RESULT 1026
ID ABL49311 standard; DNA; 6317 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 11.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6317;
Best Local Similarity 45.9%; Pred. No. 7.1;
RESULT 1027
ID ABL32832 standard; DNA; 6585 BP.
DE Human immune system associated gene SEQ ID NO: 805.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6585;
Best Local Similarity 51.9%; Pred. No. 7.2;
RESULT 1028
ID AAS61182 standard; DNA; 6585 BP.
DE Human gene regulation-associated gene oligonucleotide #137.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6585;
Best Local Similarity 51.9%; Pred. No. 7.2;
RESULT 1029
ID ABL33476 standard; DNA; 6590 BP.
DE Human immune system associated gene SEQ ID NO: 1449.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6590;
Best Local Similarity 45.8%; Pred. No. 7.2;
RESULT 1030
ID ABL33735 standard; DNA; 6942 BP.
DE Human immune system associated gene SEQ ID NO: 1708.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 6942;
Best Local Similarity 47.3%; Pred. No. 7.4;
RESULT 1031
ID AAS45403 standard; DNA; 7903 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #54.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 4; Length 7903;
Best Local Similarity 47.0%; Pred. No. 7.8;
RESULT 1032
ID ABL33363 standard; DNA; 7903 BP.
DE Human immune system associated gene SEQ ID NO: 1336.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 7903;
Best Local Similarity 47.0%; Pred. No. 7.8;
RESULT 1033
ID ABK28248 standard; DNA; 7903 BP.
DE DNA transcription associated complementary genomic DNA #61.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 7903;
Best Local Similarity 47.0%; Pred. No. 7.8;
RESULT 1034
ID ACF62816 standard; DNA; 8222 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:65.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 8; Length 8222;
Best Local Similarity 43.8%; Pred. No. 8;
RESULT 1035
ID ACF62794 standard; DNA; 8222 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:43.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 8; Length 8222;
Best Local Similarity 43.8%; Pred. No. 8;
RESULT 1036
ID ABK40075 standard; DNA; 9021 BP.
DE Human chemically pretreated gene sequence #79 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 43.4; DB 6; Length 9021;
Best Local Similarity 45.1%; Pred. No. 8.3;
RESULT 1037
ID ABL34232 standard; DNA; 9021 BP.
DE Human immune system associated gene SEQ ID NO: 2205.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 9021;
Best Local Similarity 45.1%; Pred. No. 8.3;
RESULT 1038
ID ABK33988 standard; DNA; 9021 BP.
DE Human DNA for staging of Astrocytomas #37.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 9021;
Best Local Similarity 45.1%; Pred. No. 8.3;
RESULT 1039
ID ADA20388 standard; DNA; 9021 BP.
DE Prostate tumour related genomic DNA sample #27.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 8; Length 9021;
Best Local Similarity 45.1%; Pred. No. 8.3;
RESULT 1040
ID ADAB4195 standard; DNA; 9021 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:53.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 8; Length 9021;
Best Local Similarity 45.1%; Pred. No. 8.3;
RESULT 1041
ID ADB54190 standard; DNA; 11222 BP.
DE Pretreated genomic DNA region 114.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 10; Length 11222;
Best Local Similarity 43.8%; Pred. No. 9.2;
RESULT 1042
ID ADB54318 standard; DNA; 11222 BP.
DE Pretreated genomic DNA region 242.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 10; Length 11222;
Best Local Similarity 43.8%; Pred. No. 9.2;
RESULT 1043
ID ABK39937 standard; DNA; 11422 BP.
DE Human chemically pretreated gene sequence #9 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 11422;
Best Local Similarity 49.3%; Pred. No. 9.2;
RESULT 1044
ID ABL32219 standard; DNA; 11422 BP.
DE Human immune system associated gene SEQ ID NO: 192.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 11422;
Best Local Similarity 49.3%; Pred. No. 9.2;
RESULT 1045
ID ABL33927 standard; DNA; 13427 BP.
DE Human immune system associated gene SEQ ID NO: 1900.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 13427;

Best Local Similarity 47.8%; Pred. No. 9.9;
RESULT 1046
ID ABL32190 standard; DNA; 17137 BP.
DE Human immune system associated gene SEQ ID NO: 163.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 17137;
Best Local Similarity 46.1%; Pred. No. 11;
RESULT 1047
ID ABL70570 standard; DNA; 24939 BP.
DE Chemically treated cell signalling DNA sequence complementary to#230.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 24939;
Best Local Similarity 48.2%; Pred. No. 13;
RESULT 1048
ID ABD33520 standard; DNA; 34722 BP.
DE Human cancer-associated (CA) gene HD07-102.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 43.4; DB 13; Length 34722;
Best Local Similarity 45.7%; Pred. No. 15;
RESULT 1049
ID ACN44638 standard; DNA; 35680 BP.
DE Human genomic sequence hCG17117.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 43.4; DB 11; Length 35680;
Best Local Similarity 51.9%; Pred. No. 15;
RESULT 1050
ID ABQ67150 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.4; DB 6; Length 40324;
Best Local Similarity 45.7%; Pred. No. 16;
RESULT 1051
ID ABS52847 standard; DNA; 90541 BP.
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.
PN US2002094560-A1.
PD 18-JUL-2002.
PA (ABUT/) ABU-THREIDEH J.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 1.8%; Score 43.4; DB 6; Length 90541;
Best Local Similarity 53.2%; Pred. No. 23;
RESULT 1052
ID ADJ37690 standard; DNA; 90541 BP.
DE Human kinase genomic DNA.
PN US2003175927-A1.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 43.4; DB 10; Length 90541;
Best Local Similarity 53.2%; Pred. No. 23;
RESULT 1053
ID ADR31219 standard; DNA; 90541 BP.
DE Human SRPK2 kinase protein alternative splice form genomic DNA.
PN US2004157297-A1.
PD 12-AUG-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 43.4; DB 13; Length 90541;
Best Local Similarity 53.2%; Pred. No. 23;
RESULT 1054
ID AAL54213 standard; DNA; 113033 BP.
DE SR protein-specific kinase-1 DNA, SEQ ID No 5.
PN WO200299427-A1.

PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC. 1.8%; Score 43.4; DB 8; Length 113033;
Query Match
Best Local Similarity 53.2%; Pred. No. 25;
RESULT 1055
ID ADL17884 standard; cDNA; 158001 BP.
DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
PN US2004023906-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 1.8%; Score 43.4; DB 12; Length 158001;
RESULT 1056
ID ABV56638 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 56629.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 5; Length 469;
RESULT 1057
ID ACN55408 standard; cDNA; 499 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 13; Length 499;
RESULT 1058
ID AAV40736 standard; cDNA; 1982 BP.
DE C. felis esterase, nFE51982, coding sequence complementary strand.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 2; Length 1982;
RESULT 1059
ID AAV40735 standard; cDNA; 1982 BP.
DE C. felis esterase, nFE51982, coding sequence.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 2; Length 1982;
RESULT 1060
ID AAD21167 standard; cDNA; 1982 BP.
DE Ctenocephalides felis carboxylesterase cDNA, nFE51982.
PN US6291222-B1.
PD 18-SEP-2001.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 4; Length 1982;
RESULT 1061
ID AAV40758 standard; cDNA; 2144 BP.
DE C. felis esterase, nFE52144, coding sequence.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 2; Length 2144;
RESULT 1062
ID AAV40759 standard; cDNA; 2144 BP.
DE C. felis esterase, nFE52144, coding sequence complementary strand.
PN WO9821324-A1.
PD 22-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 2; Length 2144;
RESULT 1063
ID AAD21182 standard; cDNA; 2144 BP.

DE Ctenocephalides felis carboxylesterase cDNA, nFE52144.
PN US6291222-B1.
PD 18-SEP-2001.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 4; Length 2144;
RESULT 1064
ID ADB54116 standard; DNA; 2501 BP.
DE Pretreated genomic DNA region 40.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 10; Length 2501;
RESULT 1065
ID ADS89272 standard; DNA; 2501 BP.
DE Oligonucleotide of the invention SEQ ID NO:288.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 13; Length 2501;
RESULT 1066
ID ABZ81728 standard; cDNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 8; Length 2652;
RESULT 1067
ID ABZ81727 standard; cDNA; 2652 BP.
DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 8; Length 2652;
RESULT 1068
ID ADK67781 standard; DNA; 2652 BP.
DE Rat glycosylation-variant BEHAB isoform coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 2652;
RESULT 1069
ID ADK67780 standard; DNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 2652;
RESULT 1070
ID ADB59097 standard; DNA; 3077 BP.
DE Toxicity-related gene, SEQ ID 4123.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 10; Length 3077;
RESULT 1071
ID ADP72861 standard; DNA; 3077 BP.
DE Renal toxin progression gene marker #1450.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 3077;

Best Local Similarity 51.6%; Pred. No. 5.8;
RESULT 1072
ID ADF09331 standard; DNA; 3552 BP.
DE Swinepox virus (SPV) DNA sequence #1.
PN JP2003111591-A.
PD 15-APR-2003.
PA (JAPG) NIPPON ZEON KK.
Query Match 1.8%; Score 43.2; DB 10; Length 3552;
Best Local Similarity 52.2%; Pred. No. 6.2;
RESULT 1073
ID ADH51190 standard; DNA; 4597 BP.
DE Soybean FAD2-2B gene intron 1.
PN WO2004001000-A2.
PD 31-DEC-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 1.8%; Score 43.2; DB 12; Length 4597;
Best Local Similarity 44.2%; Pred. No. 6.9;
RESULT 1074
ID ADI03851 standard; DNA; 4597 BP.
DE Soybean FAD2-2B intron 1 sequence.
PN WO2004001001-A2.
PD 31-DEC-2003.
PA (CALJ) CALGENE LLC.
Query Match 1.8%; Score 43.2; DB 12; Length 4597;
Best Local Similarity 44.2%; Pred. No. 6.9;
RESULT 1075
ID ABL33070 standard; DNA; 5294 BP.
DE Human immune system associated gene SEQ ID NO: 1043.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 5294;
Best Local Similarity 45.9%; Pred. No. 7.4;
RESULT 1076
ID ABK31282 standard; DNA; 5294 BP.
DE Signal transduction associated gene modified DNA #63.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 5294;
Best Local Similarity 45.9%; Pred. No. 7.4;
RESULT 1077
ID AAA70199 standard; DNA; 6042 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:332.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.8%; Score 43.2; DB 3; Length 6042;
Best Local Similarity 44.8%; Pred. No. 7.8;
RESULT 1078
ID AAS46310 standard; DNA; 6095 BP.
DE Tumour suppressor gene derived chemically modified sequence #32.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 4; Length 6095;
Best Local Similarity 48.9%; Pred. No. 7.8;
RESULT 1079
ID ABL32361 standard; DNA; 6095 BP.
DE Human immune system associated gene SEQ ID NO: 334.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6095;
Best Local Similarity 48.9%; Pred. No. 7.8;
RESULT 1080
ID ABL34475 standard; DNA; 6095 BP.
DE Human metastasis associated gene SEQ ID NO: 28.
PN WO200177376-A2.
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6095;
Best Local Similarity 48.9%; Pred. No. 7.8;
RESULT 1081
ID ABL70150 standard; DNA; 6095 BP.
DE Chemically treated cell signalling DNA sequence complementary to#20.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6095;
Best Local Similarity 48.9%; Pred. No. 7.8;
RESULT 1082
ID ADS99736 standard; DNA; 6095 BP.
DE Complement of bisulphite treated metastasis-associated human gene #14.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 43.2; DB 7; Length 6095;
Best Local Similarity 48.9%; Pred. No. 7.8;
RESULT 1083
ID ADH51189 standard; DNA; 6220 BP.
DE Soybean FAD2-2 partial genomic clone.
PN WO2004001000-A2.
PD 31-DEC-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 1.8%; Score 43.2; DB 12; Length 6220;
Best Local Similarity 44.2%; Pred. No. 7.9;
RESULT 1084
ID ADI03850 standard; DNA; 6220 BP.
DE Soybean FAD2-2 partial genomic sequence.
PN WO2004001001-A2.
PD 31-DEC-2003.
PA (CALJ) CALGENE LLC.
Query Match 1.8%; Score 43.2; DB 12; Length 6220;
Best Local Similarity 44.2%; Pred. No. 7.9;
RESULT 1085
ID ABL33496 standard; DNA; 6285 BP.
DE Human immune system associated gene SEQ ID NO: 1469.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6285;
Best Local Similarity 45.4%; Pred. No. 8;
RESULT 1086
ID AAS46591 standard; DNA; 6286 BP.
DE Tumour suppressor gene derived chemically modified sequence #313.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 4; Length 6286;
Best Local Similarity 43.8%; Pred. No. 8;
RESULT 1087
ID ABL32315 standard; DNA; 6641 BP.
DE Human immune system associated gene SEQ ID NO: 288.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6641;
Best Local Similarity 42.3%; Pred. No. 8.1;
RESULT 1088
ID ABL54336 standard; DNA; 6641 BP.
DE Chemically treated apoptosis gene complementary to gene #18.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6641;
Best Local Similarity 42.3%; Pred. No. 8.1;
RESULT 1089
ID ABK31323 standard; DNA; 6880 BP.
DE Signal transduction associated gene modified complementary DNA #83.
PN WO200200926-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6880;
Best Local Similarity 46.9%; Pred. No. 8.3;
RESULT 1090
ID ABL70294 standard; DNA; 6880 BP.
DE Chemically treated cell signalling DNA sequence complementary to#92.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6880;
Best Local Similarity 46.9%; Pred. No. 8.3;
RESULT 1091
ID AAS61224 standard; DNA; 6880 BP.
DE Human gene regulation-associated gene oligonucleotide #179.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 6880;
Best Local Similarity 46.9%; Pred. No. 8.3;
RESULT 1092
ID ABL32893 standard; DNA; 10710 BP.
DE Human immune system associated gene SEQ ID NO: 866.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 10710;
Best Local Similarity 46.0%; Pred. No. 10;
RESULT 1093
ID ADS89562 standard; DNA; 11029 BP.
DE Oligonucleotide of the invention SEQ ID NO:578.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 13; Length 11029;
Best Local Similarity 45.4%; Pred. No. 10;
RESULT 1094
ID ABL54326 standard; DNA; 11670 BP.
DE Chemically treated apoptosis gene complementary to gene #13.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 11670;
Best Local Similarity 46.0%; Pred. No. 10;
RESULT 1095
ID ABL33531 standard; DNA; 13712 BP.
DE Human immune system associated gene SEQ ID NO: 1504.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 13712;
Best Local Similarity 43.6%; Pred. No. 11;
RESULT 1096
ID ABL32729 standard; DNA; 14307 BP.
DE Human immune system associated gene SEQ ID NO: 702.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 14307;
Best Local Similarity 48.1%; Pred. No. 11;
RESULT 1097
ID ABL32467 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 440.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 15373;
Best Local Similarity 45.5%; Pred. No. 12;
RESULT 1098
ID ABL32625 standard; DNA; 16217 BP.
DE Human immune system associated gene SEQ ID NO: 598.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 16217;
Best Local Similarity 46.2%; Pred. No. 12;
RESULT 1099
ID ABL34027 standard; DNA; 17594 BP.
DE Human immune system associated gene SEQ ID NO: 2000.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 17594;
Best Local Similarity 49.1%; Pred. No. 13;
RESULT 1100
ID AAC58017 standard; DNA; 20674 BP.
DE Arachidonic acid metabolism related genomic biallelic marker #651.
PN WO200047771-A2.
PD 17-AUG-2000.
PA (GEST) GENSET.
Query Match 1.8%; Score 43.2; DB 3; Length 20674;
Best Local Similarity 50.0%; Pred. No. 13;
RESULT 1101
ID ABL70570 standard; DNA; 24939 BP.
DE Chemically treated cell signalling DNA sequence complementary to#230.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43.2; DB 6; Length 24939;
Best Local Similarity 46.2%; Pred. No. 15;
RESULT 1102
ID AAS16905 standard; DNA; 74586 BP.
DE Genomic DNA encoding human transporter polypeptide.
PN WO200181413-A2.
Query Match 1.8%; Score 43.2; DB 6; Length 74586;
Best Local Similarity 49.6%; Pred. No. 24;
RESULT 1103
ID ACN47472 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 43; DB 13; Length 560;
Best Local Similarity 45.4%; Pred. No. 3.1;
RESULT 1104
ID ABZ15647 standard; DNA; 1132 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3452.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 43; DB 6; Length 1132;
Best Local Similarity 47.6%; Pred. No. 4.2;
RESULT 1105
ID ADS89486 standard; DNA; 4001 BP.
DE Oligonucleotide of the invention SEQ ID NO:502.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 13; Length 4001;
Best Local Similarity 48.2%; Pred. No. 7.3;
RESULT 1106
ID ABL33266 standard; DNA; 5218 BP.
DE Human immune system associated gene SEQ ID NO: 1239.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 5218;
Best Local Similarity 48.5%; Pred. No. 8.2;
RESULT 1107
ID ABK33945 standard; DNA; 5942 BP.
DE Human DNA for staging of Astrocytomas, complement, #14.
PN WO200202808-A2.

PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1108
ID ABK31223 standard; DNA; 5942 BP.
DE Signal transduction associated gene modified complementary DNA #33.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1109
ID ABL70534 standard; DNA; 5942 BP.
DE Chemically treated cell signalling DNA sequence complementary to#212.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1110
ID AAS61135 standard; DNA; 5942 BP.
DE Human gene regulation-associated gene oligonucleotide #90.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1111
ID ABZ10002 standard; DNA; 5942 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #142.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1112
ID ABZ10234 standard; DNA; 5942 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #374.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1113
ID ABZ10088 standard; DNA; 5942 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #228.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1114
ID ABZ10148 standard; DNA; 5942 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #288.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1115
ID ADA20351 standard; DNA; 5942 BP.
DE Prostate tumour related genomic DNA complement sample #8.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1116
ID ADA84158 standard; DNA; 5942 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:16.
PN WO2002103041-A2.
PD 27-DEC-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 8; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1117
ID ADE84068 standard; DNA; 5942 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #4.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1118
ID ADE84144 standard; DNA; 5942 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #80.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 5942;
Best Local Similarity 47.2%; Pred. No. 8.7;
RESULT 1119
ID ABL33246 standard; DNA; 6077 BP.
DE Human immune system associated gene SEQ ID NO: 1219.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 6077;
Best Local Similarity 44.2%; Pred. No. 8.8;
RESULT 1120
ID AAS46573 standard; DNA; 6126 BP.
DE Tumour suppressor gene derived chemically modified sequence #295.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 4; Length 6126;
Best Local Similarity 45.2%; Pred. No. 8.8;
RESULT 1121
ID ABL33830 standard; DNA; 6126 BP.
DE Human immune system associated gene SEQ ID NO: 1803.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 6126;
Best Local Similarity 45.2%; Pred. No. 8.8;
RESULT 1122
ID AAS46498 standard; DNA; 6233 BP.
DE Tumour suppressor gene derived chemically modified sequence #220.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 4; Length 6233;
Best Local Similarity 49.0%; Pred. No. 8.9;
RESULT 1123
ID ABL32409 standard; DNA; 6317 BP.
DE Human immune system associated gene SEQ ID NO: 382.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 6317;
Best Local Similarity 43.4%; Pred. No. 8.9;
RESULT 1124
ID ABL49312 standard; DNA; 6317 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 12.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 6317;
Best Local Similarity 43.4%; Pred. No. 8.9;
RESULT 1125
ID ABK40057 standard; DNA; 7441 BP.
DE Human chemically pretreated gene sequence #70 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 43; DB 6; Length 7441;
Best Local Similarity 49.5%; Pred. No. 9.6;
RESULT 1126
ID AAS63344 standard; DNA; 7479 BP.
DE Chemically pretreated metabolism associated gene #39.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 7479;
Best Local Similarity 49.5%; Pred. No. 9.6;
RESULT 1127
ID AAS46760 standard; DNA; 7900 BP.
DE Tumour suppressor gene derived chemically modified sequence #484.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 4; Length 7900;
Best Local Similarity 44.6%; Pred. No. 9.9;
RESULT 1128
ID ABL33983 standard; DNA; 8592 BP.
DE Human immune system associated gene SEQ ID NO: 1956.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 8592;
Best Local Similarity 46.2%; Pred. No. 10;
RESULT 1129
ID ADS89411 standard; DNA; 8900 BP.
DE Oligonucleotide of the invention SEQ ID NO:427.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 13; Length 8900;
Best Local Similarity 48.2%; Pred. No. 10;
RESULT 1130
ID ABL32427 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 400.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 9810;
Best Local Similarity 46.1%; Pred. No. 11;
RESULT 1131
ID ABL92243 standard; DNA; 11787 BP.
DE Chemically treated DNA repair gene fragment complementary to#26.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 11787;
Best Local Similarity 45.0%; Pred. No. 12;
RESULT 1132
ID ADB54202 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 126.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 11787;
Best Local Similarity 45.0%; Pred. No. 12;
RESULT 1133
ID ABL33316 standard; DNA; 13574 BP.
DE Human immune system associated gene SEQ ID NO: 1289.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 13574;
Best Local Similarity 46.3%; Pred. No. 13;
RESULT 1134
ID ABL70459 standard; DNA; 16228 BP.
DE Chemically treated cell signalling DNA sequence#175.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 16228;

Best Local Similarity 45.9%; Pred. No. 14;
RESULT 1135
ID AAS61424 standard; DNA; 16228 BP.
DE Human gene regulation-associated gene oligonucleotide #379.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 16228;
Best Local Similarity 45.9%; Pred. No. 14;
RESULT 1136
ID ADB54118 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 42.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 16579;
Best Local Similarity 43.1%; Pred. No. 14;
RESULT 1137
ID ADE37763 standard; DNA; 16579 BP.
DE Human Chemically treated TPEF nucleotide sequence SEQ ID NO:9.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 16579;
Best Local Similarity 43.1%; Pred. No. 14;
RESULT 1138
ID ADS89274 standard; DNA; 16579 BP.
DE Oligonucleotide of the invention SEQ ID NO:290.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 13; Length 16579;
Best Local Similarity 43.1%; Pred. No. 14;
RESULT 1139
ID ABL32627 standard; DNA; 19082 BP.
DE Human immune system associated gene SEQ ID NO: 600.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 19082;
Best Local Similarity 44.3%; Pred. No. 15;
RESULT 1140
ID ABL32627 standard; DNA; 19082 BP.
DE Human immune system associated gene SEQ ID NO: 600.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 19082;
Best Local Similarity 53.6%; Pred. No. 15;
RESULT 1141
ID ABQ67124 standard; DNA; 20933 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 154.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 20933;
Best Local Similarity 44.3%; Pred. No. 15;
RESULT 1142
ID ADB37661 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:3.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 10; Length 29993;
Best Local Similarity 43.7%; Pred. No. 18;
RESULT 1143
ID ABQ67078 standard; DNA; 37184 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 108.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 37184;
Best Local Similarity 43.7%; Pred. No. 20;

RESULT 1144
ID AAS46746 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #470.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 4; Length 38342;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1145
ID ABK31507 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified complementary DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 43; DB 6; Length 38342;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1146
ID ABL56202 standard; DNA; 50000 BP.
DE AmEPV genome fragment#4.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 1.8%; Score 43; DB 6; Length 50000;
Best Local Similarity 46.5%; Pred. No. 22;
RESULT 1147
ID ADQ97764 standard; DNA; 79544 BP.
DE Human cancer associated sequence HD10-042, SEQ ID 741.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 43; DB 12; Length 79544;
Best Local Similarity 55.8%; Pred. No. 27;
RESULT 1148
ID ABZ16071 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3876.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 2000;
Best Local Similarity 54.4%; Pred. No. 6;
RESULT 1149
ID ABL32899 standard; DNA; 5204 BP.
DE Human immune system associated gene SEQ ID NO: 872.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 5204;
Best Local Similarity 47.6%; Pred. No. 9.2;
RESULT 1150
ID AAA70236 standard; DNA; 5454 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:369.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.8%; Score 42.8; DB 3; Length 5454;
Best Local Similarity 45.3%; Pred. No. 9.4;
RESULT 1151
ID ABQ67069 standard; DNA; 5611 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 99.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 5611;
Best Local Similarity 44.6%; Pred. No. 9.5;
RESULT 1152
ID ABL34086 standard; DNA; 5928 BP.
DE Human immune system associated gene SEQ ID NO: 2059.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 5928;
Best Local Similarity 50.8%; Pred. No. 9.8;
RESULT 1153
ID ABL32194 standard; DNA; 6208 BP.
DE Human immune system associated gene SEQ ID NO: 167.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 6208;
Best Local Similarity 44.1%; Pred. No. 10;
RESULT 1154
ID ABL32359 standard; DNA; 6237 BP.
DE Human immune system associated gene SEQ ID NO: 332.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 6237;
Best Local Similarity 46.9%; Pred. No. 10;
RESULT 1155
ID AAS45344 standard; DNA; 6815 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #25.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 4; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1156
ID ABL32670 standard; DNA; 6815 BP.
DE Human immune system associated gene SEQ ID NO: 643.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1157
ID ABK28175 standard; DNA; 6815 BP.
DE DNA transcription associated genomic DNA #25.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1158
ID ADB54195 standard; DNA; 6815 BP.
DE Pretreated genomic DNA region 119.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 10; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1159
ID ADB54323 standard; DNA; 6815 BP.
DE Pretreated genomic DNA region 247.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 10; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1160
ID ADE84207 standard; DNA; 6815 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #143.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 10; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1161
ID ADE84131 standard; DNA; 6815 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #67.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42.8; DB 10; Length 6815;
Best Local Similarity 51.6%; Pred. No. 10;
RESULT 1162
ID AAS46532 standard; DNA; 7008 BP.
DE Tumour suppressor gene derived chemically modified sequence #254.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 4; Length 7008;
Best Local Similarity 44.4%; Pred. No. 11;
RESULT 1163
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 7346;
Best Local Similarity 43.4%; Pred. No. 11;
RESULT 1164
ID ABK28131 standard; DNA; 7450 BP.
DE DNA transcription associated genomic DNA #3.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 7450;
Best Local Similarity 50.5%; Pred. No. 11;
RESULT 1165
ID ABL33761 standard; DNA; 7851 BP.
DE Human immune system associated gene SEQ ID NO: 1734.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 7851;
Best Local Similarity 45.2%; Pred. No. 11;
RESULT 1166
ID ABL32203 standard; DNA; 8246 BP.
DE Human immune system associated gene SEQ ID NO: 176.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 8246;
Best Local Similarity 46.7%; Pred. No. 11;
RESULT 1167
ID AAS45469 standard; DNA; 8588 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #87.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 4; Length 8588;
Best Local Similarity 49.1%; Pred. No. 11;
RESULT 1168
ID ABK28325 standard; DNA; 8588 BP.
DE DNA transcription associated genomic DNA #100.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 8588;
Best Local Similarity 49.1%; Pred. No. 11;
RESULT 1169
ID ABL33241 standard; DNA; 9888 BP.
DE Human immune system associated gene SEQ ID NO: 1214.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 9888;
Best Local Similarity 47.7%; Pred. No. 12;
RESULT 1170
ID ABL34241 standard; DNA; 11691 BP.
DE Human immune system associated gene SEQ ID NO: 2214.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 11691;

Best Local Similarity 45.5%; Pred. No. 13;
RESULT 1171
ID ABK28332 standard; DNA; 11745 BP.
DE DNA transcription associated complementary genomic DNA #103.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 11745;
Best Local Similarity 43.8%; Pred. No. 13;
RESULT 1172
ID ADB54256 standard; DNA; 12781 BP.
DE Pretreated genomic DNA region 180.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 10; Length 12781;
Best Local Similarity 43.8%; Pred. No. 14;
RESULT 1173
ID ABL32583 standard; DNA; 13376 BP.
DE Human immune system associated gene SEQ ID NO: 556.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 13376;
Best Local Similarity 46.8%; Pred. No. 14;
RESULT 1174
ID AAS45415 standard; DNA; 14649 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #60.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 4; Length 14649;
Best Local Similarity 47.3%; Pred. No. 15;
RESULT 1175
ID ABK28268 standard; DNA; 14649 BP.
DE DNA transcription associated complementary genomic DNA #71.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 14649;
Best Local Similarity 47.3%; Pred. No. 15;
RESULT 1176
ID ABK31170 standard; DNA; 17293 BP.
DE Signal transduction associated gene modified DNA #7.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 17293;
Best Local Similarity 44.5%; Pred. No. 16;
RESULT 1177
ID ABL70125 standard; DNA; 17293 BP.
DE Chemically treated cell signalling DNA sequence#8.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 17293;
Best Local Similarity 44.5%; Pred. No. 16;
RESULT 1178
ID AAS61057 standard; DNA; 17293 BP.
DE Human gene regulation-associated gene oligonucleotide #12.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.8; DB 6; Length 17293;
Best Local Similarity 44.5%; Pred. No. 16;
RESULT 1179
ID ABA92787 standard; DNA; 640681 BP.
DE Buchnera sp. genomic DNA SEQ ID NO:1.
PN JP2001292771-A.
PD 23-OCT-2001.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 1.8%; Score 42.8; DB 6; Length 110000;
Best Local Similarity 56.3%; Pred. No. 35;

RESULT 1180
ID ABQ88198 standard; cDNA; 154902 BP.
DE Human osteoblast differentiation related cdNA SEQ ID NO 105.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 1.8%; Score 42.8; DB 6; Length 154902;
Best Local Similarity 45.6%; Pred. No. 41;
RESULT 1181
ID ABV46406 standard; cDNA; 535 BP.
DE Human prostate expression marker cDNA 46397.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 42.6; DB 5; Length 535;
Best Local Similarity 51.9%; Pred. No. 3.8;
RESULT 1182
ID AA59475 standard; DNA; 1117 BP.
DE Nucleotide sequence of a soybean type III glutathione-S-transferase.
PN WO200047728-A2.
PD 17-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.8%; Score 42.6; DB 3; Length 1117;
Best Local Similarity 50.2%; Pred. No. 5.2;
RESULT 1183
ID AAA97037 standard; DNA; 2486 BP.
DE Nucleotide sequence encoding 48kD i-antigen.
PN WO200046373-A1.
PD 10-AUG-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
PA (LINT/) LIN T.
Query Match 1.8%; Score 42.6; DB 3; Length 2486;
Best Local Similarity 46.4%; Pred. No. 7.5;
RESULT 1184
ID ABK33946 standard; DNA; 2580 BP.
DE Human DNA for staging of Astrocytomas #15.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 2580;
Best Local Similarity 52.5%; Pred. No. 7.6;
RESULT 1185
ID ADA20402 standard; DNA; 2580 BP.
DE Prostate tumour related genomic DNA sample #34.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 2580;
Best Local Similarity 52.5%; Pred. No. 7.6;
RESULT 1186
ID AD484209 standard; DNA; 2580 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:67.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 2580;
Best Local Similarity 52.5%; Pred. No. 7.6;
RESULT 1187
ID AB210191 standard; DNA; 3287 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #331.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 3287;
Best Local Similarity 44.4%; Pred. No. 8.4;
RESULT 1188
ID ABL33066 standard; DNA; 5107 BP.
DE Human immune system associated gene SEQ ID NO: 1039.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5107;
Best Local Similarity 51.3%; Pred. No. 10;
RESULT 1189
ID ABL32348 standard; DNA; 5145 BP.
DE Human immune system associated gene SEQ ID NO: 321.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5145;
Best Local Similarity 46.7%; Pred. No. 10;
RESULT 1190
ID ABL34464 standard; DNA; 5145 BP.
DE Human metastasis associated gene SEQ ID NO: 17.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5145;
Best Local Similarity 46.7%; Pred. No. 10;
RESULT 1191
ID ADS99725 standard; DNA; 5145 BP.
DE Bisulphite treated human gene associated with metastasis #9.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 42.6; DB 7; Length 5145;
Best Local Similarity 46.7%; Pred. No. 10;
RESULT 1192
ID ABL34021 standard; DNA; 5542 BP.
DE Human immune system associated gene SEQ ID NO: 1994.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5542;
Best Local Similarity 58.1%; Pred. No. 11;
RESULT 1193
ID ABL33577 standard; DNA; 5925 BP.
DE Human immune system associated gene SEQ ID NO: 1550.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5925;
Best Local Similarity 48.2%; Pred. No. 11;
RESULT 1194
ID ABL32708 standard; DNA; 5929 BP.
DE Human immune system associated gene SEQ ID NO: 681.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 5929;
Best Local Similarity 46.9%; Pred. No. 11;
RESULT 1195
ID AAS46337 standard; DNA; 6063 BP.
DE Tumour suppressor gene derived chemically modified sequence #59.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 4; Length 6063;
Best Local Similarity 45.9%; Pred. No. 11;
RESULT 1196
ID ABL70595 standard; DNA; 6075 BP.
DE Chemically treated cell signalling DNA sequence#243.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6075;
Best Local Similarity 53.6%; Pred. No. 11;
RESULT 1197
ID AAS61316 standard; DNA; 6075 BP.
DE Human gene regulation-associated gene oligonucleotide #271.

PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6075;
Best Local Similarity 53.6%; Pred. No. 11;
RESULT 1198
ID ABL70590 standard; DNA; 6129 BP.
DE Chemically treated cell signalling DNA sequence complementary to#240.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6129;
Best Local Similarity 49.8%; Pred. No. 11;
RESULT 1199
ID AAS61301 standard; DNA; 6129 BP.
DE Human gene regulation-associated gene oligonucleotide #256.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6129;
Best Local Similarity 49.8%; Pred. No. 11;
RESULT 1200
ID ABL33307 standard; DNA; 6175 BP.
DE Human immune system associated gene SEQ ID NO: 1280.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6175;
Best Local Similarity 44.4%; Pred. No. 11;
RESULT 1201
ID ABL33393 standard; DNA; 6494 BP.
DE Human immune system associated gene SEQ ID NO: 1366.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6494;
Best Local Similarity 45.8%; Pred. No. 11;
RESULT 1202
ID AAD28391 standard; DNA; 6494 BP.
DE Human chemically treated genomic DNA #32.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6494;
Best Local Similarity 45.8%; Pred. No. 11;
RESULT 1203
ID ABL33709 standard; DNA; 6533 BP.
DE Human immune system associated gene SEQ ID NO: 1682.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 6533;
Best Local Similarity 46.2%; Pred. No. 11;
RESULT 1204
ID ABL33815 standard; DNA; 7312 BP.
DE Human immune system associated gene SEQ ID NO: 1788.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 7312;
Best Local Similarity 44.6%; Pred. No. 12;
RESULT 1205
ID ABL70402 standard; DNA; 7312 BP.
DE Chemically treated cell signalling DNA sequence complementary to#146.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 7312;
Best Local Similarity 44.6%; Pred. No. 12;
RESULT 1206
ID AAS61350 standard; DNA; 7312 BP.
DE Human gene regulation-associated gene oligonucleotide #305.
PN WO200177375-A2.

PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 7312;
Best Local Similarity 44.6%; Pred. No. 12;
RESULT 1207
ID AAS46436 standard; DNA; 8093 BP.
DE Tumour suppressor gene derived chemically modified sequence #158.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 4; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1208
ID ABK33974 standard; DNA; 8093 BP.
DE Human DNA for staging of Astrocytomas, complement, #29.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1209
ID ABL92237 standard; DNA; 8093 BP.
DE Chemically treated DNA repair gene fragment complementary to#23.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1210
ID ABL49332 standard; DNA; 8093 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 32.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1211
ID ABZ10032 standard; DNA; 8093 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #172.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1212
ID ADA20361 standard; DNA; 8093 BP.
DE Prostate tumour related genomic DNA complement sample #13.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1213
ID ADAB4168 standard; DNA; 8093 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:26.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1214
ID ADB54140 standard; DNA; 8093 BP.
DE Pretreated genomic DNA region 64.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 8; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1215
ID ADE84114 standard; DNA; 8093 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #50.
PN WO2003044226-A2.
PD 30-MAY-2003.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 10; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1216
ID ADS89292 standard; DNA; 8093 BP.
DE Oligonucleotide of the invention SEQ ID NO:308.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 13; Length 8093;
Best Local Similarity 47.2%; Pred. No. 13;
RESULT 1217
ID ABL33491 standard; DNA; 8392 BP.
DE Human immune system associated gene SEQ ID NO: 1464.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 8392;
Best Local Similarity 44.1%; Pred. No. 13;
RESULT 1218
ID ABL32990 standard; DNA; 9731 BP.
DE Human immune system associated gene SEQ ID NO: 963.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 9731;
Best Local Similarity 58.1%; Pred. No. 14;
RESULT 1219
ID ADF50895 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 3).
PN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 10; Length 11097;
Best Local Similarity 45.0%; Pred. No. 14;
RESULT 1220
ID ADF50897 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 5).
PN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 10; Length 11097;
Best Local Similarity 45.0%; Pred. No. 14;
RESULT 1221
ID AAS46698 standard; DNA; 11694 BP.
DE Tumour suppressor gene derived chemically modified sequence #421.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 4; Length 11694;
Best Local Similarity 45.7%; Pred. No. 15;
RESULT 1222
ID ABL34493 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 46.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 11996;
Best Local Similarity 48.2%; Pred. No. 15;
RESULT 1223
ID ADS99754 standard; DNA; 11996 BP.
DE Complement of bisulphite treated metastasis-associated human gene #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 42.6; DB 7; Length 11996;
Best Local Similarity 48.2%; Pred. No. 15;
RESULT 1224
ID AAS45331 standard; DNA; 12405 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #18.
PN WO200168911-A2.

PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 4; Length 12405;
Best Local Similarity 44.3%; Pred. No. 15;
RESULT 1225
ID ABK28170 standard; DNA; 12405 BP.
DE DNA transcription associated complementary genomic DNA #22.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 12405;
Best Local Similarity 44.3%; Pred. No. 15;
RESULT 1226
ID AAS61144 standard; DNA; 12405 BP.
DE Human gene regulation-associated gene oligonucleotide #99.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 12405;
Best Local Similarity 44.3%; Pred. No. 15;
RESULT 1227
ID ABN80146 standard; DNA; 14920 BP.
DE Human chemically modified disease associated gene SEQ ID NO 163.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 6; Length 14920;
Best Local Similarity 47.9%; Pred. No. 16;
RESULT 1228
ID AAS46665 standard; DNA; 17144 BP.
DE Tumour suppressor gene derived chemically modified sequence #387.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.6; DB 4; Length 17144;
Best Local Similarity 52.5%; Pred. No. 17;
RESULT 1229
ID ADP84152 standard; DNA; 42347 BP.
DE Human CAL25 genomic DNA extracellular repeat sequence SeqID 2.
Query Match 1.8%; Score 42.6; DB 12; Length 42347;
Best Local Similarity 46.2%; Pred. No. 26;
RESULT 1230
ID AAL48890 standard; DNA; 53332 BP.
DE Human Pftaire family kinase gene.
PN WO200261060-A2.
PD 08-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 42.6; DB 6; Length 53332;
Best Local Similarity 45.2%; Pred. No. 29;
RESULT 1231
ID AAI61370 standard; DNA; 127197 BP.
DE Soybean 515O02 region G2, SEQ ID NO: 1.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 1.8%; Score 42.6; DB 5; Length 127197;
Best Local Similarity 47.0%; Pred. No. 42;
RESULT 1232
ID ADL11800 standard; cDNA; 275 BP.
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #2205.
PN US2004067516-A1.
PD 08-APR-2004.
PA (BRAN/) BRANDT K S.
PA (GAIN/) GAINES P J.
PA (STIN/) STINCHCOMB D T.
PA (WISN/) WISNEWSKI N.
Query Match 1.8%; Score 42.4; DB 12; Length 275;
Best Local Similarity 49.1%; Pred. No. 3.2;
RESULT 1233
ID ADL11674 standard; cDNA; 549 BP.
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #2079.
PN US2004067516-A1.
PD 08-APR-2004.

PA (BRAN/) BRANDT K S.
PA (GAIN/) GAINES P J.
PA (STIN/) STINCHCOMB D T.
PA (WISN/) WISNEWSKI N.
Query Match 1.8%; Score 42.4; DB 12; Length 549;
Best Local Similarity 46.0%; Pred. No. 4.3;
RESULT 1234
ID ACN45312 standard; cDNA; 552 BP.
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-C5, SEQ:93.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 42.4; DB 13; Length 552;
Best Local Similarity 41.7%; Pred. No. 4.3;
RESULT 1235
ID ADR01846 standard; DNA; 828 BP.
DE A. gossypii genomic DNA PAG1375RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.4; DB 2; Length 828;
Best Local Similarity 48.7%; Pred. No. 5.2;
RESULT 1236
ID ADP10611 standard; DNA; 1843 BP.
DE Reference mRNA sequences for marker probe #288.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 1.8%; Score 42.4; DB 12; Length 1843;
Best Local Similarity 51.0%; Pred. No. 7.3;
RESULT 1237
ID ABL21456 standard; DNA; 4377 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15841.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 42.4; DB 4; Length 4377;
Best Local Similarity 44.6%; Pred. No. 11;
RESULT 1238
ID ABX63337 standard; cDNA; 4537 BP.
DE Human cDNA #337 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 1.8%; Score 42.4; DB 8; Length 4537;
Best Local Similarity 60.3%; Pred. No. 11;
RESULT 1239
ID ABL32258 standard; DNA; 6079 BP.
DE Human immune system associated gene SEQ ID NO: 231.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 6079;
Best Local Similarity 45.7%; Pred. No. 12;
RESULT 1240
ID ABL33366 standard; DNA; 6104 BP.
DE Human immune system associated gene SEQ ID NO: 1339.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 6104;
Best Local Similarity 48.1%; Pred. No. 12;
RESULT 1241
ID AAS46344 standard; DNA; 6179 BP.
DE Tumour suppressor gene derived chemically modified sequence #66.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 4; Length 6179;
Best Local Similarity 45.3%; Pred. No. 13;

RESULT 1242
ID ABK31251 standard; DNA; 6179 BP.
DE Signal transduction associated gene modified complementary DNA #47.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 6179;
Best Local Similarity 45.3%; Pred. No. 13;
RESULT 1243
ID AAS46498 standard; DNA; 6233 BP.
DE Tumour suppressor gene derived chemically modified sequence #220.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 4; Length 6233;
Best Local Similarity 49.5%; Pred. No. 13;
RESULT 1244
ID ABL32089 standard; DNA; 6283 BP.
DE Human immune system associated gene SEQ ID NO: 62.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 6283;
Best Local Similarity 44.6%; Pred. No. 13;
RESULT 1245
ID AAS46591 standard; DNA; 6286 BP.
DE Tumour suppressor gene derived chemically modified sequence #313.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 4; Length 6286;
Best Local Similarity 44.2%; Pred. No. 13;
RESULT 1246
ID AAS46735 standard; DNA; 6292 BP.
DE Tumour suppressor gene derived chemically modified sequence #459.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 4; Length 6292;
Best Local Similarity 46.8%; Pred. No. 13;
RESULT 1247
ID ABL49326 standard; DNA; 6583 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 26.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 6583;
Best Local Similarity 51.0%; Pred. No. 13;
RESULT 1248
ID ABK39996 standard; DNA; 7108 BP.
DE Human chemically pretreated gene sequence #39 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 7108;
Best Local Similarity 47.1%; Pred. No. 13;
RESULT 1249
ID ABL33989 standard; DNA; 8238 BP.
DE Human immune system associated gene SEQ ID NO: 1962.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 8238;
Best Local Similarity 45.6%; Pred. No. 14;
RESULT 1250
ID AAS63349 standard; DNA; 8238 BP.
DE Chemically pretreated metabolism associated gene #44.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 8238;
Best Local Similarity 45.6%; Pred. No. 14;
RESULT 1251

ID AAK86270 standard; DNA; 9706 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 42.4; DB 4; Length 9706;
Best Local Similarity 44.9%; Pred. No. 15;
RESULT 1252
ID ABK31243 standard; DNA; 9760 BP.
DE Signal transduction associated gene modified complementary DNA #43.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 9760;
Best Local Similarity 47.9%; Pred. No. 15;
RESULT 1253
ID ABL70198 standard; DNA; 9760 BP.
DE Chemically treated cell signalling DNA sequence complementary to#44.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 9760;
Best Local Similarity 47.9%; Pred. No. 15;
RESULT 1254
ID AAS61156 standard; DNA; 9760 BP.
DE Human gene regulation-associated gene oligonucleotide #111.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 9760;
Best Local Similarity 47.9%; Pred. No. 15;
RESULT 1255
ID ABL33263 standard; DNA; 12393 BP.
DE Human immune system associated gene SEQ ID NO: 1236.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 12393;
Best Local Similarity 44.0%; Pred. No. 17;
RESULT 1256
ID ABK40038 standard; DNA; 16258 BP.
DE Human chemically pretreated gene sequence #60 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 16258;
Best Local Similarity 44.1%; Pred. No. 19;
RESULT 1257
ID ABL70376 standard; DNA; 16258 BP.
DE Chemically treated cell signalling DNA sequence complementary to#133.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 16258;
Best Local Similarity 44.1%; Pred. No. 19;
RESULT 1258
ID ABL32619 standard; DNA; 16373 BP.
DE Human immune system associated gene SEQ ID NO: 592.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 16373;
Best Local Similarity 44.1%; Pred. No. 19;
RESULT 1259
ID AAD28383 standard; DNA; 16373 BP.
DE Human chemically treated genomic DNA #24.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 16373;
Best Local Similarity 44.1%; Pred. No. 19;
RESULT 1260
ID ABL32387 standard; DNA; 18598 BP.

DE Human immune system associated gene SEQ ID NO: 360.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 18598;
Best Local Similarity 52.2%; Pred. No. 20;
RESULT 1261
ID ABL34495 standard; DNA; 18817 BP.
DE Human metastasis associated gene SEQ ID NO: 48.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 18817;
Best Local Similarity 46.1%; Pred. No. 20;
RESULT 1262
ID ABL70162 standard; DNA; 18817 BP.
DE Chemically treated cell signalling DNA sequence complementary to#26.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 18817;
Best Local Similarity 46.1%; Pred. No. 20;
RESULT 1263
ID ADS99756 standard; DNA; 18817 BP.
DE Complement of bisulphite treated metastasis-associated human gene #24.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 42.4; DB 7; Length 18817;
Best Local Similarity 46.1%; Pred. No. 20;
RESULT 1264
ID ABQ67059 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 34688;
Best Local Similarity 48.6%; Pred. No. 27;
RESULT 1265
ID ABQ66998 standard; DNA; 37515 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 28.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 37515;
Best Local Similarity 45.5%; Pred. No. 28;
RESULT 1266
ID ABD32684 standard; DNA; 41991 BP.
DE Human cancer-associated genomic DNA HD13-117.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 42.4; DB 13; Length 41991;
Best Local Similarity 44.9%; Pred. No. 29;
RESULT 1267
ID ABL34175 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2148.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.4; DB 6; Length 113515;
Best Local Similarity 45.7%; Pred. No. 45;
RESULT 1268
ID ADO43653 standard; DNA; 127432 BP.
DE Nucleotide sequence of BAC-64.
PN WO2004039988-A1.
PD 13-MAY-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 1.8%; Score 42.4; DB 12; Length 127432;
Best Local Similarity 45.3%; Pred. No. 47;
RESULT 1269

ID AAQ04525 standard; DNA; 134525 BP.
DE Total base sequence of rice plant chloroplast DNA.
PN JP02100682-A.
PD 12-APR-1990.
PA (MITK) MITSUI TOATSU CHEM INC.
Query Match 1.8%; Score 42.4; DB 2; Length 134525;
Best Local Similarity 49.5%; Pred. No. 49;
RESULT 1270
ID ADS36467 standard; DNA; 154799 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1681.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 42.4; DB 13; Length 154799;
Best Local Similarity 46.4%; Pred. No. 52;
RESULT 1271
ID ADL37508 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #11398.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 42.2; DB 5; Length 294;
Best Local Similarity 47.7%; Pred. No. 3.7;
RESULT 1272
ID ADI72364 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #5106.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 42.2; DB 5; Length 294;
Best Local Similarity 47.7%; Pred. No. 3.7;
RESULT 1273
ID ACN53339 standard; cDNA; 537 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-D9, SEQ:8120.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 42.2; DB 13; Length 537;
Best Local Similarity 43.2%; Pred. No. 4.8;
RESULT 1274
ID ACN47472 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 42.2; DB 13; Length 560;
Best Local Similarity 51.3%; Pred. No. 4.9;
RESULT 1275
ID AAL14642 standard; cDNA; 796 BP.
DE Human breast cancer expressed polynucleotide 7099.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 42.2; DB 4; Length 796;
Best Local Similarity 48.0%; Pred. No. 5.7;
RESULT 1276
ID ACN84679 standard; DNA; 839 BP.
DE Breast cancer related marker, seq id 5829.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 42.2; DB 11; Length 839;
Best Local Similarity 48.0%; Pred. No. 5.8;
RESULT 1277
ID ADA69044 standard; DNA; 2000 BP.
DE Arabidopsis thaliana gene, SEQ ID 2367.
PN WO2003000898-A1.

PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42.2; DB 8; Length 2000;
Best Local Similarity 51.0%; Pred. No. 8.5;
RESULT 1278
ID ADB54244 standard; DNA; 2501 BP.
DE Pretreated genomic DNA region 168.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 10; Length 2501;
Best Local Similarity 46.4%; Pred. No. 9.4;
RESULT 1279
ID ADS89546 standard; DNA; 2501 BP.
DE Oligonucleotide of the invention SEQ ID NO:562.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 13; Length 2501;
Best Local Similarity 46.4%; Pred. No. 9.4;
RESULT 1280
ID ABL32801 standard; DNA; 5070 BP.
DE Human immune system associated gene SEQ ID NO: 774.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 5070;
Best Local Similarity 47.9%; Pred. No. 13;
RESULT 1281
ID ABN80030 standard; DNA; 5942 BP.
DE Human chemically modified disease associated gene SEQ ID NO 47.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 5942;
Best Local Similarity 56.2%; Pred. No. 14;
RESULT 1282
ID ABK31361 standard; DNA; 6013 BP.
DE Signal transduction associated gene modified complementary DNA #102.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 6013;
Best Local Similarity 46.2%; Pred. No. 14;
RESULT 1283
ID AAS61265 standard; DNA; 6013 BP.
DE Human gene regulation-associated gene oligonucleotide #220.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 6013;
Best Local Similarity 46.2%; Pred. No. 14;
RESULT 1284
ID AAS61405 standard; DNA; 6014 BP.
DE Human gene regulation-associated gene oligonucleotide #360.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 6014;
Best Local Similarity 44.1%; Pred. No. 14;
RESULT 1285
ID ABL32421 standard; DNA; 6079 BP.
DE Human immune system associated gene SEQ ID NO: 394.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 6079;
Best Local Similarity 48.5%; Pred. No. 14;
RESULT 1286
ID AAS46449 standard; DNA; 6337 BP.
DE Tumour suppressor gene derived chemically modified sequence #171.
PN WO200168912-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 4; Length 6337;
Best Local Similarity 47.3%; Pred. No. 14;
RESULT 1287
ID ABL33310 standard; DNA; 6337 BP.
DE Human immune system associated gene SEQ ID NO: 1283.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 6337;
Best Local Similarity 47.3%; Pred. No. 14;
RESULT 1288
ID AAS46336 standard; DNA; 7348 BP.
DE Tumour suppressor gene derived chemically modified sequence #58.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 4; Length 7348;
Best Local Similarity 45.0%; Pred. No. 15;
RESULT 1289
ID ABX77219 standard; DNA; 10094 BP.
DE 5' sequence flanking human MDR1 contig.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Query Match 1.8%; Score 42.2; DB 10; Length 10094;
Best Local Similarity 49.9%; Pred. No. 17;
RESULT 1290
ID AAS45315 standard; DNA; 11260 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #10.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 4; Length 11260;
Best Local Similarity 44.1%; Pred. No. 18;
RESULT 1291
ID ABX28154 standard; DNA; 11260 BP.
DE DNA transcription associated complementary genomic DNA #14.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 11260;
Best Local Similarity 44.1%; Pred. No. 18;
RESULT 1292
ID ABN80039 standard; DNA; 11260 BP.
DE Human chemically modified disease associated gene SEQ ID NO 56.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 11260;
Best Local Similarity 44.1%; Pred. No. 18;
RESULT 1293
ID ABL33943 standard; DNA; 12138 BP.
DE Human immune system associated gene SEQ ID NO: 1916.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 12138;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1294
ID ABX28336 standard; DNA; 12138 BP.
DE DNA transcription associated complementary genomic DNA #105.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 12138;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1295
ID AAS63312 standard; DNA; 12409 BP.
DE Chemically pretreated metabolism associated gene #7.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42.2; DB 6; Length 12409;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1296
ID ABL32298 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 271.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 12507;
Best Local Similarity 45.7%; Pred. No. 19;
RESULT 1297
ID ABL70458 standard; DNA; 15161 BP.
DE Chemically treated cell signalling DNA sequence complementary to#174.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 15161;
Best Local Similarity 48.8%; Pred. No. 21;
RESULT 1298
ID AAS61423 standard; DNA; 15161 BP.
DE Human gene regulation-associated gene oligonucleotide #378.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 15161;
Best Local Similarity 48.8%; Pred. No. 21;
RESULT 1299
ID ABL32466 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 439.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 15373;
Best Local Similarity 48.2%; Pred. No. 21;
RESULT 1300
ID ABL33157 standard; DNA; 17538 BP.
DE Human immune system associated gene SEQ ID NO: 1130.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 17538;
Best Local Similarity 44.0%; Pred. No. 22;
RESULT 1301
ID ABL32571 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 544.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 18997;
Best Local Similarity 51.0%; Pred. No. 23;
RESULT 1302
ID ABK33949 standard; DNA; 18997 BP.
DE Human DNA for staging of Astrocytomas, complement, #16.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 18997;
Best Local Similarity 51.0%; Pred. No. 23;
RESULT 1303
ID ADA20353 standard; DNA; 18997 BP.
DE Prostate tumour related genomic DNA complement sample #9.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 8; Length 18997;
Best Local Similarity 51.0%; Pred. No. 23;
RESULT 1304
ID ADA84160 standard; DNA; 18997 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:18.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 8; Length 18997;
Best Local Similarity 51.0%; Pred. No. 23;

Best Local Similarity 51.0%; Pred. No. 23;
RESULT 1305
ID ABL33451 standard; DNA; 19787 BP.
DE Human immune system associated gene SEQ ID NO: 1424.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 19787;
Best Local Similarity 42.5%; Pred. No. 23;
RESULT 1306
ID ADB37661 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:3.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 10; Length 29993;
Best Local Similarity 46.7%; Pred. No. 28;
RESULT 1307
ID AAS46746 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #470.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 4; Length 38342;
Best Local Similarity 46.7%; Pred. No. 31;
RESULT 1308
ID ABK31507 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified complementary DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42.2; DB 6; Length 38342;
Best Local Similarity 46.7%; Pred. No. 31;
RESULT 1309
ID ACN44642 standard; DNA; 69081 BP.
DE Human genomic sequence hCG17195.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 42.2; DB 11; Length 69081;
Best Local Similarity 46.6%; Pred. No. 41;
RESULT 1310
ID ABD33611 standard; DNA; 89567 BP.
DE Human cancer-associated (CA) gene HD07-124.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 42.2; DB 13; Length 89567;
Best Local Similarity 45.3%; Pred. No. 46;
RESULT 1311
Query Match 1.8%; Score 42.2; DB 2; Length 110000;
Best Local Similarity 47.5%; Pred. No. 50;
RESULT 1312
ID ACF62751 standard; DNA; 177380 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 1.8%; Score 42.2; DB 8; Length 177380;
Best Local Similarity 49.9%; Pred. No. 62;
RESULT 1313
ID ADB20870 standard; DNA; 177380 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 1.8%; Score 42.2; DB 8; Length 177380;
Best Local Similarity 49.9%; Pred. No. 62;
RESULT 1314
ID ADB87959 standard; DNA; 177380 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:683.
PN WO2003013536-A2.
PD 20-FEB-2003.

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 1.8%; Score 42.2; DB 10; Length 177380;
Best Local Similarity 49.9%; Pred. No. 62;
RESULT 1315
ID ADB96942 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 1.8%; Score 42.2; DB 10; Length 177380;
Best Local Similarity 49.9%; Pred. No. 62;
RESULT 1316
ID ADB92133 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 1.8%; Score 42.2; DB 10; Length 177380;
Best Local Similarity 49.9%; Pred. No. 62;
RESULT 1317
ID ADR02445 standard; DNA; 636 BP.
DE A. Gossypii genomic DNA PAG1692RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 42; DB 2; Length 636;
Best Local Similarity 44.8%; Pred. No. 5.8;
RESULT 1318
ID AAX00617 standard; DNA; 683 BP.
DE Human secreted protein gene 7 clone HBHBL77.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 42; DB 2; Length 683;
Best Local Similarity 47.7%; Pred. No. 6;
RESULT 1319
ID AAI97306 standard; cDNA; 804 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3381.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 1.8%; Score 42; DB 4; Length 804;
Best Local Similarity 43.8%; Pred. No. 6.4;
RESULT 1320
ID AAC59297 standard; cDNA; 887 BP.
DE Human secreted protein cDNA #21.
PN WO200056753-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 42; DB 3; Length 887;
Best Local Similarity 47.4%; Pred. No. 6.7;
RESULT 1321
ID AAZ37079 standard; DNA; 1431 BP.
DE DNA sequence encoding a modified yeast SceI endonuclease.
PN EP972836-A2.
PD 19-JAN-2000.
PA (RIKA) INST PHYSICAL & CHEM RES.
Query Match 1.8%; Score 42; DB 3; Length 1431;
Best Local Similarity 45.9%; Pred. No. 8.3;
RESULT 1322
ID ABS67963 standard; DNA; 1431 BP.
DE Platelet activating factor acetylhydrolase (PAF-AH) DNA.
PN US2002102231-A1.
PD 01-AUG-2002.
PA (ICOS-) ICOS CORP.
Query Match 1.8%; Score 42; DB 6; Length 1431;
Best Local Similarity 45.9%; Pred. No. 8.3;
RESULT 1323
ID ADG34448 standard; DNA; 1431 BP.
DE Platelet activating factor associated Yeast DNA sequence.
PN US2003215439-A1.
PD 20-NOV-2003.

PA (DIET/) DIETSCH G N.
PA (PETE/) PETERMAN G M.
PA (YUAS/) YU A S.
Query Match 1.8%; Score 42; DB 10; Length 1431;
Best Local Similarity 45.9%; Pred. No. 8.3;
RESULT 1324
ID ACC60976 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 734.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 1.8%; Score 42; DB 10; Length 2000;
Best Local Similarity 50.5%; Pred. No. 9.6;
RESULT 1325
ID ADK62537 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #394.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 1.8%; Score 42; DB 10; Length 2000;
Best Local Similarity 50.5%; Pred. No. 9.6;
RESULT 1326
ID ADQ63205 standard; cDNA; 3708 BP.
DE Novel human cDNA sequence #366.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 42; DB 12; Length 3708;
Best Local Similarity 50.8%; Pred. No. 13;
RESULT 1327
ID ABL34109 standard; DNA; 5467 BP.
DE Human immune system associated gene SEQ ID NO: 2082.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 5467;
Best Local Similarity 45.3%; Pred. No. 15;
RESULT 1328
ID ABL33773 standard; DNA; 5666 BP.
DE Human immune system associated gene SEQ ID NO: 1746.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 5666;
Best Local Similarity 47.7%; Pred. No. 15;
RESULT 1329
ID AAS61186 standard; DNA; 5666 BP.
DE Human gene regulation-associated gene oligonucleotide #141.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 5666;
Best Local Similarity 45.8%; Pred. No. 15;
RESULT 1330
ID ABL49329 standard; DNA; 5666 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 29.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 5666;
Best Local Similarity 45.8%; Pred. No. 15;
RESULT 1331
ID ADA20417 standard; DNA; 5881 BP.
DE Prostate tumour related genomic DNA complement sample #41.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 8; Length 5881;
Best Local Similarity 43.9%; Pred. No. 15;
RESULT 1332
ID ADA84224 standard; DNA; 5881 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:82.
PN WO2002103041-A2.

PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 8; Length 5881;
Best Local Similarity 43.9%; Pred. No. 15;
RESULT 1333
ID ABL33614 standard; DNA; 6127 BP.
DE Human immune system associated gene SEQ ID NO: 1587.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6127;
Best Local Similarity 46.7%; Pred. No. 16;
RESULT 1334
ID ABL32891 standard; DNA; 6131 BP.
DE Human immune system associated gene SEQ ID NO: 864.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6131;
Best Local Similarity 45.5%; Pred. No. 16;
RESULT 1335
ID AAS46644 standard; DNA; 6261 BP.
DE Tumour suppressor gene derived chemically modified sequence #366.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 4; Length 6261;
Best Local Similarity 49.5%; Pred. No. 16;
RESULT 1336
ID ABK31161 standard; DNA; 6261 BP.
DE Signal transduction associated gene modified complementary DNA #2.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6261;
Best Local Similarity 49.5%; Pred. No. 16;
RESULT 1337
ID ABL33872 standard; DNA; 6270 BP.
DE Human immune system associated gene SEQ ID NO: 1845.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6270;
Best Local Similarity 59.3%; Pred. No. 16;
RESULT 1338
ID ABN80070 standard; DNA; 6325 BP.
DE Human chemically modified disease associated gene SEQ ID NO 87.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6325;
Best Local Similarity 45.3%; Pred. No. 16;
RESULT 1339
ID ABK31188 standard; DNA; 6509 BP.
DE Signal transduction associated gene modified DNA #16.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6509;
Best Local Similarity 44.8%; Pred. No. 16;
RESULT 1340
ID AAS61085 standard; DNA; 6509 BP.
DE Human gene regulation-associated gene oligonucleotide #40.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6509;
Best Local Similarity 44.8%; Pred. No. 16;
RESULT 1341
ID ABL32639 standard; DNA; 6650 BP.
DE Human immune system associated gene SEQ ID NO: 612.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6650;
Best Local Similarity 47.0%; Pred. No. 16;
RESULT 1342
ID ABL32155 standard; DNA; 6681 BP.
DE Human immune system associated gene SEQ ID NO: 128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6681;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 1343
ID ABL32155 standard; DNA; 6681 BP.
DE Human immune system associated gene SEQ ID NO: 128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6681;
Best Local Similarity 45.3%; Pred. No. 16;
RESULT 1344
ID ABL54304 standard; DNA; 6681 BP.
DE Chemically treated apoptosis gene complementary to gene #2.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6681;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 1345
ID ABL54304 standard; DNA; 6681 BP.
DE Chemically treated apoptosis gene complementary to gene #2.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6681;
Best Local Similarity 45.3%; Pred. No. 16;
RESULT 1346
ID ABL32453 standard; DNA; 6980 BP.
DE Human immune system associated gene SEQ ID NO: 426.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 6980;
Best Local Similarity 48.4%; Pred. No. 17;
RESULT 1347
ID ABK31451 standard; DNA; 7131 BP.
DE Signal transduction associated gene modified complementary DNA #147.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7131;
Best Local Similarity 65.3%; Pred. No. 17;
RESULT 1348
ID ABL70428 standard; DNA; 7131 BP.
DE Chemically treated cell signalling DNA sequence complementary to#159.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7131;
Best Local Similarity 65.3%; Pred. No. 17;
RESULT 1349
ID AAS61361 standard; DNA; 7131 BP.
DE Human gene regulation-associated gene oligonucleotide #316.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7131;
Best Local Similarity 65.3%; Pred. No. 17;
RESULT 1350
ID ABL32746 standard; DNA; 7384 BP.
DE Human immune system associated gene SEQ ID NO: 719.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42; DB 6; Length 7384;
Best Local Similarity 44.2%; Pred. No. 17;
RESULT 1351
ID AAS45477 standard; DNA; 7657 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #91.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 4; Length 7657;
Best Local Similarity 46.3%; Pred. No. 17;
RESULT 1352
ID ABL34022 standard; DNA; 7657 BP.
DE Human immune system associated gene SEQ ID NO: 1995.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7657;
Best Local Similarity 46.3%; Pred. No. 17;
RESULT 1353
ID AAS45489 standard; DNA; 7823 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #97.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 4; Length 7823;
Best Local Similarity 45.0%; Pred. No. 17;
RESULT 1354
ID ABL34060 standard; DNA; 7823 BP.
DE Human immune system associated gene SEQ ID NO: 2033.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7823;
Best Local Similarity 45.0%; Pred. No. 17;
RESULT 1355
ID ABK31492 standard; DNA; 7823 BP.
DE Signal transduction associated gene modified DNA #168.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7823;
Best Local Similarity 45.0%; Pred. No. 17;
RESULT 1356
ID ABK28417 standard; DNA; 7823 BP.
DE DNA transcription associated genomic DNA #146.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 7823;
Best Local Similarity 45.0%; Pred. No. 17;
RESULT 1357
ID ABL33793 standard; DNA; 8166 BP.
DE Human immune system associated gene SEQ ID NO: 1766.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 8166;
Best Local Similarity 46.5%; Pred. No. 18;
RESULT 1358
ID ABL33569 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1542.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 8305;
Best Local Similarity 45.3%; Pred. No. 18;
RESULT 1359
ID AAZ29911 standard; DNA; 8310 BP.
DE cDNA encoding a SC4 protein of soybean.
PN WO9953067-A2.
PD 21-OCT-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 1.8%; Score 42; DB 2; Length 8310;

Best Local Similarity 46.9%; Pred. No. 18;
RESULT 1360
ID ABL34229 standard; DNA; 8576 BP.
DE Human immune system associated gene SEQ ID NO: 2202.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 8576;
Best Local Similarity 46.3%; Pred. No. 18;
RESULT 1361
ID ABK28366 standard; DNA; 9238 BP.
DE DNA transcription associated complementary genomic DNA #120.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 9238;
Best Local Similarity 44.5%; Pred. No. 19;
RESULT 1362
ID ABL34161 standard; DNA; 10189 BP.
DE Human immune system associated gene SEQ ID NO: 2134.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 10189;
Best Local Similarity 43.8%; Pred. No. 20;
RESULT 1363
ID AAS46360 standard; DNA; 10609 BP.
DE Tumour suppressor gene derived chemically modified sequence #82.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 4; Length 10609;
Best Local Similarity 46.9%; Pred. No. 20;
RESULT 1364
ID ABK31269 standard; DNA; 10609 BP.
DE Signal transduction associated gene modified complementary DNA #56.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 10609;
Best Local Similarity 46.9%; Pred. No. 20;
RESULT 1365
ID ABL32605 standard; DNA; 11155 BP.
DE Human immune system associated gene SEQ ID NO: 578.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 11155;
Best Local Similarity 47.5%; Pred. No. 20;
RESULT 1366
ID ABK31422 standard; DNA; 13123 BP.
DE Signal transduction associated gene modified DNA #133.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 13123;
Best Local Similarity 44.4%; Pred. No. 22;
RESULT 1367
ID ABL54363 standard; DNA; 13123 BP.
DE Chemically treated apoptosis gene #32.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 13123;
Best Local Similarity 44.4%; Pred. No. 22;
RESULT 1368
ID ABL34141 standard; DNA; 15698 BP.
DE Human immune system associated gene SEQ ID NO: 2114.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 15698;
Best Local Similarity 48.6%; Pred. No. 24;

RESULT 1369
ID ADB54306 standard; DNA; 17897 BP.
DE Pretreated genomic DNA region 230.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 10; Length 17897;
Best Local Similarity 49.5%; Pred. No. 25;
RESULT 1370
ID ADB54178 standard; DNA; 17897 BP.
DE Pretreated genomic DNA region 102.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 10; Length 17897;
Best Local Similarity 49.5%; Pred. No. 25;
RESULT 1371
ID ADS89328 standard; DNA; 17897 BP.
DE Oligonucleotide of the invention SEQ ID NO:344.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 13; Length 17897;
Best Local Similarity 49.5%; Pred. No. 25;
RESULT 1372
ID ADS89602 standard; DNA; 17897 BP.
DE Oligonucleotide of the invention SEQ ID NO:618.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 13; Length 17897;
Best Local Similarity 49.5%; Pred. No. 25;
RESULT 1373
ID ABL32035 standard; DNA; 18011 BP.
DE Human immune system associated gene SEQ ID NO: 8.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 18011;
Best Local Similarity 45.7%; Pred. No. 25;
RESULT 1374
ID ABQ67059 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 1.8%; Score 42; DB 6; Length 34688;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 1375
Query Match 1.8%; Score 42; DB 6; Length 40681;
Best Local Similarity 51.0%; Pred. No. 36;
RESULT 1376
ID ADA03026 standard; DNA; 96588 BP.
DE Human MBNL carcinoma associated gene, SEQ ID NO:1544.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 42; DB 9; Length 96588;
Best Local Similarity 45.9%; Pred. No. 53;
RESULT 1377
ID ADB72764 standard; DNA; 96588 BP.
DE Human MBNL gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 42; DB 10; Length 96588;
Best Local Similarity 45.9%; Pred. No. 53;
RESULT 1378
ID ADC85506 standard; DNA; 96588 BP.
DE Human Mbnl genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 1.8%; Score 42; DB 10; Length 96588;
Best Local Similarity 45.9%; Pred. No. 53;
RESULT 1379
ID ADM74621 standard; DNA; 96588 BP.
DE Human carcinoma associated (CA) nucleic acid #145.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 1.8%; Score 42; DB 12; Length 96588;
Best Local Similarity 45.9%; Pred. No. 53;
RESULT 1380
ID ABD32992 standard; DNA; 99764 BP.
DE Human cancer-associated genomic DNA HD21-017.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 42; DB 13; Length 99764;
Best Local Similarity 44.6%; Pred. No. 54;
RESULT 1381
ID ABA92787 standard; DNA; 640681 BP.
DE Buchnera sp. genomic DNA SEQ ID NO:1.
PN JP2001292771-A.
PD 23-OCT-2001.
PA (RIKA) RIKAKAKU KENKYUSHO.
Query Match 1.8%; Score 42; DB 6; Length 110000;
Best Local Similarity 46.3%; Pred. No. 56;
RESULT 1382
ID ABD32653 standard; DNA; 117750 BP.
DE Human cancer-associated genomic DNA HD13-060.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 42; DB 13; Length 117750;
Best Local Similarity 45.6%; Pred. No. 58;
RESULT 1383
ID ADQ97523 standard; DNA; 215974 BP.
DE Human cancer associated sequence HD09-008, SEQ ID 500.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.8%; Score 42; DB 12; Length 215974;
Best Local Similarity 57.7%; Pred. No. 75;
RESULT 1384
ID ADD25213 standard; DNA; 271990 BP.
DE Fertility restorer protein genomic DNA sequence.
PN WO2003006622-A2.
PD 23-JAN-2003.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
Query Match 1.8%; Score 42; DB 10; Length 271990;
Best Local Similarity 46.6%; Pred. No. 84;
RESULT 1385
ID ADN61228 standard; DNA; 271990 BP.
DE Radish nuclear fertility restorer Rfo Rfo locus SEQ ID NO:87.
PN WO2004006655-A2.
PD 22-JAN-2004.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 1.8%; Score 42; DB 12; Length 271990;
Best Local Similarity 46.6%; Pred. No. 84;
RESULT 1386
ID ADL37641 standard; DNA; 375 BP.
DE Human ovarian cancer DNA marker #11531.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 41.8; DB 5; Length 375;
Best Local Similarity 41.7%; Pred. No. 5.1;
RESULT 1387
ID ADI72502 standard; DNA; 375 BP.
DE Human ovarian cancer DNA marker #5244.

PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 41.8; DB 5; Length 375;
Best Local Similarity 41.7%; Pred. No. 5.1;
RESULT 1388
ID AAZ94422 standard; DNA; 1444 BP.
DE Plasmodium falciparum ycf 24 gene.
PN WO200016758-A2.
PD 30-MAR-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 1.8%; Score 41.8; DB 3; Length 1444;
Best Local Similarity 47.2%; Pred. No. 9.3;
RESULT 1389
ID AAX99552 standard; DNA; 2478 BP.
DE Nucleic acid sequence from U. urealyticum.
PN WO9939007-A1.
PD 05-AUG-1999.
PA (UABR-) UAB RES FOUND.
Query Match 1.8%; Score 41.8; DB 2; Length 2478;
Best Local Similarity 44.0%; Pred. No. 12;
RESULT 1390
ID AAA97037 standard; DNA; 2486 BP.
DE Nucleotide sequence encoding 48kD i-antigen.
PN WO200046373-A1.
PD 10-AUG-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
PA (LINT/) LIN T.
Query Match 1.8%; Score 41.8; DB 3; Length 2486;
Best Local Similarity 45.2%; Pred. No. 12;
RESULT 1391
ID ADD93413 standard; cDNA; 2622 BP.
DE Human lipid-associated molecule LIPAM-1 polynucleotide.
PN WO2003083081-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 41.8; DB 10; Length 2622;
Best Local Similarity 50.8%; Pred. No. 12;
RESULT 1392
ID AAA70149 standard; DNA; 3744 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:282.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 1.8%; Score 41.8; DB 3; Length 3744;
Best Local Similarity 49.8%; Pred. No. 14;
RESULT 1393
ID ABZ10146 standard; DNA; 5033 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #286.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 8; Length 5033;
Best Local Similarity 43.7%; Pred. No. 16;
RESULT 1394
ID ABZ10000 standard; DNA; 5033 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #140.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 8; Length 5033;
Best Local Similarity 43.7%; Pred. No. 16;
RESULT 1395
ID ABL33066 standard; DNA; 5107 BP.
DE Human immune system associated gene SEQ ID NO: 1039.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 5107;
Best Local Similarity 57.1%; Pred. No. 16;
RESULT 1396
ID ABL32979 standard; DNA; 6068 BP.
DE Human chemically modified disease associated gene SEQ ID NO 222.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6068;
Best Local Similarity 49.1%; Pred. No. 18;
RESULT 1397
ID ABL92289 standard; DNA; 6156 BP.
DE Chemically treated DNA repair gene fragment complementary to#49.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6156;
Best Local Similarity 44.5%; Pred. No. 18;
RESULT 1398
ID ABL49360 standard; DNA; 6156 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 60.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6156;
Best Local Similarity 44.5%; Pred. No. 18;
RESULT 1399
ID ABL32591 standard; DNA; 6195 BP.
DE Human immune system associated gene SEQ ID NO: 564.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6195;
Best Local Similarity 46.5%; Pred. No. 18;
RESULT 1400
ID ABL33145 standard; DNA; 6823 BP.
DE Human immune system associated gene SEQ ID NO: 1118.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6823;
Best Local Similarity 59.8%; Pred. No. 18;
RESULT 1401
ID ABL33239 standard; DNA; 6894 BP.
DE Human immune system associated gene SEQ ID NO: 1212.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6894;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1402
ID ABK33970 standard; DNA; 6894 BP.
DE Human DNA for staging of Astrocytomas, complement, #27.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6894;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1403
ID ADA20365 standard; DNA; 6894 BP.
DE Prostate tumour related genomic DNA complement sample #15.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 8; Length 6894;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1404
ID ADA84172 standard; DNA; 6894 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:30.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.8; DB 8; Length 6894;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1405
ID ABL32979 standard; DNA; 6963 BP.
DE Human immune system associated gene SEQ ID NO: 952.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 6963;
Best Local Similarity 43.4%; Pred. No. 19;
RESULT 1406
ID ABK40051 standard; DNA; 7058 BP.
DE Human chemically pretreated gene sequence #67 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 7058;
Best Local Similarity 47.2%; Pred. No. 19;
RESULT 1407
ID AAS46423 standard; DNA; 7135 BP.
DE Tumour suppressor gene derived chemically modified sequence #145.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 4; Length 7135;
Best Local Similarity 53.3%; Pred. No. 19;
RESULT 1408
ID AAS46308 standard; DNA; 8033 BP.
DE Tumour suppressor gene derived chemically modified sequence #30.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 4; Length 8033;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1409
ID ABK31203 standard; DNA; 8033 BP.
DE Signal transduction associated gene modified complementary DNA #23.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8033;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1410
ID ABL70170 standard; DNA; 8033 BP.
DE Chemically treated cell signalling DNA sequence complementary to#30.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8033;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1411
ID AAS61117 standard; DNA; 8033 BP.
DE Human gene regulation-associated gene oligonucleotide #72.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8033;
Best Local Similarity 43.7%; Pred. No. 20;
RESULT 1412
ID ABL34514 standard; DNA; 8197 BP.
DE Human metastasis associated gene SEQ ID NO: 67.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8197;
Best Local Similarity 46.4%; Pred. No. 20;
RESULT 1413
ID ABL70541 standard; DNA; 8197 BP.
DE Chemically treated cell signalling DNA sequence#216.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8197;

Best Local Similarity 46.4%; Pred. No. 20;
RESULT 1414
ID ADS99775 standard; DNA; 8197 BP.
DE Bisulphite treated human gene associated with metastasis #34.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 41.8; DB 7; Length 8197;
Best Local Similarity 46.4%; Pred. No. 20;
RESULT 1415
ID ABK40068 standard; DNA; 8776 BP.
DE Human chemically pretreated gene sequence #75 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8776;
Best Local Similarity 50.8%; Pred. No. 21;
RESULT 1416
ID AAS45437 standard; DNA; 8801 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #71.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 4; Length 8801;
Best Local Similarity 50.2%; Pred. No. 21;
RESULT 1417
ID ABL33741 standard; DNA; 8801 BP.
DE Human immune system associated gene SEQ ID NO: 1714.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8801;
Best Local Similarity 50.2%; Pred. No. 21;
RESULT 1418
ID ABK28286 standard; DNA; 8801 BP.
DE DNA transcription associated complementary genomic DNA #80.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 8801;
Best Local Similarity 50.2%; Pred. No. 21;
RESULT 1419
ID AAK86271 standard; DNA; 9599 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41083.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 41.8; DB 4; Length 9599;
Best Local Similarity 48.2%; Pred. No. 21;
RESULT 1420
ID ABL33799 standard; DNA; 9848 BP.
DE Human immune system associated gene SEQ ID NO: 1772.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 9848;
Best Local Similarity 45.2%; Pred. No. 22;
RESULT 1421
ID ABL34043 standard; DNA; 10039 BP.
DE Human immune system associated gene SEQ ID NO: 2016.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 10039;
Best Local Similarity 46.7%; Pred. No. 22;
RESULT 1422
ID ABL34187 standard; DNA; 11944 BP.
DE Human immune system associated gene SEQ ID NO: 2160.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.8; DB 6; Length 11944;
Best Local Similarity 46.4%; Pred. No. 24;
RESULT 1423
ID ABL33052 standard; DNA; 17131 BP.
DE Human immune system associated gene SEQ ID NO: 1025.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 17131;
Best Local Similarity 46.7%; Pred. No. 28;
RESULT 1424
ID AAD52172 standard; DNA; 26000 BP.
DE Human interferon gamma receptor 1 (IFNGR1) gene.
PN WO200288162-A1.
PD 07-NOV-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 1.8%; Score 41.8; DB 10; Length 26000;
Best Local Similarity 48.2%; Pred. No. 33;
RESULT 1425
ID ACN44852 standard; DNA; 34200 BP.
DE Mouse genomic sequence MCG4860.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 41.8; DB 11; Length 34200;
Best Local Similarity 47.2%; Pred. No. 38;
RESULT 1426
ID ABL55857 standard; DNA; 34337 BP.
DE Human GABA transporter protein gene.
PN US2002031800-A1.
PD 14-MAR-2002.
PA (LIZZ/) LI Z.
PA (CHAT/) CHATURVEDI K.
PA (ZHUS/) ZHU S.
PA (WOOD/) WOODAGE T.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 1.8%; Score 41.8; DB 6; Length 34337;
Best Local Similarity 48.2%; Pred. No. 38;
RESULT 1427
ID ADG88376 standard; DNA; 34337 BP.
DE Human transporter gene.
PN US2003157649-A1.
PD 21-AUG-2003.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 41.8; DB 10; Length 34337;
Best Local Similarity 48.2%; Pred. No. 38;
RESULT 1428
ID ABQ67094 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.8; DB 6; Length 83391;
Best Local Similarity 47.7%; Pred. No. 56;
RESULT 1429
ID ADI72102 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #4844.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 41.6; DB 5; Length 299;
Best Local Similarity 45.3%; Pred. No. 5.2;
RESULT 1430
ID ADL37251 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #11141.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 41.6; DB 5; Length 299;
Best Local Similarity 45.3%; Pred. No. 5.2;

RESULT 1431
ID AAH93356 standard; DNA; 366 BP.
DE Human chromosome 16 BAC clone CIT987SK-A-248F7 SEQ ID NO 77.
PN WO200152616-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 41.6; DB 4; Length 366;
Best Local Similarity 48.7%; Pred. No. 5.7;
RESULT 1432
ID ACN52913 standard; cDNA; 411 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 41.6; DB 13; Length 411;
Best Local Similarity 49.5%; Pred. No. 6;
RESULT 1433
ID ACN62049 standard; cDNA; 469 BP.
DE Cotton gynoeceium tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 41.6; DB 13; Length 469;
Best Local Similarity 47.1%; Pred. No. 6.4;
RESULT 1434
ID ADL43972 standard; DNA; 539 BP.
DE Human ovarian cancer DNA marker #17862.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 1.8%; Score 41.6; DB 5; Length 539;
Best Local Similarity 48.0%; Pred. No. 6.8;
RESULT 1435
ID ABT18873 standard; DNA; 1569 BP.
DE Aspergillus fumigatus essential gene #1231.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 1569;
Best Local Similarity 52.3%; Pred. No. 11;
RESULT 1436
ID ABT20693 standard; DNA; 1569 BP.
DE Aspergillus fumigatus essential gene #3051.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 1569;
Best Local Similarity 52.3%; Pred. No. 11;
RESULT 1437
ID ABT20095 standard; DNA; 1689 BP.
DE Aspergillus fumigatus essential gene #2453.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 1689;
Best Local Similarity 52.3%; Pred. No. 11;
RESULT 1438
ID ABT18279 standard; DNA; 1714 BP.
DE Aspergillus fumigatus essential gene #637.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 1714;
Best Local Similarity 52.3%; Pred. No. 11;
RESULT 1439
ID AAV38373 standard; cDNA; 2115 BP.
DE Beta(1 -> 4)-N-acetylglucosaminyl-transferase (GnT-IV)a encoding cDNA.

PN WO9826053-A1.
PD 18-JUN-1998.
PA (KIRI) KIRIN BEER KK.
Query Match 1.8%; Score 41.6; DB 2; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1440
ID AAD63209 standard; DNA; 2115 BP.
DE Human DNA #34 used in the method for diagnosing cancer.
PN US2003190656-A1.
PD 09-OCT-2003.
PA (WANG/) WANG Y.
Query Match 1.8%; Score 41.6; DB 10; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1441
ID AAD62810 standard; DNA; 2115 BP.
DE Human DNA #23 used in the method for diagnosing cancer.
PN US2003194733-A1.
PD 16-OCT-2003.
PA (WANG/) WANG Y.
Query Match 1.8%; Score 41.6; DB 10; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1442
ID ADP88305 standard; cDNA; 2115 BP.
DE Metastatic breast cancer marker gene MGAT4A, SEQ ID NO:82.
PN EP1349104-A2.
PD 01-OCT-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 1.8%; Score 41.6; DB 11; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1443
ID ADR25531 standard; DNA; 2115 BP.
DE Breast cancer prognosis marker #1392.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 1.8%; Score 41.6; DB 13; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1444
ID ADS32721 standard; DNA; 2115 BP.
DE Human MGAT4A coding sequence.
PN WO2004074461-A2.
PD 02-SEP-2004.
PA (BOBR/) BOBROWICZ P.
PA (HAMI/) HAMILTON S R.
PA (GERN/) GERNGROSS T U.
PA (WILD/) WILDT S.
PA (CHOI/) CHOI B.
PA (NETT/) NETT J H.
PA (DAVI/) DAVIDSON R C.
Query Match 1.8%; Score 41.6; DB 13; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1445
ID ADR97303 standard; DNA; 2115 BP.
DE Human MGAT4A DNA, an apoptosis related target Seq 11.
PN WO2004078783-A2.
PD 16-SEP-2004.
PA (EIRX-) EIRX THERAPEUTICS LTD.
Query Match 1.8%; Score 41.6; DB 13; Length 2115;
Best Local Similarity 53.0%; Pred. No. 12;
RESULT 1446
ID AAD09955 standard; cDNA; 2339 BP.
DE Human drug metabolising enzyme (DME-20) cDNA.
PN WO200151638-A2.
PD 19-JUL-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.8%; Score 41.6; DB 4; Length 2339;
Best Local Similarity 53.0%; Pred. No. 13;
RESULT 1447
ID ABT19499 standard; DNA; 3689 BP.
DE Aspergillus fumigatus essential gene #1857.
PN WO200286090-A2.
PD 31-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 3689;
Best Local Similarity 52.3%; Pred. No. 16;
RESULT 1448
ID ABT17685 standard; DNA; 3714 BP.
DE Aspergillus fumigatus essential gene #43.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 41.6; DB 8; Length 3714;
Best Local Similarity 52.3%; Pred. No. 16;
RESULT 1449
ID ABL33676 standard; DNA; 5379 BP.
DE Human immune system associated gene SEQ ID NO: 1649.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5379;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1450
ID ABL34576 standard; DNA; 5379 BP.
DE Human metastasis associated gene SEQ ID NO: 129.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5379;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1451
ID ABL70369 standard; DNA; 5379 BP.
DE Chemically treated cell signalling DNA sequence#130.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5379;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1452
ID ADS99837 standard; DNA; 5379 BP.
DE Bisulphite treated human gene associated with metastasis #65.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.8%; Score 41.6; DB 7; Length 5379;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1453
ID ABZ10204 standard; DNA; 5507 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #344.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 8; Length 5507;
Best Local Similarity 43.8%; Pred. No. 19;
RESULT 1454
ID ABK31279 standard; DNA; 5526 BP.
DE Signal transduction associated gene modified complementary DNA #61.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5526;
Best Local Similarity 53.0%; Pred. No. 19;
RESULT 1455
ID ABL33396 standard; DNA; 5641 BP.
DE Human immune system associated gene SEQ ID NO: 1369.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5641;
Best Local Similarity 49.3%; Pred. No. 19;
RESULT 1456
ID ABZ10144 standard; DNA; 5660 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #284.
PN WO200277272-A2.

PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 8; Length 5660;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1457
ID ABL32697 standard; DNA; 5663 BP.
DE Human immune system associated gene SEQ ID NO: 670.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5663;
Best Local Similarity 49.5%; Pred. No. 19;
RESULT 1458
ID ABL92223 standard; DNA; 5663 BP.
DE Chemically treated DNA repair gene fragment complementary to#16.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5663;
Best Local Similarity 49.5%; Pred. No. 19;
RESULT 1459
ID ACF62812 standard; DNA; 5666 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:61.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 8; Length 5666;
Best Local Similarity 49.1%; Pred. No. 19;
RESULT 1460
ID ABL33667 standard; DNA; 5798 BP.
DE Human immune system associated gene SEQ ID NO: 1640.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5798;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1461
ID AAS61416 standard; DNA; 5887 BP.
DE Human gene regulation-associated gene oligonucleotide #371.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 5887;
Best Local Similarity 45.4%; Pred. No. 19;
RESULT 1462
ID ABK31361 standard; DNA; 6013 BP.
DE Signal transduction associated gene modified complementary DNA #102.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6013;
Best Local Similarity 47.0%; Pred. No. 20;
RESULT 1463
ID AAS61265 standard; DNA; 6013 BP.
DE Human gene regulation-associated gene oligonucleotide #220.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6013;
Best Local Similarity 47.0%; Pred. No. 20;
RESULT 1464
ID ABL92288 standard; DNA; 6156 BP.
DE Chemically treated DNA repair gene fragment#49.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6156;
Best Local Similarity 44.8%; Pred. No. 20;
RESULT 1465
ID ABL49359 standard; DNA; 6156 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 59.
PN WO200177377-A2.
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6156;
Best Local Similarity 44.8%; Pred. No. 20;
RESULT 1466
ID ABK28369 standard; DNA; 6167 BP.
DE DNA transcription associated genomic DNA #122.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6167;
Best Local Similarity 50.0%; Pred. No. 20;
RESULT 1467
ID AAS46497 standard; DNA; 6233 BP.
DE Tumour suppressor gene derived chemically modified sequence #219.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 6233;
Best Local Similarity 48.4%; Pred. No. 20;
RESULT 1468
ID AAS45445 standard; DNA; 6327 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #75.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 6327;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 1469
ID ABK28294 standard; DNA; 6327 BP.
DE DNA transcription associated complementary genomic DNA #84.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6327;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 1470
ID ABN80023 standard; DNA; 6636 BP.
DE Human chemically modified disease associated gene SEQ ID NO 40.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6636;
Best Local Similarity 44.1%; Pred. No. 20;
RESULT 1471
ID ABL32315 standard; DNA; 6641 BP.
DE Human immune system associated gene SEQ ID NO: 288.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6641;
Best Local Similarity 45.3%; Pred. No. 20;
RESULT 1472
ID ABL54336 standard; DNA; 6641 BP.
DE Chemically treated apoptosis gene complementary to gene #18.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6641;
Best Local Similarity 45.3%; Pred. No. 20;
RESULT 1473
ID ABL33894 standard; DNA; 6899 BP.
DE Human immune system associated gene SEQ ID NO: 1867.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 6899;
Best Local Similarity 54.6%; Pred. No. 21;
RESULT 1474
ID AAD28379 standard; DNA; 7340 BP.
DE Human chemically treated genomic DNA #20.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.6; DB 6; Length 7340;
Best Local Similarity 48.0%; Pred. No. 21;
RESULT 1475
ID ABK28342 standard; DNA; 8260 BP.
DE DNA transcription associated complementary genomic DNA #108.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 8260;
Best Local Similarity 46.5%; Pred. No. 23;
RESULT 1476
ID ADE54216 standard; DNA; 8404 BP.
DE Pretreated genomic DNA region 140.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 10; Length 8404;
Best Local Similarity 43.8%; Pred. No. 23;
RESULT 1477
ID ADE84152 standard; DNA; 8404 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #88.
PN WO2003042226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 10; Length 8404;
Best Local Similarity 43.8%; Pred. No. 23;
RESULT 1478
ID ADS89516 standard; DNA; 8404 BP.
DE Oligonucleotide of the invention SEQ ID NO:532.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 13; Length 8404;
Best Local Similarity 43.8%; Pred. No. 23;
RESULT 1479
ID ADB54240 standard; DNA; 8666 BP.
DE Pretreated genomic DNA region 164.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 10; Length 8666;
Best Local Similarity 49.1%; Pred. No. 23;
RESULT 1480
ID ADE84178 standard; DNA; 8666 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #114.
PN WO2003042226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 10; Length 8666;
Best Local Similarity 49.1%; Pred. No. 23;
RESULT 1481
ID ADS89542 standard; DNA; 8666 BP.
DE Oligonucleotide of the invention SEQ ID NO:558.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 13; Length 8666;
Best Local Similarity 49.1%; Pred. No. 23;
RESULT 1482
ID ABQ66990 standard; DNA; 9118 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 20.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 9118;
Best Local Similarity 45.4%; Pred. No. 24;
RESULT 1483
ID ABN80049 standard; DNA; 9543 BP.
DE Human chemically modified disease associated gene SEQ ID NO 66.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 9543;

Best Local Similarity 45.4%; Pred. No. 24;
RESULT 1484
ID ABL33323 standard; DNA; 9741 BP.
DE Human immune system associated gene SEQ ID NO: 1296.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 9741;
Best Local Similarity 45.9%; Pred. No. 24;
RESULT 1485
ID ABL32892 standard; DNA; 10710 BP.
DE Human immune system associated gene SEQ ID NO: 865.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 10710;
Best Local Similarity 45.6%; Pred. No. 25;
RESULT 1486
ID AAS46805 standard; DNA; 10996 BP.
DE Tumour suppressor gene derived chemically modified sequence #531.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 10996;
Best Local Similarity 43.0%; Pred. No. 26;
RESULT 1487
ID ABK28465 standard; DNA; 10996 BP.
DE DNA transcription associated genomic DNA #170.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 10996;
Best Local Similarity 43.0%; Pred. No. 26;
RESULT 1488
ID AAS46414 standard; DNA; 11029 BP.
DE Tumour suppressor gene derived chemically modified sequence #136.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 11029;
Best Local Similarity 45.2%; Pred. No. 26;
RESULT 1489
ID ADS89288 standard; DNA; 11029 BP.
DE Oligonucleotide of the invention SEQ ID NO:304.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 13; Length 11029;
Best Local Similarity 45.2%; Pred. No. 26;
RESULT 1490
ID AAS45479 standard; DNA; 11047 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #92.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 11047;
Best Local Similarity 45.9%; Pred. No. 26;
RESULT 1491
ID ABL33984 standard; DNA; 11047 BP.
DE Human immune system associated gene SEQ ID NO: 1957.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 11047;
Best Local Similarity 45.9%; Pred. No. 26;
RESULT 1492
ID ABK28401 standard; DNA; 11047 BP.
DE DNA transcription associated genomic DNA #138.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 11047;
Best Local Similarity 45.9%; Pred. No. 26;

RESULT 1493
ID ABK39937 standard; DNA; 11422 BP.
DE Human chemically pretreated gene sequence #9 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 11422;
Best Local Similarity 46.3%; Pred. No. 26;
RESULT 1494
ID ABL32219 standard; DNA; 11422 BP.
DE Human immune system associated gene SEQ ID NO: 192.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 11422;
Best Local Similarity 46.3%; Pred. No. 26;
RESULT 1495
ID AAS46509 standard; DNA; 12356 BP.
DE Tumour suppressor gene derived chemically modified sequence #231.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 4; Length 12356;
Best Local Similarity 49.1%; Pred. No. 27;
RESULT 1496
ID ADS89729 standard; DNA; 13286 BP.
DE Oligonucleotide of the invention SEQ ID NO:745.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 13; Length 13286;
Best Local Similarity 44.7%; Pred. No. 28;
RESULT 1497
ID ADS89455 standard; DNA; 13286 BP.
DE Oligonucleotide of the invention SEQ ID NO:471.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 13; Length 13286;
Best Local Similarity 44.7%; Pred. No. 28;
RESULT 1498
ID ABK31518 standard; DNA; 14316 BP.
DE Signal transduction associated gene modified DNA #181.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 14316;
Best Local Similarity 51.8%; Pred. No. 29;
RESULT 1499
ID ABL70605 standard; DNA; 14316 BP.
DE Chemically treated cell signalling DNA sequence#248.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 14316;
Best Local Similarity 51.8%; Pred. No. 29;
RESULT 1500
ID AAS61444 standard; DNA; 14316 BP.
DE Human gene regulation-associated gene oligonucleotide #399.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.8%; Score 41.6; DB 6; Length 14316;
Best Local Similarity 51.8%; Pred. No. 29;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 08:30:38 ; Search time 10304 Seconds
 (without alignments)
 11154.481 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccgatgctc.....ttaagcatttagaaaaactt 2372

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2372	100.0	2372	6	BD172392	BD172392 Secreted
2	2372	100.0	2372	6	BD172711	BD172711 Secreted
3	2372	100.0	2372	6	BD173030	BD173030 Secreted
4	2372	100.0	2372	6	BD173349	BD173349 Secreted
5	2372	100.0	2372	6	BD175383	BD175383 Secretory
6	2372	100.0	2372	6	AR410761	AR410761 Sequence
7	2372	100.0	2372	6	AR439125	AR439125 Sequence
8	2372	100.0	2372	6	AR473145	AR473145 Sequence
9	2372	100.0	2372	6	AR527131	AR527131 Sequence
10	2372	100.0	2372	6	AR566164	AR566164 Sequence
11	2372	100.0	2372	6	AX092274	AX092274 Sequence
12	2372	100.0	2372	6	AX454446	AX454446 Sequence
13	2372	100.0	2372	6	AX490924	AX490924 Sequence
14	2372	100.0	2372	6	AX697609	AX697609 Sequence
15	2372	100.0	2372	6	BD075532	BD075532 Secretory
16	2372	100.0	2372	9	AY358925	AY358925 Homo sapi
17	2299.4	96.9	2312	6	CQ720788	CQ720788 Sequence
18	2282.2	96.2	2313	9	AF118108	AF118108 Homo sapi
19	2245.4	94.7	2282	9	BC026231	BC026231 Homo sapi

C 239	55.4	2.3	181713	2	CR847903	Danio rer
C 240	55.4	2.3	232548	2	AC125209	Mus muscu
C 241	55.4	2.3	250078	3	AE014829	Plasmodiu
C 242	55.4	2.3	349174	1	AB063522	Wiggleswo
C 243	55.2	2.3	8056	6	AX599046	Sequence
C 244	55.2	2.3	28862	9	AC012398	Homo sapi
C 245	55.2	2.3	85779	8	SCE011856	
C 246	55.2	2.3	105940	9	AC010606	Homo sapi
C 247	55.2	2.3	110000	8	CR382138_22	
C 248	55.2	2.3	133877	2	AC120883	Continuation (23 o
C 249	55.2	2.3	135121	9	AC069525	Homo sapi
C 250	55.2	2.3	136098	9	AC006970	Homo sapi
C 251	55.2	2.3	150199	9	AC087568	Pan trogl
C 252	55.2	2.3	159066	9	AC103557	Homo sapi
C 253	55.2	2.3	176906	2	CR354587	Danio rer
C 254	55.2	2.3	182870	3	AC116960	Dictyoste
C 255	55.2	2.3	223509	2	CR388007	
C 256	55.2	2.3	337203	3	CR382401	Plasmodiu
C 257	55	2.3	1894	3	PFA428569	
C 258	55	2.3	83391	6	AX458577	Sequence
C 259	55	2.3	89086	9	AC104373	Homo sapi
C 260	55	2.3	125744	5	AL954387	Zebrafish
C 261	55	2.3	159603	2	CR762422	Danio rer
C 262	55	2.3	163809	2	CR392044	Danio rer
C 263	55	2.3	170668	9	AC104012	Homo sapi
C 264	55	2.3	176142	2	CR388010	Danio rer
C 265	55	2.3	197951	2	CR392343	Danio rer
C 266	55	2.3	254050	3	PFA929358	Plasmodiu
C 267	54.8	2.3	7079	3	AF362375	Dictyoste
C 268	54.8	2.3	14001	3	PFCOMPIRB	X95276 P.falciparu
C 269	54.8	2.3	41399	3	AC116984_5	Continuation (6 of
C 270	54.8	2.3	110000	8	CR382131_03	Continuation (4 of
C 271	54.8	2.3	120029	2	HSJ282H10	AL132672 Homo sapi
C 272	54.8	2.3	154675	2	CR354440	Danio rer
C 273	54.8	2.3	161641	9	AC109464	Homo sapi
C 274	54.8	2.3	204430	2	CR792453	Danio rer
C 275	54.8	2.3	225612	2	AC117641	Mus muscu
C 276	54.8	2.3	246589	2	CR450749	Danio rer
C 277	54.8	2.3	287510	2	CR753823	Danio rer
C 278	54.8	2.3	348600	1	AB063521	AB063521 Wiggleswo
C 279	54.8	2.3	348600	1	AB063521	AB063521 Wiggleswo
C 280	54.6	2.3	33651	3	AC114261	Dictyoste
C 281	54.6	2.3	34335	9	AC126776	Homo sapi
C 282	54.6	2.3	84550	3	PFMAL1P2_3	Continuation (4 of
C 283	54.6	2.3	110000	2	PFMAL13_23	Continuation (24 o
C 284	54.6	2.3	110000	2	PFMAL13_24	Continuation (25 o
C 285	54.6	2.3	110000	2	PFMAL8P1_05	Continuation (6 of
C 286	54.6	2.3	155609	2	CR387986	Danio rer
C 287	54.6	2.3	156395	2	CR387986	Danio rer
C 288	54.6	2.3	163735	9	AC027277	Homo sapi
C 289	54.6	2.3	163930	2	CR847885	Danio rer
C 290	54.6	2.3	175559	2	AC145101	Homo sapi
C 291	54.6	2.3	191191	2	CR847965	Danio rer
C 292	54.6	2.3	211748	2	CR392346	Danio rer
C 293	54.6	2.3	236823	2	CR394523	Danio rer
C 294	54.6	2.3	245802	2	AC006279	Plasmodiu
C 295	54.6	2.3	250029	3	AE014839	Plasmodiu
C 296	54.6	2.3	250195	3	AE014831	Plasmodiu
C 297	54.6	2.3	251762	3	AE014851	Plasmodiu
C 298	54.6	2.3	251797	2	BX890543	Danio rer
C 299	54.6	2.3	257570	2	CR354431	Danio rer
C 300	54.6	2.3	260929	3	AE014852	Plasmodiu
C 301	54.6	2.3	271546	3	AE014843	Plasmodiu
C 302	54.6	2.3	287510	2	CR753823	Danio rer
C 303	54.6	2.3	310779	2	AC005140	Plasmodiu
C 304	54.4	2.3	110000	2	BX890596_1	Continuation (2 of
C 305	54.4	2.3	110000	2	PFMAL13_04	Continuation (5 of
C 306	54.4	2.3	125632	2	CR753868	Danio rer
C 307	54.4	2.3	163167	9	AC099784	Homo sapi
C 308	54.4	2.3	167592	2	CR847845	Danio rer
C 309	54.4	2.3	170195	9	AC025452	Homo sapi
C 310	54.4	2.3	175356	2	CR354555	Danio rer
C 311	54.4	2.3	250029	3	AE014816	Plasmodiu

C 312	54.4	2.3	261771	2	CR356223	Danio rer
C 313	54.4	2.3	290874	2	CR847807	Danio rer
C 314	54.4	2.3	293431	2	PFMAL13P4	Plasmodiu
C 315	54.2	2.3	5075	3	AY171193	Caenorhab
C 316	54.2	2.3	8622	8	YSCMTCYTOC	M97514 Saccharomyc
C 317	54.2	2.3	15373	6	AX345369	Sequence
C 318	54.2	2.3	17470	3	AE001402	Plasmodiu
C 319	54.2	2.3	85779	8	SCE011856	Saccharom
C 320	54.2	2.3	110000	2	CR555291_2	Continuation (3 of
C 321	54.2	2.3	154071	3	AC115598	Dictyoste
C 322	54.2	2.3	154948	2	AC141985	Rattus no
C 323	54.2	2.3	166014	2	CR762396	Danio rer
C 324	54.2	2.3	169979	2	BX901942	Danio rer
C 325	54.2	2.3	170534	2	CR391918	Danio rer
C 326	54.2	2.3	173021	9	AC146376	Pan trogl
C 327	54.2	2.3	174198	2	CR762438	Danio rer
C 328	54.2	2.3	185409	9	AC018758	Homo sapi
C 329	54.2	2.3	196613	2	CR735105	Danio rer
C 330	54.2	2.3	349174	1	AB063522	Wiggleswo
C 331	54	2.3	25769	3	AC117267	Dictyoste
C 332	54	2.3	66448	9	AC091286	Homo sapi
C 333	54	2.3	87845	9	AL583860	Human DNA
C 334	54	2.3	113053	8	ATF12B17	Arabidops
C 335	54	2.3	144765	2	CR759966	Danio rer
C 336	54	2.3	158813	9	AC080091	Homo sapi
C 337	54	2.3	165797	2	CR847851	Danio rer
C 338	54	2.3	169850	2	CR847949	Danio rer
C 339	54	2.3	250793	2	CR388030	Danio rer
C 340	53.8	2.3	1905	3	AF336303	Ostrinia
C 341	53.8	2.3	11790	6	AX345444	Sequence
C 342	53.8	2.3	24036	3	CEY53F4A	Caenorhab
C 343	53.8	2.3	89665	9	AC063976	Homo sapi
C 344	53.8	2.3	110000	3	AC116984_1	Continuation (2 of
C 345	53.8	2.3	163660	2	AC046165	Homo sapi
C 346	53.8	2.3	163930	2	CR847885	Danio rer
C 347	53.8	2.3	170966	5	BX000991	Zebrafish
C 348	53.8	2.3	174001	2	BX927081	Danio rer
C 349	53.8	2.3	175959	2	AL450429	Homo sapi
C 350	53.8	2.3	190058	2	CR628384	Danio rer
C 351	53.8	2.3	198047	2	CR376763	Danio rer
C 352	53.8	2.3	252632	3	AE014818	Plasmodiu
C 353	53.8	2.3	254436	3	AE014827	Plasmodiu
C 354	53.8	2.3	349418	3	CR382398	Plasmodiu
C 355	53.8	2.3	349751	3	PFMAL4P3	Plasmodiu
C 356	53.6	2.3	631	3	JALMTTGMDDL	L16849 Jalmenus ev
C 357	53.6	2.3	700	6	AX183285	Sequence
C 358	53.6	2.3	46491	8	AP005666	Lotus cor
C 359	53.6	2.3	48488	3	AF106589	Caenorhab
C 360	53.6	2.3	88295	9	AC004612	AC004612 Homo sapi
C 361	53.6	2.3	110000	2	PFMAL8P1_08	Continuation (9 of
C 362	53.6	2.3	110000	3	AC116305_3	Continuation (4 of
C 363	53.6	2.3	112811	5	BX005301	Zebrafish
C 364	53.6	2.3	147056	2	CR846095	Danio rer
C 365	53.6	2.3	152224	2	AC141680	Apis mell
C 366	53.6	2.3	155024	5	BX649446	Zebrafish
C 367	53.6	2.3	156851	2	CR751546	Danio rer
C 368	53.6	2.3	157865	2	CR450836	Danio rer
C 369	53.6	2.3	167320	2	CR450810	Danio rer
C 370	53.6	2.3	178427	2	CR392006	Danio rer
C 371	53.6	2.3	203595	2	CR385054	Danio rer
C 372	53.6	2.3	205190	2	CR391979	Danio rer
C 373	53.6	2.3	205828	2	BX649409	Danio rer
C 374	53.6	2.3	250029	3	AE014820	Plasmodiu
C 375	53.6	2.3	271546	3	AE014843	Plasmodiu
C 376	53.6	2.3	297798	2	CR396591	Danio rer
C 377	53.4	2.3	403	3	AF102765	Mirax sp.
C 378	53.4	2.3	1156	3	AF044862	Phoebis a
C 379	53.4	2.3	1192	9	HSA323759	Homo sapi
C 380	53.4	2.3	110000	2	PFMAL7P1_07	Continuation (8 of
C 381	53.4	2.3	110000	3	PFMAL1P2_1	Continuation (2 of
C 382	53.4	2.3	121024	8	CHMPXX	X04465 Marchantia
C 383	53.4	2.3	155490	2	CR749749	Danio rer
C 384	53.4	2.3	160645	2	CR391949	Danio rer

385	53.4	2.3	165445	5	BX321870	BX321870 Zebrafish	458	52.6	2.2	116256	9	AL139101	AL139101 Human DNA
386	53.4	2.3	169850	2	CR847949	Danio rer	459	52.6	2.2	118642	9	AC126283	AC126283 Homo sapi
387	53.4	2.3	186552	2	CR392001	Danio rer	c 460	52.6	2.2	132500	2	AC141435	AC141435 Medicago
c 388	53.4	2.3	198693	2	AC113912	Rattus no	c 461	52.6	2.2	141423	2	CR628324	CR628324 Danio rer
389	53.4	2.3	226345	9	AC005406	AC005406 Homo sapi	c 462	52.6	2.2	148385	2	CR749764	CR749764 Danio rer
c 390	53.4	2.3	248977	2	AC136952	Danio rer	c 463	52.6	2.2	156557	2	CR405705	CR405705 Danio rer
391	53.4	2.3	250707	3	AE014848	AE014848 Plasmodiu	c 464	52.6	2.2	160835	9	AC087273	AC087273 Homo sapi
c 392	53.4	2.3	349980	6	AX344560	AX344560 Sequence	465	52.6	2.2	166763	9	AC087625	AC087625 Homo sapi
c 393	53.4	2.3	349980	6	AX344561	AX344561 Sequence	c 466	52.6	2.2	170534	2	CR391918	CR391918 Danio rer
c 394	53.2	2.2	44227	8	AF275271	AF275271 Schizosac	c 467	52.6	2.2	186898	2	CR388057	CR388057 Danio rer
395	53.2	2.2	66448	9	AC091286	AC091286 Homo sapi	468	52.6	2.2	252394	3	AE014833	AE014833 Plasmodiu
396	53.2	2.2	132943	9	AC011287	AC011287 Homo sapi	469	52.6	2.2	302156	3	AC116977	AC116977 Dictyoste
c 397	53.2	2.2	137057	9	AC004952	AC004952 Homo sapi	470	52.4	2.2	7291	1	AF211133	AF211133 Carsonell
398	53.2	2.2	154844	9	AC017000	AC017000 Homo sapi	471	52.4	2.2	28150	9	AC137733	AC137733 Homo sapi
c 399	53.2	2.2	174162	2	CR759781	CR759781 Danio rer	c 472	52.4	2.2	37906	9	AC005199	AC005199 Homo sapi
400	53.2	2.2	177560	2	CR318627	CR318627 Danio rer	473	52.4	2.2	64845	2	AC099834	AC099834 Homo sapi
401	53.2	2.2	182445	2	AC026850	AC026850 Homo sapi	c 474	52.4	2.2	72243	9	AL731858	AL731858 Human DNA
402	53.2	2.2	195958	2	BX957263	BX957263 Danio rer	c 475	52.4	2.2	135121	9	AC069525	AC069525 Homo sapi
403	53.2	2.2	228285	2	CR391925	CR391925 Danio rer	476	52.4	2.2	145032	2	BX890579	BX890579 Danio rer
404	53.2	2.2	235493	2	CR388183	CR388183 Danio rer	c 477	52.4	2.2	148878	2	CR759816	CR759816 Danio rer
c 405	53	2.2	6544	6	AX277882	AX277882 Sequence	c 478	52.4	2.2	160571	10	AL672008	AL672008 Mouse DNA
c 406	53	2.2	6544	6	AX345548	AX345548 Sequence	479	52.4	2.2	163475	2	CR628390	CR628390 Danio rer
c 407	53	2.2	8101	6	AX346881	AX346881 Sequence	c 480	52.4	2.2	166183	9	AC073048	AC073048 Homo sapi
408	53	2.2	12940	3	AE001386	AE001386 Plasmodiu	c 481	52.4	2.2	175842	9	AL731547	AL731547 Human DNA
c 409	53	2.2	13138	3	AC116305_4	Continuation (5 of	c 482	52.4	2.2	176898	9	AC117569	AC117569 Homo sapi
c 410	53	2.2	13574	6	AX346219	AX346219 Sequence	c 483	52.4	2.2	177164	9	AL365202	AL365202 Human DNA
c 411	53	2.2	19822	3	AC116918	AC116918 Dictyoste	c 484	52.4	2.2	180701	9	AC024590	AC024590 Homo sapi
c 412	53	2.2	110000	2	PFMAL7P1_06	Continuation (7 of	c 485	52.4	2.2	182518	9	AC131649	AC131649 Homo sapi
413	53	2.2	135928	9	HS434O14	AL0223398 Human DNA	c 486	52.4	2.2	185989	2	CR407587	CR407587 Danio rer
c 414	53	2.2	137889	9	AC073269	AC073269 Homo sapi	487	52.4	2.2	194028	2	AC111077	AC111077 Homo sapi
415	53	2.2	160555	5	BX296516	BX296516 Zebrafish	c 488	52.4	2.2	218311	2	CR749741	CR749741 Danio rer
c 416	53	2.2	166820	2	CR388213	CR388213 Danio rer	c 489	52.4	2.2	219727	2	AC145709	AC145709 Homo sapi
c 417	53	2.2	170632	2	BX927206	BX927206 Danio rer	490	52.4	2.2	238215	2	CR848028	CR848028 Danio rer
c 418	53	2.2	178660	2	CR847868	CR847868 Danio rer	c 491	52.4	2.2	239484	2	CR759895	CR759895 Danio rer
c 419	53	2.2	187161	5	BX088526	BX088526 Zebrafish	c 492	52.2	2.2	1181	8	MISC0X13	X14910 Yeast mitoc
c 420	53	2.2	195319	2	CR388410	CR388410 Danio rer	c 493	52.2	2.2	104229	9	AC097458	AC097458 Homo sapi
421	53	2.2	220158	2	CR678095	CR678095 Danio rer	c 494	52.2	2.2	109847	2	AC149579	AC149579 Medicago
422	53	2.2	254436	3	AE014827	AE014827 Plasmodiu	495	52.2	2.2	110000	3	AC116957_2	Continuation (3 of
423	53	2.2	266544	3	AC116956	AC116956 Dictyoste	496	52.2	2.2	146841	9	AC020549	AC020549 Homo sapi
424	53	2.2	281723	3	PF929359	AL9293359 Plasmodiu	c 497	52.2	2.2	151802	3	AC114263	AC114263 Dictyoste
c 425	52.8	2.2	3215	3	AY601895	AY601895 Daktulosp	c 498	52.2	2.2	151900	9	AC107419	AC107419 Homo sapi
c 426	52.8	2.2	4475	8	ZMZEMAGEN	X91882 Z.mays ZEMA	c 499	52.2	2.2	153947	2	CR788315	CR788315 Danio rer
427	52.8	2.2	5264	8	AB025906	AB025906 Cucumis m	500	52.2	2.2	159857	9	AC018767	AC018767 Homo sapi
c 428	52.8	2.2	106958	9	AL807813	AL807813 Human DNA	c 501	52.2	2.2	163443	2	AC006280	AC006280 Plasmodiu
429	52.8	2.2	110000	2	PFMAL7P1_00	AL8444506 Plasmodiu	502	52.2	2.2	167103	9	AC147065	AC147065 Pan trogl
430	52.8	2.2	130349	9	AC011593	AC011593 Homo sapi	c 503	52.2	2.2	174181	9	AL691517	AL691517 Human DNA
c 431	52.8	2.2	130461	2	AP002741	AP002741 Homo sapi	c 504	52.2	2.2	177423	2	CR356242	CR356242 Danio rer
c 432	52.8	2.2	133410	5	BX470202	BX470202 Zebrafish	c 505	52.2	2.2	178207	9	AC140172	AC140172 Homo sapi
433	52.8	2.2	140101	9	AC004648	AC004648 Homo sapi	c 506	52.2	2.2	181581	2	AC026621	AC026621 Homo sapi
c 434	52.8	2.2	157583	5	BX571951	BX571951 Zebrafish	507	52.2	2.2	181674	9	AC099514	AC099514 Homo sapi
435	52.8	2.2	162954	2	BX548252	BX548252 Danio rer	508	52.2	2.2	186175	2	CR318664	CR318664 Danio rer
c 436	52.8	2.2	163724	2	CR788299	CR788299 Danio rer	c 509	52.2	2.2	205544	2	CR847834	CR847834 Danio rer
c 437	52.8	2.2	165797	2	CR847851	CR847851 Danio rer	510	52.2	2.2	217063	2	CR749178	CR749178 Danio rer
c 438	52.8	2.2	181447	2	CR388121	CR388121 Danio rer	511	52.2	2.2	218548	9	AL158035	AL158035 Human DNA
439	52.8	2.2	184794	5	AL929229	AL929229 Zebrafish	512	52.2	2.2	250029	3	AE014839	AE014839 Plasmodiu
c 440	52.8	2.2	192187	3	AC117072	AC117072 Dictyoste	513	52.2	2.2	250663	3	AE014826	AE014826 Plasmodiu
441	52.8	2.2	195422	2	CR450745	CR450745 Danio rer	514	52.2	2.2	253132	3	AE014846	AE014846 Plasmodiu
c 442	52.8	2.2	206504	9	AC012491	AC012491 Homo sapi	515	52.2	2.2	335050	3	PF929356	AL9293356 Plasmodiu
c 443	52.8	2.2	337203	3	CR382401	CR382401 Plasmodiu	516	52.2	2.2	343050	3	PF929353	AL9293353 Plasmodiu
c 444	52.8	2.2	349980	6	AX344555	AX344555 Sequence	517	52.2	2.2	347582	3	PFMAL4P1	AL034557 Plasmodiu
c 445	52.6	2.2	1818	1	AF280098	AF280098 Candidatu	c 518	52.2	2.2	348174	3	CR382399	CR382399 Plasmodiu
c 446	52.6	2.2	3392	3	AF300334	AF300334 Dictyoste	c 519	52	2.2	40180	9	AC008977	AC008977 Homo sapi
447	52.6	2.2	3614	8	MISC02	V00683 Yeast mitoc	c 520	52	2.2	110000	2	PFMAL7P1_00	AL8444506 Plasmodiu
c 448	52.6	2.2	4617	3	SFAJ5398	AJ005398 Dictyoste	c 521	52	2.2	110000	3	AC116305_2	Continuation (3 of
449	52.6	2.2	35077	3	CEY38H8A	AL021483 Caenorhab	522	52	2.2	115998	9	AL672311	AL672311 Human DNA
c 450	52.6	2.2	53932	2	AC023371	AC023371 Homo sapi	523	52	2.2	146704	2	CR774192	CR774192 Danio rer
451	52.6	2.2	62268	9	HS1178121	AL109852 Human DNA	524	52	2.2	151143	2	AC141740	AC141740 Apis mell
452	52.6	2.2	76568	3	MBREV	AF538053 Monosiga	c 525	52	2.2	157176	2	AC084716	AC084716 Homo sapi
453	52.6	2.2	86826	3	PFMAL3P5	AL034556 Plasmodiu	c 526	52	2.2	174482	2	AC139870	AC139870 Rattus no
454	52.6	2.2	97315	9	AL662866	AL662866 Human DNA	c 527	52	2.2	185342	2	CR387989	CR387989 Danio rer
455	52.6	2.2	110000	2	PFMAL13_03	Continuation (4 of	528	52	2.2	186431	2	AC022281	AC022281 Homo sapi
456	52.6	2.2	110000	2	PFMAL8P1_01	Continuation (2 of	529	52	2.2	201659	2	AC146419	AC146419 Pan trogl
c 457	52.6	2.2	110000	2	PFMAL8P1_04	Continuation (5 of	530	52	2.2	249943	3	AE014823	AE014823 Plasmodiu

C 531	52	2.2	250029	3	AE014830	AE014830 Plasmodiu
C 532	52	2.2	250053	3	AE014825	AE014825 Plasmodiu
C 533	52	2.2	250823	3	AE014821	AE014821 Plasmodiu
C 534	51.8	2.2	721	3	AMU35790	U35790 Anopheles m
C 535	51.8	2.2	809	3	AF293659	AF293659 Anopheles
C 536	51.8	2.2	9832	6	AX345558	AX345558 Sequence
C 537	51.8	2.2	96630	9	AC120055	AC120055 Homo sapi
C 538	51.8	2.2	103344	9	HS1100E15	AL035551 Human DNA
C 539	51.8	2.2	110000	2	PFMAL13_25	Continuation (26 o
540	51.8	2.2	110000	2	PFMAL8P1_00	AL844507 Plasmodiu
541	51.8	2.2	110000	2	PFMAL8P1_09	Continuation (10 o
C 542	51.8	2.2	110000	3	AC116957_1	Continuation (2 of
C 543	51.8	2.2	114000	5	BX572104	BX572104 Zebrafish
C 544	51.8	2.2	138342	2	CR376794	CR376794 Danio rer
C 545	51.8	2.2	142012	9	AL591428	AL591428 Human DNA
C 546	51.8	2.2	148394	2	CR753884	CR753884 Danio rer
547	51.8	2.2	156975	2	CR394534	CR394534 Danio rer
C 548	51.8	2.2	162954	2	BX548252	BX548252 Danio rer
C 549	51.8	2.2	163377	9	BS000042	BS000042 Pan trogl
550	51.8	2.2	166719	9	AC136957	AC136957 Homo sapi
551	51.8	2.2	170597	9	CNS01DRR	AL118556 Human chr
552	51.8	2.2	180629	2	CR388025	CR388025 Danio rer
553	51.8	2.2	185926	5	BX548066	BX548066 Zebrafish
554	51.8	2.2	198434	9	AC109994	AC109994 Homo sapi
C 555	51.8	2.2	209491	2	CR392365	CR392365 Danio rer
556	51.8	2.2	212528	2	BX914219	BX914219 Danio rer
C 557	51.8	2.2	212881	2	CR450705	CR450705 Danio rer
C 558	51.8	2.2	245072	2	CR381551	CR381551 Danio rer
C 559	51.8	2.2	248140	2	BX901898	BX901898 Danio rer
560	51.8	2.2	346940	2	AC107420	AC107420 Homo sapi
C 561	51.6	2.2	715	3	AMU35794	U35794 Anopheles m
C 562	51.6	2.2	1809	1	AF267221	AF267221 Candidatu
C 563	51.6	2.2	9424	8	SDO404228	AJ404228 Saccharom
C 564	51.6	2.2	16750	6	AX251068	AX251068 Sequence
C 565	51.6	2.2	16750	6	AX345423	AX345423 Sequence
566	51.6	2.2	47812	9	HS127L4	Z83839 Human DNA s
C 567	51.6	2.2	73666	9	HSJ333B15	AL109954 Human DNA
C 568	51.6	2.2	89357	9	AC109472	AC109472 Homo sapi
C 569	51.6	2.2	91012	2	AC147363	AC147363 Medicago
C 570	51.6	2.2	101628	9	AF130350	AF130350 Homo sapi
571	51.6	2.2	110000	2	PFMAL7P1_08	Continuation (9 Of
C 572	51.6	2.2	110621	2	CR762468	CR762468 Danio rer
573	51.6	2.2	113880	3	PFMAL3P4	AL008970 Plasmodiu
574	51.6	2.2	118018	9	AF227510	AF227510 Homo sapi
575	51.6	2.2	151151	5	BX005294	BX005294 Zebrafish
C 576	51.6	2.2	151370	9	AC147148	AC147148 Pan trogl
C 577	51.6	2.2	153477	2	AC006278	AC006278 Plasmodiu
578	51.6	2.2	156849	2	CR405684	CR405684 Danio rer
579	51.6	2.2	170664	5	BX276096	BX276096 Zebrafish
C 580	51.6	2.2	180346	9	AC092615	AC092615 Homo sapi
C 581	51.6	2.2	181381	2	CR450818	CR450818 Danio rer
582	51.6	2.2	181792	9	AC098822	AC098822 Homo sapi
583	51.6	2.2	197054	2	CR450840	CR450840 Danio rer
584	51.6	2.2	209195	5	AL954309	AL954309 Zebrafish
C 585	51.6	2.2	217307	2	BX324165	BX324165 Danio rer
C 586	51.6	2.2	256172	2	AC005139	AC005139 Plasmodiu
587	51.6	2.2	311860	2	BX537353	BX537353 Danio rer
588	51.6	2.2	340000	9	HS21C048	AL163248 Homo sapi
589	51.6	2.2	349980	6	AX951695	AX951695 Sequence
590	51.4	2.2	1449	3	AF151384	AF151384 Cochliomy
C 591	51.4	2.2	6591	8	YSCWTCG06	L36890 Saccharomyc
592	51.4	2.2	17429	3	AE001416	AE001416 Plasmodiu
593	51.4	2.2	18168	3	PF13PB1	AL929365 Plasmodiu
C 594	51.4	2.2	18556	9	AY527817	AY527817 Homo sapi
595	51.4	2.2	47601	9	AC078802	AC078802 Homo sapi
596	51.4	2.2	47916	8	YL1307410	AJ307410 Yarrowia
597	51.4	2.2	53932	2	AC023371	AC023371 Homo sapi
598	51.4	2.2	74406	8	F2P3	AF080120 Arabidops
C 599	51.4	2.2	87731	9	AC105148	AC105148 Homo sapi
C 600	51.4	2.2	108598	8	ATT22B4	AL049876 Arabidops
C 601	51.4	2.2	115990	5	BX890614	BX890614 Zebrafish
C 602	51.4	2.2	116810	9	AC112657	AC112657 Homo sapi
603	51.4	2.2	145306	2	BX899179	BX899179 Danio rer

C 604	51.4	2.2	145553	5	AL9335272	AL9335272 Zebrafish
605	51.4	2.2	150882	5	CR392344	CR392344 Zebrafish
606	51.4	2.2	151391	9	HSJ730H16	AL122006 Human DNA
C 607	51.4	2.2	155076	2	CR391987	CR391987 Danio rer
608	51.4	2.2	157176	2	AC084716	AC084716 Homo sapi
C 609	51.4	2.2	157845	5	BX005079	BX005079 Zebrafish
610	51.4	2.2	165979	2	CR376741	CR376741 Danio rer
C 611	51.4	2.2	174225	5	BX005071	BX005071 Zebrafish
C 612	51.4	2.2	174741	9	AC040977	AC040977 Homo sapi
613	51.4	2.2	176032	2	BX510656	BX510656 Danio rer
C 614	51.4	2.2	179266	2	CR847966	CR847966 Danio rer
615	51.4	2.2	183498	5	BX072578	BX072578 Zebrafish
C 616	51.4	2.2	198301	8	ATCHRIV31	AL161531 Arabidops
C 617	51.4	2.2	199296	2	CR753895	CR753895 Danio rer
C 618	51.4	2.2	205807	2	CR388418	CR388418 Danio rer
C 619	51.4	2.2	206216	2	AC148586	AC148586 Pan trogl
620	51.4	2.2	217621	2	BX901924	BX901924 Danio rer
621	51.4	2.2	245072	2	CR381551	CR381551 Danio rer
C 622	51.4	2.2	343050	3	PFA929353	AL929353 Plasmodiu
C 623	51.4	2.2	349980	6	AX344569	AX344569 Sequence
624	51.2	2.2	724	6	A86024	A86024 Sequence 68
625	51.2	2.2	724	6	AR155517	AR155517 Sequence
626	51.2	2.2	724	6	E66042	E66042 Genome DNA
C 627	51.2	2.2	738	8	AF264668	AF264668 Cryptomit
C 628	51.2	2.2	963	8	YSCMTREP2	AF503869 Plasmodiu
629	51.2	2.2	1536	3	AF503869	AF503869 Plasmodiu
C 630	51.2	2.2	2305	3	DTMTRNA	X54011 D.teissieri
C 631	51.2	2.2	4601	3	DMU11584	U11584 Drosophila
C 632	51.2	2.2	19517	3	DMU37541	U37541 Drosophila
633	51.2	2.2	67970	3	PFMAL1P3	AL031746 Plasmodiu
634	51.2	2.2	71217	9	AL590306	AL590306 Human DNA
635	51.2	2.2	73639	2	AC055834	AC055834 Homo sapi
636	51.2	2.2	104791	9	AC084364	AC084364 Homo sapi
C 637	51.2	2.2	108902	2	AC011430	AC011430 Homo sapi
C 638	51.2	2.2	110000	3	AC116305_1	Continuation (2 Of
639	51.2	2.2	122986	9	AC004915	AC004915 Homo sapi
640	51.2	2.2	125623	3	AC115599	AC115599 Dictyooste
641	51.2	2.2	147640	5	BX323035	BX323035 Zebrafish
642	51.2	2.2	151802	3	AC114263	AC114263 Dictyooste
C 643	51.2	2.2	152878	3	CEY18D10A	AL034393 Caenorhab
644	51.2	2.2	160645	2	CR391949	CR391949 Danio rer
645	51.2	2.2	164262	2	AC147723	AC147723 Pongo pyg
646	51.2	2.2	167336	2	AC021350	AC021350 Homo sapi
647	51.2	2.2	168054	2	BX936460	BX936460 Danio rer
C 648	51.2	2.2	168103	2	CR751601	CR751601 Danio rer
C 649	51.2	2.2	168538	5	BX537314	BX537314 Zebrafish
650	51.2	2.2	168686	9	AC097066	AC097066 Homo sapi
C 651	51.2	2.2	169842	2	BX914195	BX914195 Danio rer
652	51.2	2.2	173288	2	AC138859	AC138859 Homo sapi
C 653	51.2	2.2	174765	2	AC073103	AC073103 Homo sapi
C 654	51.2	2.2	175959	2	AL450429	AL450429 Homo sapi
C 655	51.2	2.2	180450	3	AE014835	AE014835 Plasmodiu
C 656	51.2	2.2	182738	2	CR407564	CR407564 Danio rer
C 657	51.2	2.2	185085	2	CR762404	CR762404 Danio rer
C 658	51.2	2.2	185926	5	BX548066	BX548066 Zebrafish
659	51.2	2.2	209515	2	BX571687	BX571687 Danio rer
C 660	51.2	2.2	213891	2	CR387983	CR387983 Danio rer
661	51.2	2.2	237869	5	BX537326	BX537326 Zebrafish
C 662	51.2	2.2	253924	3	AE014822	AE014822 Plasmodiu
663	51	2.2	1141	6	AX083744	AX083744 Sequence
664	51	2.2	19209	1	AF274444	AF274444 Carsonell
665	51	2.2	20579	6	AX458558	AX458558 Sequence
C 666	51	2.2	64394	9	AL928596	AL928596 Human DNA
C 667	51	2.2	79170	9	AC026705	AC026705 Homo sapi
C 668	51	2.2	92348	5	AL935295	AL935295 Zebrafish
669	51	2.2	94384	9	AC011718	AC011718 Homo sapi
670	51	2.2	110000	2	BX649285_0	BX649285 Danio rer
671	51	2.2	110000	2	PFMAL7P1_02	Continuation (3 Of
C 672	51	2.2	110000	2	PFMAL7P1_05	Continuation (6 Of
673	51	2.2	110000	3	AC116957_1	Continuation (2 Of
674	51	2.2	110001	9	BX005439	BX005439 Human DNA
C 675	51	2.2	127560	5	BX005077	BX005077 Zebrafish
676	51	2.2	134597	2	CR391983	CR391983 Danio rer

C 823	50.2	2.1	158548	3	PFMAL3P2	AL034558	Plasmodiu
C 824	50.2	2.1	159448	2	CR627500	CR627500	Danio rer
825	50.2	2.1	162884	9	AC016558	AC016558	Homo sapi
826	50.2	2.1	162884	9	AC020936	AC020936	Homo sapi
C 827	50.2	2.1	165277	5	AL954184	AL954184	Zebrafish
C 828	50.2	2.1	166189	2	CR847575	CR847575	Danio rer
C 829	50.2	2.1	166281	2	CR790386	CR790386	Danio rer
830	50.2	2.1	167373	2	CR354397	CR354397	Danio rer
831	50.2	2.1	170425	5	BX465867	BX465867	Zebrafish
832	50.2	2.1	171255	9	AL691447	AL691447	Human DNA
C 833	50.2	2.1	173288	2	AC138859	AC138859	Homo sapi
C 834	50.2	2.1	174187	10	AC121781	AC121781	Mus muscu
C 835	50.2	2.1	175916	9	AC018842	AC018842	Homo sapi
C 836	50.2	2.1	176704	2	CR628364	CR628364	Danio rer
837	50.2	2.1	197310	10	BX005240	BX005240	Mouse DNA
C 838	50.2	2.1	206258	2	CR450701	CR450701	Danio rer
839	50.2	2.1	209360	5	BX470128	BX470128	Zebrafish
C 840	50.2	2.1	245046	2	CR846103	CR846103	Danio rer
C 841	50.2	2.1	273275	3	AE014828	AE014828	Plasmodiu
842	50.2	2.1	330050	3	PFA929355	AL929355	Plasmodiu
843	50.2	2.1	333321	3	AC116986	AC116986	Dictyoste
C 844	50.2	2.1	335050	3	PFA929356	AL929356	Plasmodiu
845	50	2.1	50	6	BD172396	BD172396	Secreted
846	50	2.1	50	6	BD172715	BD172715	Secreted
847	50	2.1	50	6	BD173034	BD173034	Secreted
848	50	2.1	50	6	BD173353	BD173353	Secreted
849	50	2.1	50	6	BD175387	BD175387	Secretory
850	50	2.1	50	6	AR410765	AR410765	Sequence
851	50	2.1	50	6	AR439129	AR439129	Sequence
852	50	2.1	50	6	AR473149	AR473149	Sequence
853	50	2.1	50	6	AR527135	AR527135	Sequence
854	50	2.1	50	6	AR566168	AR566168	Sequence
855	50	2.1	50	6	AX697614	AX697614	Sequence
856	50	2.1	50	6	BD075536	BD075536	Secretory
857	50	2.1	542	4	AF165781	AF165781	Aepyceros
C 858	50	2.1	1647	3	AF275219	AF275219	Gryllopro
859	50	2.1	15635	3	AB083339	AB083339	Bombyx mo
860	50	2.1	15643	3	AF149768	AF149768	Bombyx mo
861	50	2.1	15656	3	AB070264	AB070264	Bombyx mo
862	50	2.1	15664	3	AY048187	AY048187	Bombyx mo
C 863	50	2.1	26565	2	AC119399	AC119399	Homo sapi
864	50	2.1	34750	3	AY217738	AY217738	Eimeria t
C 865	50	2.1	36977	2	AC092304	AC092304	Homo sapi
C 866	50	2.1	37515	6	AX458482	AX458482	Sequence
867	50	2.1	57203	3	AC115581	AC115581	Dictyoste
C 868	50	2.1	96106	9	AC074119	AC074119	Homo sapi
C 869	50	2.1	103775	9	AC091439	AC091439	Homo sapi
C 870	50	2.1	108451	2	AP002739	AP002739	Homo sapi
871	50	2.1	110000	2	PFMAL13_11	Continuation (12 o	
C 872	50	2.1	110000	2	PFMAL13_12	Continuation (13 o	
873	50	2.1	110000	2	PFMAL13_25	Continuation (26 o	
C 874	50	2.1	110000	2	PFMAL8PI_06	Continuation (7 of	
875	50	2.1	116696	3	PFMAL3P3	Z98547 Plasmodium	
876	50	2.1	118758	9	HS450C20	Z84720 Human DNA s	
C 877	50	2.1	124330	3	PFMAL1P1	AL031744 Plasmodiu	
878	50	2.1	132427	5	BX323806	BX323806 Zebrafish	
879	50	2.1	137028	2	BS000643	BS000643 Pan trogl	
C 880	50	2.1	139111	9	AL158048	AL158048 Human DNA	
881	50	2.1	143802	9	AL161431	AL161431 Human DNA	
C 882	50	2.1	146285	9	AC005083	AC005083 Homo sapi	
C 883	50	2.1	155106	9	AC104069	AC104069 Homo sapi	
C 884	50	2.1	155758	2	CR792441	CR792441 Danio rer	
C 885	50	2.1	163816	9	AC012308	AC012308 Homo sapi	
886	50	2.1	172862	2	AL645796	AL645796 Homo sapi	
C 887	50	2.1	175919	2	CR786574	CR786574 Danio rer	
888	50	2.1	181435	2	BX927092	BX927092 Danio rer	
C 889	50	2.1	183584	9	AC012492	AC012492 Homo sapi	
890	50	2.1	186335	2	CR788251	CR788251 Danio rer	
891	50	2.1	189646	2	AC140909	AC140909 Homo sapi	
C 892	50	2.1	193047	9	CNS0000Q	AL049874 Human chr	
C 893	50	2.1	194513	2	CR524482	CR524482 Danio rer	
894	50	2.1	199551	2	AC006281	AC006281 Plasmodiu	
895	50	2.1	216648	2	BX901972	BX901972 Danio rer	

896	50	2.1	217006	2	BX248241	
897	50	2.1	218074	9	AC023283	
C 898	50	2.1	249995	3	AE014840	
899	50	2.1	250029	3	AE014838	
900	50	2.1	257109	3	AC116963	
901	50	2.1	293431	2	PFMAL13P4	
902	49.8	2.1	1162	3	AF044851	
903	49.8	2.1	1260	1	AF086618	
C 904	49.8	2.1	1809	1	AF267216	
905	49.8	2.1	14851	2	PFMAL1P5	
C 906	49.8	2.1	61052	2	AC123513	
C 907	49.8	2.1	67970	3	PFMAL1P3	
C 908	49.8	2.1	68887	2	AC067755	
C 909	49.8	2.1	87731	9	AC105148	
C 910	49.8	2.1	88549	3	AC116924	
C 911	49.8	2.1	110000	2	PFMAL13_06	
912	49.8	2.1	110000	2	PFMAL13_21	
913	49.8	2.1	110000	2	PFMAL8P1_0	
914	49.8	2.1	116121	2	CR352337	
915	49.8	2.1	119483	5	BX470158	
C 916	49.8	2.1	124497	9	AC120053	
917	49.8	2.1	136240	3	AC117070	
C 918	49.8	2.1	136503	2	AC068939	
C 919	49.8	2.1	137457	9	AC067947	
C 920	49.8	2.1	144041	2	CR392045	
C 921	49.8	2.1	149223	2	CR382382	
922	49.8	2.1	150830	5	BX470190	
923	49.8	2.1	157088	5	AL935300	
C 924	49.8	2.1	157544	9	AC098590	
C 925	49.8	2.1	157613	9	AC018769	
926	49.8	2.1	159621	9	AC083801	
927	49.8	2.1	161233	2	BX927409	
928	49.8	2.1	163443	2	AC006280	
929	49.8	2.1	165326	9	AL159974	
C 930	49.8	2.1	166904	9	AL627309	
931	49.8	2.1	169448	2	CR385039	
932	49.8	2.1	170102	9	AC008079	
933	49.8	2.1	172476	9	AC007736	
934	49.8	2.1	179066	2	CR450782	
935	49.8	2.1	180861	2	CR391970	
936	49.8	2.1	181880	9	BS000198	
C 937	49.8	2.1	182871	3	AC117176	
C 938	49.8	2.1	187466	2	CR388371	
939	49.8	2.1	188248	2	AC119128	
940	49.8	2.1	200260	2	CR753814	
941	49.8	2.1	209215	2	CR751543	
942	49.8	2.1	218311	2	CR749741	
943	49.8	2.1	226450	2	CR522882	
944	49.8	2.1	226957	2	BX572639	
945	49.8	2.1	245802	2	AC006279	
C 946	49.8	2.1	252394	3	AE014833	
C 947	49.8	2.1	252650	3	AE014847	
948	49.8	2.1	253151	3	AE014842	
C 949	49.8	2.1	260929	3	AE014852	
950	49.8	2.1	263169	2	BX927111	
951	49.8	2.1	266371	2	AC020619	
952	49.8	2.1	286208	2	AC117140	
C 953	49.8	2.1	288385	2	AC092430	
954	49.8	2.1	318221	2	PFMAL13P3	
955	49.6	2.1	7137	9	HUMAGPRO	
C 956	49.6	2.1	9043	1	AF263924	
C 957	49.6	2.1	14867	3	AE001398	
C 958	49.6	2.1	16022	3	AF260826	
C 959	49.6	2.1	23564	8	AE016821	
960	49.6	2.1	34119	8	AF222718	
C 961	49.6	2.1	47108	6	AX344507	
C 962	49.6	2.1	68444	9	AL731768	
C 963	49.6	2.1	70788	2	AL353144	
C 964	49.6	2.1	73345	8	ALO294725	
C 965	49.6	2.1	82139	3	AC115684	
C 966	49.6	2.1	103728	9	AL445219	
967	49.6	2.1	104992	2	AC005504	
C 968	49.6	2.1	110000	2	PFMAL13_05	

969	49.6	2.1	113201	9	AC117509	AC117509 Homo sapi
c 970	49.6	2.1	138504	9	AC092665	Homo sapi
971	49.6	2.1	144361	2	CR318608	Danio rer
972	49.6	2.1	144644	8	AP006155	Oryza sat
973	49.6	2.1	144734	2	AC148922	Dasyypus n
c 974	49.6	2.1	146478	2	AC032036	Homo sapi
c 975	49.6	2.1	148782	9	AP006213	Homo sapi
976	49.6	2.1	150317	8	AP005739	Oryza sat
c 977	49.6	2.1	161078	9	AP003500	Homo sapi
978	49.6	2.1	161286	2	AC025120	Homo sapi
c 979	49.6	2.1	167103	9	AC147065	Pan trogl
c 980	49.6	2.1	169524	2	AC023111	Homo sapi
981	49.6	2.1	169546	2	AC004157	Plasmodiu
982	49.6	2.1	169894	2	CR762466	Danio rer
983	49.6	2.1	170627	2	AC125567	Rattus no
c 984	49.6	2.1	172285	2	CR381538	Danio rer
985	49.6	2.1	176063	9	AC022911	Homo sapi
986	49.6	2.1	178273	2	AC005308	Plasmodiu
987	49.6	2.1	183648	3	AC117081	Dictyoste
c 988	49.6	2.1	187466	9	AC016322	Homo sapi
c 989	49.6	2.1	188406	2	CR381547	Danio rer
990	49.6	2.1	191528	9	AC104260	Homo sapi
991	49.6	2.1	205242	9	AC146375	Pan trogl
992	49.6	2.1	205479	2	CR847506	Danio rer
993	49.6	2.1	206784	9	HS93L7	Human DNA
c 994	49.6	2.1	215231	2	CR385085	Danio rer
995	49.6	2.1	234796	2	CR318626	Danio rer
996	49.6	2.1	250029	3	AE014816	Plasmodiu
c 997	49.6	2.1	250421	3	AE014849	Plasmodiu
998	49.6	2.1	251237	2	CR812792	Danio rer
c 999	49.4	2.1	1055	6	AX083745	Sequence
1000	49.4	2.1	1072	5	AF332869	Anas plat
1001	49.4	2.1	1183	4	RABAGGRECA	Oryctolagus
1002	49.4	2.1	1314	3	AF489476	Schletter
1003	49.4	2.1	1618	5	AY029553	Anas plat
c1004	49.4	2.1	2872	3	DDIUBIRPB	Slime mold
c1005	49.4	2.1	4362	3	U60170	Dictyosteli
c1006	49.4	2.1	7347	1	AF211124	Carsonell
c1007	49.4	2.1	8305	6	AX346471	Sequence
c1008	49.4	2.1	11929	2	AE001431	Plasmodiu
1009	49.4	2.1	12600	2	AC013952	Drosophil
c1010	49.4	2.1	15959	3	AE001390	Plasmodiu
1011	49.4	2.1	30630	3	AC116032	Dictyoste
1012	49.4	2.1	47841	6	AX504842	Sequence
c1013	49.4	2.1	73334	6	AX347027	Sequence
c1014	49.4	2.1	73334	6	AX356494	Sequence
1015	49.4	2.1	82139	3	AC115684	Dictyoste
c1016	49.4	2.1	91875	9	AL512286	Human DNA
1017	49.4	2.1	110000	2	PFMAL13_14	Continuation (15 o
c1018	49.4	2.1	110000	2	PFMAL13P2_1	Continuation (2 of
c1019	49.4	2.1	110000	2	PFMAL8P1_01	Continuation (2 of
c1020	49.4	2.1	110000	3	PFMAL1P2_0	Continuation (15 o
1021	49.4	2.1	140677	9	AC005922	Homo sapi
c1022	49.4	2.1	146610	2	CR387981	Danio rer
1023	49.4	2.1	144765	2	CR759966	Danio rer
1024	49.4	2.1	144784	9	AC009224	Homo sapi
1025	49.4	2.1	149603	9	AC022100	Homo sapi
c1026	49.4	2.1	150656	5	BX649530	Zebrafish
1027	49.4	2.1	155106	9	AC104069	Homo sapi
c1028	49.4	2.1	155711	3	VYIVD10	Plasmodiu
1029	49.4	2.1	158548	3	PFMAL3P2	Plasmodiu
c1030	49.4	2.1	160896	9	AC025540	Homo sapi
1031	49.4	2.1	163448	2	CR846088	Danio rer
1032	49.4	2.1	163809	2	CR392044	Danio rer
1033	49.4	2.1	172738	9	AC091953	Homo sapi
1034	49.4	2.1	174162	2	CR759781	Danio rer
1035	49.4	2.1	174412	2	CR381542	Danio rer
1036	49.4	2.1	174482	2	AC139870	Rattus no
c1037	49.4	2.1	180096	2	CR391999	Danio rer
c1038	49.4	2.1	180124	2	CR450699	Danio rer
1039	49.4	2.1	180540	2	CR847859	Danio rer
1040	49.4	2.1	182871	3	AC117176	Dictyoste
1041	49.4	2.1	191191	2	CR847965	Danio rer

1042	49.4	2.1	202533	2	CR392031	Danio rer
1043	49.4	2.1	202634	2	CR339052	Danio rer
1044	49.4	2.1	203958	5	AL954339	Zebrafish
1045	49.4	2.1	216185	5	BX842696	Zebrafish
1046	49.4	2.1	220888	2	CR450804	Danio rer
c1047	49.4	2.1	227073	2	CR846086	Danio rer
1048	49.4	2.1	229435	2	CR457452	Danio rer
1049	49.4	2.1	261771	2	CR356223	Danio rer
c1050	49.2	2.1	663	6	A85532	Sequence 19
c1051	49.2	2.1	663	6	AR155025	Sequence
c1052	49.2	2.1	663	6	E65550	Genome DNA
1053	49.2	2.1	669	3	AF504324	Andrena b
1054	49.2	2.1	732	6	A86377	Sequence 10
1055	49.2	2.1	732	6	AR155870	Sequence
1056	49.2	2.1	732	6	E66395	Genome DNA
c1057	49.2	2.1	854	6	A85875	Sequence 53
c1058	49.2	2.1	854	6	AR155368	Sequence
c1059	49.2	2.1	854	6	E65893	Genome DNA
c1060	49.2	2.1	1098	3	OFU560796	Sequence
c1061	49.2	2.1	1098	3	OFU560797	Ostrinia
c1062	49.2	2.1	1099	3	OFU560800	Ostrinia
1063	49.2	2.1	2418	3	DDRASGG	D.discoidu
1064	49.2	2.1	7038	3	PFGP195A	Plasmodium
1065	49.2	2.1	7347	1	AF211124	Carsonell
c1066	49.2	2.1	7461	6	AX346686	Sequence
1067	49.2	2.1	14374	3	AC024748	Caenorhab
c1068	49.2	2.1	21354	6	AX251544	Sequence
c1069	49.2	2.1	37957	8	U17009	Phytophthor
1070	49.2	2.1	62028	9	AC010371	Homo sapi
c1071	49.2	2.1	81035	8	AB025631	Arabidops
c1072	49.2	2.1	90373	3	AC115680	Dictyoste
1073	49.2	2.1	93122	8	AC006283	Arabidops
1074	49.2	2.1	101800	9	AC021659	Homo sapi
c1075	49.2	2.1	101970	2	CR383670	Danio rer
1076	49.2	2.1	103244	3	AC090524	Caenorhab
1077	49.2	2.1	110000	2	BX324168_1	Continuation (2 of
c1078	49.2	2.1	110000	2	PFMAL13_10	Continuation (11 o
1079	49.2	2.1	110000	2	PFMAL13_19	Continuation (20 o
c1080	49.2	2.1	110000	2	PFMAL8P1_09	Continuation (10 o
c1081	49.2	2.1	111037	2	AC090067	Homo sapi
1082	49.2	2.1	111728	5	BX470096	Zebrafish
c1083	49.2	2.1	127392	9	AC008570	Homo sapi
c1084	49.2	2.1	138964	2	BX950176	Danio rer
1085	49.2	2.1	145160	2	CR847935	Danio rer
c1086	49.2	2.1	145299	5	BX005348	Zebrafish
1087	49.2	2.1	148061	9	AC010727	Homo sapi
1088	49.2	2.1	148929	2	CR847848	Danio rer
c1089	49.2	2.1	149238	2	CR847833	Danio rer
1090	49.2	2.1	149450	2	AC067880	Homo sapi
c1091	49.2	2.1	153300	9	AC073387	Homo sapi
c1092	49.2	2.1	154792	2	BX511299	Danio rer
c1093	49.2	2.1	155443	9	AC106740	Homo sapi
1094	49.2	2.1	159618	9	AC096750	Homo sapi
c1095	49.2	2.1	160621	5	BX005014	Zebrafish
1096	49.2	2.1	163288	2	CR812925	Danio rer
c1097	49.2	2.1	163957	9	AC104786	Homo sapi
c1098	49.2	2.1	164819	9	AC092335	Homo sapi
1099	49.2	2.1	169122	9	AC106803	Homo sapi
c1100	49.2	2.1	170736	2	AC013658	Homo sapi
1101	49.2	2.1	175946	9	AC141000	Homo sapi
1102	49.2	2.1	179380	9	AL354803	Human DNA
1103	49.2	2.1	179400	9	AC087481	Homo sapi
1104	49.2	2.1	186979	2	CR631129	Danio rer
c1105	49.2	2.1	187647	2	AC073220	Homo sapi
1106	49.2	2.1	193806	2	AC148824	Pan trogl
1107	49.2	2.1	204609	2	BX322531	Danio rer
c1108	49.2	2.1	204652	2	PFMAL13P6	Plasmodiu
1109	49.2	2.1	206513	5	AL928728	Zebrafish
1110	49.2	2.1	206832	2	CR759927	Danio rer
c1111	49.2	2.1	229081	2	CR753897	Danio rer
c1112	49.2	2.1	229237	5	BX323548	Zebrafish
1113	49.2	2.1	238266	2	CR392026	Danio rer
1114	49.2	2.1	246007	2	BX914205	Danio rer

CR392031	Danio rer
CR339052	Danio rer
AL954339	Zebrafish
BX842696	Zebrafish
CR450804	Danio rer
CR846086	Danio rer
CR457452	Danio rer
CR356223	Danio rer
A85532	Sequence 19
AR155025	Sequence
E65550	Genome DNA
AF504324	Andrena b
A86377	Sequence 10
AR155870	Sequence
E66395	Genome DNA
A85875	Sequence 53
AR155368	Sequence
E65893	Genome DNA
AJ560796	Ostrinia
AJ560797	Ostrinia
AJ560800	Ostrinia
Z11533	D.discoidu
X15063	Plasmodium
AF211124	Carsonell
AX346686	Sequence
AC024748	Caenorhab
AX251544	Sequence
U17009	Phytophthor
AC010371	Homo sapi
AB025631	Arabidops
AC115680	Dictyoste
AC006283	Arabidops
AC021659	Homo sapi
CR383670	Danio rer
AC090524	Caenorhab
Continuation (2 of	
Continuation (11 o	
Continuation (20 o	
Continuation (10 o	
AC090067	Homo sapi
BX470096	Zebrafish
AC008570	Homo sapi
BX950176	Danio rer
CR847935	Danio rer
BX005348	Zebrafish
AC010727	Homo sapi
CR847848	Danio rer
CR847833	Danio rer
AC067880	Homo sapi
AC073387	Homo sapi
BX511299	Danio rer
AC106740	Homo sapi
AC096750	Homo sapi
BX005014	Zebrafish
CR812925	Danio rer
AC104786	Homo sapi
AC092335	Homo sapi
AC106803	Homo sapi
AC013658	Homo sapi
AC141000	Homo sapi
AL354803	Human DNA
AC087481	Homo sapi
CR631129	Danio rer
AC073220	Homo sapi
AC148824	Pan trogl
BX322531	Danio rer
PFMAL13P6	Plasmodiu
AL928728	Zebrafish
CR759927	Danio rer
CR753897	Danio rer
BX323548	Zebrafish
CR392026	Danio rer
BX914205	Danio rer

c1115	49.2	2.1	281723	3	PFA929359	AL929359 Plasmodiu	1188	49	2.1	212889	2	CR392341	CR392341	Danio rer
c1116	49.2	2.1	302250	6	AX335531	AX335531 Sequence	1189	49	2.1	213056	9	AC103590	AC103590	Homo sapi
c1117	49.2	2.1	324604	9	U82671	U82671 Homo sapien	c1190	49	2.1	214035	2	AC148503	AC148503	Callithri
1118	49.2	2.1	341303	2	AC129003	AC129003 Rattus no	1191	49	2.1	215480	2	AC135781	AC135781	Homo sapi
1119	49	2.1	1165	3	AF044856	AF044856 Colias er	c1192	49	2.1	227211	2	CR847561	CR847561	Danio rer
c1120	49	2.1	5371	8	YSCMTTGS	J01462 Yeast (S.ce	1193	49	2.1	228968	2	AC107571	AC107571	Rattus no
c1121	49	2.1	5430	6	AX251046	AX251046 Sequence	1194	49	2.1	234009	2	CR383672	CR383672	Danio rer
1122	49	2.1	6106	6	AX251183	AX251183 Sequence	c1195	49	2.1	241486	2	AC130137	AC130137	Rattus no
1123	49	2.1	6106	6	AX346374	AX346374 Sequence	c1196	49	2.1	250029	3	AE014820	AE014820	Plasmodiu
1124	49	2.1	6106	6	AX348418	AX348418 Sequence	c1197	49	2.1	257109	3	AC116963	AC116963	Dictyoste
c1125	49	2.1	14422	3	AF466146	AF466146 Melipona	c1198	49	2.1	313050	3	PFA929352	AL929352	Plasmodiu
1126	49	2.1	15767	6	AX281442	AX281442 Sequence	c1199	49	2.1	340552	3	PFA929354	AL929354	Plasmodiu
1127	49	2.1	15767	6	AX346109	AX346109 Sequence	1200	49	2.1	341153	2	BX914212	BX914212	Danio rer
1128	49	2.1	15894	3	AY383557	AY383557 Cherax de	c1201	48.8	2.1	713	3	AMU35788	U35788	Anopheles m
1129	49	2.1	48306	9	AL590675	AL590675 Human DNA	c1202	48.8	2.1	860	6	A85628	A85628	Sequence 28
c1130	49	2.1	59847	9	AL136112	AL136112 Human DNA	c1203	48.8	2.1	860	6	AR155121	AR155121	Sequence
1131	49	2.1	61052	2	AC123513	AC123513 Dictyoste	c1204	48.8	2.1	860	6	E65646	E65646	Genome DNA
c1132	49	2.1	68054	9	AL592300	AL592300 Human DNA	c1205	48.8	2.1	1095	3	OFU560798	AJ560798	Ostrinia
c1133	49	2.1	70204	9	AC010737	AC010737 Homo sapi	c1206	48.8	2.1	1096	3	OFU560799	AJ560799	Ostrinia
1134	49	2.1	88549	3	AC116924	AC116924 Dictyoste	1207	48.8	2.1	2426	8	SDU49822	U49822	Saccharomyc
c1135	49	2.1	89086	9	AC104373	AC104373 Homo sapi	1208	48.8	2.1	4617	3	SFAJ5398	AJ005398	Dictyoste
c1136	49	2.1	105574	2	AC013308	AC013308 Homo sapi	c1209	48.8	2.1	9810	6	AX345328	AX345328	Sequence
1137	49	2.1	108908	3	PFMAL3P8	AL034560 Plasmodiu	c1210	48.8	2.1	12025	6	AX346201	AX346201	Sequence
1138	49	2.1	110000	2	AL928982_2	Continuation (3 of	1211	48.8	2.1	12029	3	AE001395	AE001395	Plasmodiu
c1139	49	2.1	110000	2	PFMAL13_15	Continuation (16 o	c1212	48.8	2.1	13202	6	AX346387	AX346387	Sequence
c1140	49	2.1	110000	2	PFMAL13_16	Continuation (17 o	1213	48.8	2.1	13712	6	AX346432	AX346432	Sequence
1141	49	2.1	110000	2	PFMAL13_24	Continuation (25 o	c1214	48.8	2.1	32392	6	AX392737	AX392737	Sequence
1142	49	2.1	110000	2	PFMAL7PI_01	Continuation (2 of	c1215	48.8	2.1	65970	9	AP000282	AP000282	Homo sapi
c1143	49	2.1	110000	2	PFMAL8PI_07	Continuation (8 of	c1216	48.8	2.1	85916	3	AC117080	AC117080	Dictyoste
1144	49	2.1	110000	3	PFMAL1P2_0	AL031745 Plasmodiu	1217	48.8	2.1	88932	2	AC022680	AC022680	Homo sapi
c1145	49	2.1	110000	9	AF438327_0	AF438327 Homo sapi	1218	48.8	2.1	90550	9	AL592166	AL592166	Human DNA
c1146	49	2.1	114252	5	BX649441_0	BX649441 Zebrafish	c1219	48.8	2.1	97211	5	CR556710	CR556710	Zebrafish
c1147	49	2.1	114276	9	AC011355	AC011355 Homo sapi	c1220	48.8	2.1	99241	8	AC069160	AC069160	Arabidops
c1148	49	2.1	124615	2	AC124956	AC124956 Medicago	c1221	48.8	2.1	100000	9	AP000040	AP000040	Homo sapi
1149	49	2.1	136176	5	AL929119	AL929119 Zebrafish	c1222	48.8	2.1	100000	9	AP000108	AP000108	Homo sapi
c1150	49	2.1	136240	3	AC117070	AC117070 Dictyoste	c1223	48.8	2.1	100000	9	AP000184	AP000184	Homo sapi
c1151	49	2.1	136723	9	AC074000	AC074000 Homo sapi	c1224	48.8	2.1	110000	2	CR753903_0	CR753903	Danio rer
1152	49	2.1	144658	9	AL138969	AL138969 Human DNA	c1225	48.8	2.1	110000	2	PFMAL13_26	Continuation (27 o	
1153	49	2.1	145135	9	AC007094	AC007094 Homo sapi	c1226	48.8	2.1	110000	2	PFMAL7PI_02	Continuation (3 of	
c1154	49	2.1	145992	9	AC134919	AC134919 Homo sapi	c1227	48.8	2.1	110000	2	PFMAL7PI_03	Continuation (4 of	
1155	49	2.1	146928	2	AC135775	AC135775 Homo sapi	1228	48.8	2.1	110000	3	AC116957_0	AC116957 Dictyoste	
c1156	49	2.1	147728	10	AC116774	AC116774 Mus muscu	1229	48.8	2.1	122620	2	CR382299	CR382299	Danio rer
1157	49	2.1	151941	9	AC108131	AC108131 Homo sapi	c1230	48.8	2.1	132254	3	AC116330	AC116330	Dictyoste
c1158	49	2.1	152686	2	CR762419	CR762419 Danio rer	1231	48.8	2.1	139409	9	AC069181	AC069181	Homo sapi
1159	49	2.1	156351	9	AC092133	AC092133 Homo sapi	c1232	48.8	2.1	148435	9	AC073973	AC073973	Homo sapi
1160	49	2.1	161398	9	AC092804	AC092804 Homo sapi	1233	48.8	2.1	152103	2	AC012130	AC012130	Homo sapi
c1161	49	2.1	162195	2	BX957331	BX957331 Danio rer	1234	48.8	2.1	158699	9	AP006183	AP006183	Homo sapi
1162	49	2.1	162377	9	AL683870	AL683870 Human DNA	1235	48.8	2.1	160138	9	AC008551	AC008551	Homo sapi
c1163	49	2.1	163448	2	CR846088	CR846088 Danio rer	1236	48.8	2.1	162554	2	CR626901	CR626901	Danio rer
1164	49	2.1	163597	9	AC098870	AC098870 Homo sapi	c1237	48.8	2.1	163595	2	AC022076	AC022076	Homo sapi
c1165	49	2.1	164278	2	AC073126	AC073126 Homo sapi	c1238	48.8	2.1	168069	2	CR812470	CR812470	Danio rer
c1166	49	2.1	164564	2	CR847897	CR847897 Danio rer	1239	48.8	2.1	173882	9	HSFAF001550	AF001550	Homo sapi
c1167	49	2.1	166695	5	BX005440	BX005440 Zebrafish	c1240	48.8	2.1	176077	5	BX530089	BX530089	Zebrafish
c1168	49	2.1	168438	2	AC024632	AC024632 Homo sapi	1241	48.8	2.1	176291	9	AC024610	AC024610	Homo sapi
1169	49	2.1	168546	9	AC135776	AC135776 Homo sapi	c1242	48.8	2.1	177560	2	CR318627	CR318627	Danio rer
c1170	49	2.1	169539	2	AC080095	AC080095 Homo sapi	1243	48.8	2.1	177867	2	BX936329	BX936329	Danio rer
c1171	49	2.1	170668	9	AC104012	AC104012 Homo sapi	c1244	48.8	2.1	178670	9	AC104073	AC104073	Homo sapi
c1172	49	2.1	173927	2	CR812798	CR812798 Danio rer	1245	48.8	2.1	178686	2	AC151308	AC151308	Xenopus t
c1173	49	2.1	174001	2	BX927081	BX927081 Danio rer	c1246	48.8	2.1	180465	9	AC074011	AC074011	Homo sapi
c1174	49	2.1	177045	2	BX957238	BX957238 Danio rer	1247	48.8	2.1	182614	5	AL928830	AL928830	Zebrafish
c1175	49	2.1	178457	5	AL935031	AL935031 Zebrafish	1248	48.8	2.1	184257	5	AL929013	AL929013	Zebrafish
c1176	49	2.1	181430	2	CR407555	CR407555 Danio rer	1249	48.8	2.1	189598	2	BX957347	BX957347	Danio rer
1177	49	2.1	184927	2	AL683875	AL683875 Homo sapi	1250	48.8	2.1	190612	10	AC118212	AC118212	Mus muscu
1178	49	2.1	186972	9	AC137794	AC137794 Homo sapi	c1251	48.8	2.1	192337	2	CR762383	CR762383	Danio rer
c1179	49	2.1	187174	9	AC109484	AC109484 Homo sapi								

c1261	48.8	2.1	211429	2	BX324152	BX324152	Danio rer	c1334	48.6	2.0	221637	2	AC097553	AC097553	Rattus no
1262	48.8	2.1	226160	5	BX004838	BX004838	Zebrafish	c1335	48.6	2.0	239335	2	AC146635	AC146635	Otolemur
c1263	48.8	2.1	232392	14	AF250284	AF250284	Amsacta m	c1336	48.6	2.0	250707	3	AE014848	AE014848	Plasmodiu
1264	48.8	2.1	239484	2	CR759895	CR759895	Danio rer	c1337	48.6	2.0	282355	2	AC104401	AC104401	Rattus no
1265	48.8	2.1	241111	2	CR385051	CR385051	Danio rer	1338	48.6	2.0	300050	1	AP004171	AP004171	Mycoplasma
c1266	48.8	2.1	246651	2	CR847857	CR847857	Danio rer	c1339	48.6	2.0	340000	9	AP001667	AP001667	Homo sapi
c1267	48.8	2.1	250022	3	AE014824	AE014824	Plasmodiu	1340	48.6	2.0	349980	6	AX344555	AX344555	Sequence
c1268	48.8	2.1	251237	2	CR812792	CR812792	Danio rer	c1341	48.4	2.0	716	3	AMU35786	U35786	Anopheles m
1269	48.8	2.1	253305	3	PFMAL3P7	AL034559	Plasmodiu	c1342	48.4	2.0	1154	3	AF044864	AF044864	Pieris ra
c1270	48.8	2.1	253755	2	CR812465	CR812465	Danio rer	c1343	48.4	2.0	1442	8	MTSDATP9A	Z25399	S.douglasii
c1271	48.8	2.1	254449	3	AE014817	AE014817	Plasmodiu	c1344	48.4	2.0	1815	1	AF267201	AF267201	Candidatu
c1272	48.8	2.1	256879	3	AC116982	AC116982	Dictyoste	1345	48.4	2.0	5500	3	PFAMDF	M29154	P.falciparu
c1273	48.8	2.1	263615	5	BX927240	BX927240	Zebrafish	c1346	48.4	2.0	6775	6	AX458644	AX458644	Sequence
c1274	48.8	2.1	272698	3	PFMAL4P4	AL035477	Plasmodiu	c1347	48.4	2.0	8574	3	AF057019	AF057019	Dictyoste
1275	48.8	2.1	273275	3	AE014828	AE014828	Plasmodiu	c1348	48.4	2.0	8633	3	PFPFMDR1	X56851	P.falciparu
c1276	48.8	2.1	340000	9	AP001715	AP001715	Homo sapi	c1349	48.4	2.0	14535	3	AF442957	AF442957	Ostrinia
c1277	48.6	2.0	718	3	AQU35792	U35792	Anopheles q	c1350	48.4	2.0	14536	3	AF467260	AF467260	Ostrinia
1278	48.6	2.0	1717	3	DDISP70B	M98546	Dictyosteli	1351	48.4	2.0	20816	3	AY325300	AY325300	Parameciu
c1279	48.6	2.0	1865	8	MISCAAP1	X00960	Yeast mitoc	c1352	48.4	2.0	26561	9	AL929515	AL929515	Human DNA
1280	48.6	2.0	1958	8	RCH296505	AJ296505	Reyemia c	c1353	48.4	2.0	29143	3	AC115594	AC115594	Dictyoste
1281	48.6	2.0	4197	3	AF163835	AF163835	Dictyoste	c1354	48.4	2.0	30849	3	AC117082	AC117082	Dictyoste
1282	48.6	2.0	6154	6	AX251808	AX251808	Sequence	c1355	48.4	2.0	55372	2	CR759965	CR759965	Danio rer
1283	48.6	2.0	6154	6	AX344196	AX344196	Sequence	1356	48.4	2.0	73666	9	HSJ333B15	AL109954	Human DNA
1284	48.6	2.0	6154	6	AX348599	AX348599	Sequence	1357	48.4	2.0	102306	5	BX571980	BX571980	Zebrafish
c1285	48.6	2.0	11172	6	AX346955	AX346955	Sequence	c1358	48.4	2.0	104153	2	BX890590_3	Continuation (4 of	
1286	48.6	2.0	14591	3	AE001406	AE001406	Plasmodiu	c1359	48.4	2.0	105940	9	AC010606	AC010606	Homo sapi
1287	48.6	2.0	15575	3	AY242996	AY242996	Plasmodiu	c1360	48.4	2.0	107635	8	AC136955	Medicago	
c1288	48.6	2.0	15723	3	AY521251	AY521251	Aleurodic	c1361	48.4	2.0	108908	3	PFMAL3P8	AL034560	Plasmodiu
1289	48.6	2.0	17137	6	AX345093	AX345093	Sequence	c1362	48.4	2.0	110000	2	PFMAL13_14	Continuation (15 o	
c1290	48.6	2.0	24565	9	AL162498	AL162498	Human DNA	1363	48.4	2.0	110000	2	PFMAL7P1_06	Continuation (7 of	
c1291	48.6	2.0	34750	3	AY217738	AY217738	Eimeria t	c1364	48.4	2.0	110000	3	AC116984_4	Continuation (5 of	
1292	48.6	2.0	36849	1	AE000788	AE000788	Borrelia	1365	48.4	2.0	110000	6	AR409405_3	Continuation (4 of	
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
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JIAN ZHENG,
PI JEAN YUAN
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FEATURES
source

ORIGIN

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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 2372)				
TITLE	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.				
	Secreted and transmembrane polypeptides and nucleic acids encoding the same				

JOURNAL Patent: JP 2002238587-A 165 27-AUG-2002;
 GENENTECH INC
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 PN JP 2002238587-A/165
 PD 27-AUG-2002
 PF 18-DEC-2001 JP 2001385248
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QY	2281	CAAAATGTATCACTAGCCCTCCTTTTCCCAACAAGAGGGACTGAGAGATGCAGAAAATATT	2340
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RESULT 4
BD173349
LOCUS

BD173349 2372 bp DNA linear PAT 18-FEB-2003

DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173349		
VERSION	BD173349.1 GI:28414660		
KEYWORDS	JP 2002238588-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2372) Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238588-A 165 27-AUG-2002; GENENTECH INC		
COMMENT	OS Homo sapiens (human) PN JP 2002238588-A/165 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385315 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/435,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19), PC (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers FT source 1..2372 FT /organism='Homo sapiens (human)'. FEATURES source Location/Qualifiers 1..2372 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAGTGGC 120
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Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTTCAGCCGTG 180
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Db 421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCAAACCCCAAGTGTGGG 480
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BD175383			
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DEFINITION	Secretory and transmembrane polypeptide and nucleic acid encoding the same.		
ACCESSION	BD175383		
VERSION	BD175383.1	GI:29121079	
KEYWORDS	JP 2002253280-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	(bases 1 to 2372)	
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same		
JOURNAL	Patent: JP 2002253280-A 165 10-SEP-2002; GENENTECH INC		
COMMENT	OS Homo sapiens (human) PN JP 2002253280-A/165 PD 10-SEP-2002 PF 18-DEC-2001 JP 2001385319 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC A61P25/00, PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18, PC C07K19/00, PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395, PC A61P43/00, PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10, PC C12R1:91), PC C12N15/00,A61K37/02,(C12N5/00,C12R1:91) CC Secretory and transmembrane polypeptide and nucleic acid encoding the same FH Key Location/Qualifiers		

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Db 1981 TTTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTC 2040
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RESULT 6
AR410761
LOCUS AR410761 2372 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Ashkenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..2372
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
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Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACCATGGCCAGGTGCTTCAGCCTG 180
Qy 181 GTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
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Db	1321		

Db	1321	CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT	1380
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Db	2341		

AR439125 LOCUS AR439125 2372 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 200 from patent US 6664376.
ACCESSION AR439125
VERSION AR439125.1 GI:42664974
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2372)
Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6664376-A 200 16-DEC-2003;
FEATURES Location/Qualifiers
source 1..2372
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
RESULT 9
AR527131
LOCUS AR527131 2372 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 200 from patent US 6723535.
ACCESSION AR527131
VERSION AR527131.1 GI:53914048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6723535-A 200 20-APR-2004;
FEATURES Location/Qualifiers
source 1..2372
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGGAAATCCGGATGTCCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Db 1 AGCAGGGAAATCCGGATGTCCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
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Db	1201	ATCAAAAGGSCCAAAGAACCAAAGAAAGATCCACCTTGGTTCTTAACCTGGAATCAGC	1260
Qy	1261	TCAGGACTGCCATTGGACTATGGAGTGCACAAAGAGAAATGCCCTTCTCCTTATTGTAAC	1320
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 VERSION AR566164.1 GI:53983074
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 ORGANISM Unknown.
 REFERENCE Unclassified.
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 AUTHORS Desnoyers, L., Goddard, A., Godowski, P. J., Gurney, A. L. and Wood, W. I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: US 6767995-A 200 27-JUL-2004;
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Db	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGSCCAGGTGCTTCAGCCTG	180						
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Qy	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	300						
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Qy	301	GCGAACCAAGCAGCTGAATTTCACAGAACTAAGGAGGCTGTAGGCTGTGGACTAAGT	360						
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AX454446

LOCUS AX454446 2372 bp DNA linear PAT 06-JUL-2002

DEFINITION Sequence 31 from Patent WO0208284.

ACCESSION AX454446

VERSION AX454446.1 GI:21713847

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

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Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

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LOCUS	AX490924	2372 bp	DNA linear PAT 16-AUG-2002
DEFINITION	Sequence 31 from Patent WO0200690.		
ACCESSION	AX490924		
VERSION	AX490924.1 GI:22323799		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
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AUTHORS	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,		
	Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,		
TITLE	Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.		
	and Ye,W.		
	Compositions and methods for the diagnosis and treatment of		
JOURNAL	disorders involving angiogenesis		
	Patent: WO 0200690-A 31 03-JAN-2002;		
	Genentech, Inc. (US)		
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Best Local Similarity		100.0%;	Pred. No. 0;				
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Qy	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120				
Db	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC	120				
Qy	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG	180				
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Qy	181	GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240				
Db	181	GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240				
Qy	241	GAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAG	300				
Db	241	GAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAG	300				
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Qy	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420				
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Qy	481	AAAAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGAGCCTAT	540				
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Db	841	AATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC	900				
Qy	901	TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT	960				
Db	901	TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT	960				
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Db	961	TTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAGTAGTAAAGGAGAG	1020				
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Qy	1381	GTCTTAATAATATCCCACCTGGAGAAAAGGAGTTTGTCAAAGTGCAAAGGACCTAAAAATC	1440	
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DEFINITION	Sequence 200 from Patent WO0104311.		
ACCESSION	AX697609		
VERSION	AX697609.1 GI:29498705		
KEYWORDS			
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ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1		
AUTHORS	Ashkenazi, A.J., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,		
	Filvaroff, E., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,		
	Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J.,		
TITLE	Kljasin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,		
	Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.		
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	Genentech Inc. (US)		
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Db	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC	1320
QY	1321	CCTGTCTGGATCCTATCCTACCTCCAAGCTTCCCACGGCCTTCTAGCCTGGCTAT	1380
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Db	1681	TCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA	1740
Qy	1741	GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT	1800
Db	1741	GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT	1800
Qy	1801	CACGTCTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Db	1801	CACGTCTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Qy	1861	AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
Db	1861	AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
Qy	1921	GAGTTACAGAAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	1980
Db	1921	GAGTTACAGAAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	1980
Qy	1981	TTCAACAAACATTTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC	2040
Db	1981	TTCAACAAACATTTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC	2040
Qy	2041	TGTAATTGAATATTATTCCTCAAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
Db	2041	TGTAATTGAATATTATTCCTCAAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT	2100
Qy	2101	TTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTGCTGA	2160
Db	2101	TTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTGCTGA	2160
Qy	2161	GACTAATCTTATTCATTTTTCTTAATATGGCAACCATTATATAACCTTAATTTATTATAAC	2220
Db	2161	GACTAATCTTATTCATTTTTCTTAATATGGCAACCATTATATAACCTTAATTTATTATAAC	2220
Qy	2221	ATACCTAAGAAGTACATTGTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA	2280
Db	2221	ATACCTAAGAAGTACATTGTGTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA	2280
Qy	2281	CAAAATGTATCACTAGCCCTCCTTTTTTCCAAACAAGAAGGACTGAGAGATGCAGAAAAATT	2340
Db	2281	CAAAATGTATCACTAGCCCTCCTTTTTTCCAAACAAGAAGGACTGAGAGATGCAGAAAAATT	2340

Oy 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372
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Db 2341 TGTGACAAAAAATTAAAGCATTTAGAAAACTT 2372

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